

1057

ACAGGTGGCG TTCTGACTGG TCGAGATGCC TTTGAACACA TCCTCTGTGG AGCAAGTATG 7260  
GTGCAGGTGG GAACGACCCT TCACAAAGAA GCGGTCAGTG CTTTGTACCG CATTACCAAT 7320  
GAACTGAAAG CAATCATGGT GGAAAAAGGC TACGAGAGCT TAGAAGATTT CCGTGGGAAA 7380  
TTGCGCTATA TTGACTAAAT TAAATCGAAA AATCTGAAGA AAGGAGAGAC GATGCTAGCC 7440  
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ACAGATCAGG GTCAGTTTGA AGTGATGAAG AGTCAAATGT TGAAACAGAT TGGGTATGAT 7560  
TCTGCTGACC TCAACTTTGC CTACTTTGAT ATGAAAGAAG TAGTTTACAA GGATGTGGAA 7620  
CTGGAGTTGG TCAGCCTTCC TTTCTTTGCG GATGAGAAAA TCGTGATATT AGATTATTTT 7680  
ATGGATATCA CGACTGCTAA GAAACGCTTT TTGACAGATG ATGAGCTTAA GTCATTTGAG 7740  
GAATACCTTG ACAATCCTTC TCCAACAACC AAGTTGATAA TCTTTGCAGA AGGAAAGCTG 7800  
GATAGCAAAA GACGGTTAGT CAAATTACTT AAGCGTGATG CCAAGGCCTT CGATGCAGTA 7860  
GAAGTAAAAG AACAAGAATT GCGCCAGTAC TTCCAAAAGT GGAGTCAGAA ACAAGGTCTG 7920  
CAGTTTACCA ATCATTCTTT TGAAAATCTC CTCATCAAGT CGGGGTTTCA ATTTAGCGAA 7980  
ATCCAGAAAA ATCTTCTCTT TTTACAGTCC TATAAGCCGA ATTCTGTTAT TGAGGAAGAG 8040  
GATATTGTTA ACGCAATTCC CAAGACTTGC AGGACAATAT TTTTGATTTA ACTCAGTTTA 8100  
TTCTGACTAA AAAGATGGAT CAGGCGCGCG ATTTGGTGAG AGACTTGACC TTGCAAGGGG 8160  
AAGATGAAAT CAAACTGATT GCAGTCATGC TGGGACAATT TCGGACTTTT ACTCAGGTGA 8220  
AGATTTTGGC GGAGTCTGGC CAAACAGAAT CGCAGATTGC AAGTAGTTTA GGTAGTTATC 8280  
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CAGGTCTTTA TGAAAAGGT TTCCTTTTGT AAAAGGCACT CTTACAGATT GCTAGTCAGG 8460  
TCAATTGACA TTTGTTGAAA CTACTAACCC GCGG 8494

## (2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CCGGTCAGTT CGTTCAGTAC AAGGAATCAT AATGAACGAT CAATCAGAAA AAAAGACTAG 60

1058

AAAGAAGACT GTATGGATAA TCGACCAATT GGTTTTTTGG ATTCTGGGTGT CGGGGGCTTG	120
ACCGTTGTGC GCGAGCTCAT GCGCCAGCTT CCCCATGAAG AAATCGTCTA TATTGGAGAT	180
TCGGCGCGGG CGCCCTATGG CCCCCGTCCT GCTGAGCAAA TTCGTGAATA TACTTGGCAG	240
CTGGTCAACT TTCTCTTGAC CAAGGATGTC AAAATGATTG TCATTGCTTG TAACACTGCC	300
ACTGCGGTCTG TCTGGGAAGA AATCAAGGCT CAACTAGATA TTCCTGTCTT GGGTGTAATT	360
TTGCCAGGAG CTTCGGCAGC CATCAAGTCC AGTCAAGGTG GGAAAATCGG AGTGATTGGA	420
ACGCCCCATGA CGGTACAATC AGACATATAC CGTCAGAAAA TCCATGATCT GGATCCCGAC	480
TTACAGGTGG AGAGCTTGGC CTGTCCCAAG TTTGCTCCCT TGGTTGAGTC AGGTGCCCTG	540
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GATAGCCTGA TTTTGGGCTG TACTCATTAT CCACTCCTTC GCCCTATTAT CCAAATGTG	660
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TTACTCAATT ATTTTGAAAT CAATCGTGGT CGCGATGCTG GACCACTCCA TCACCGTTTT	780
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ATTCATGTGG AGCATGTAGA ATTATGACAA ATAAAATTTA TGAATATAAG GATGACCAGG	900
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TTTCAGTTAC TGTTTTACGC TATGGTTCTA TCTACCGTTT GTTCTCCTTT GTGGTAGACA	1080
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TGGTTGAAAA TGGGCAACTC TTGTATGTAG AATTGCCTAA AGAAGGGGTC AATGTTTCATG	1200
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AAACCAAGGA ATTCCGAGCT ATCTTTGATA AGTTAGGCTA CGATGTGGAA AATCTTAATG	1320
ACTACCCTGA CCTGCCTGAA GTAGCAGAAA CAGGTATGAC CTTTGAAGAA AATGCCCGCC	1380
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TCAAAGTCGA TGTCTTGGT GGCTTACCAG GCGTCTGGTC AGCTCGTTTC GCAGGTGTGG	1500
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CCCTGGAAGA AAAAAATAGT CAATCTCACC GTGCCTTAGC CGTTAAGAAA CTTTGGAGG	1800
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1059

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CGATTCTGAA CTACGTCCGG ATTCTCCACT TTGGGAGGGC ATCCGCGTTG TTAAAGGGAA	1980
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TATCCAAACT CATGGTCACT TGTGTGACAT CAATTTCAAC TTTCAAAAGT TGGACTACTG	2100
GGCTCAGGAG GAAGAGGCCG CTATCTGCCT CTATGGTCAC TTGCATGTGC CAAGTGCTTG	2160
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CAGAGAATGT CTCTATGCTC GTGTGGAGAT TGATGATAGT TACTTCAAAG TGGACTTTTT	2280
GACACGAGAT CACGAGGTGT ATCCAGGTTT GTCCAAGGAG TTTAGCCGAT GATTGCCAAG	2340
GAGTTTGAGA CTTTCTTGTT GGGGCAGGAG GAAACTTTTT TGACCCCTGC TAAAAATCTA	2400
GCTGTGTTGA TTGATACCCA CAATGCGGAT CATGCGACCC TCTTGCTCAG TCAGATGACC	2460
TATACCCGTG TTCCCGTTGT GACAGATGAA AAACAGTTTG TTGGGACGAT TGGACTCAGA	2520
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ATCGTTCATA TGACAAAAAC GGACGTAGCG GTTGTTTCGC CTGATTTTAC CATTACGGAG	2640
GTCTTGACA AGCTAGTAGA TGAGTCCTTC TTACCGGTTG TGGATGCAGA GGGTATTTTC	2700
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AGCAGGGCTT GTCTGTCAAT TCCAAGCAGT CCTATAAGTA TGATTTGGAG CAATTTTATAG	2880
ACATGGTAGG TGAGCGGATT TCTGAGACCA GTCTCAAGAT TTACCAAGCC CAGCTAGCCA	2940
ATCTAAAAAT CAGCGCCCAG AAGCGAAAGA TTTCGGCCTG TAACCAATTT CTATACTTTC	3000
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CAGAGGGCCG CTTGCTAGCG CTCTTAATCC TAGAAATGGG GCTCTTGCCC AGTGAGATTT	3180
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CCCAACAGAG GATTGTCACC ATTCCCACGG CCTTGCTTTC AGAATTGGAA CCCTTGATGG	3300
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TTTGAAGGA CCCCTGGACT TGCTCTTGCA TCTGGTTTCT AAGTACCAGA TGGATATCTA	3600

1060

CGATGTGCCC ATTACGGAAG TCATCGAACA GTATCTAGCC TATGTCTCAA CCCTGCAGGC	3660
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GAGTCGTAAA CTCCTTCCGA AGGTAGCAGA AGTGACAGAC TTGGGGGATG ACCTGGAGCA	3780
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AGCCAAGCAC CAAGAACGGG CCCAGTATTA TTCCAAAGCG CCGACAGAGT TGATTTACGA	3900
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CTTGCAAGAT TTGTTCAAGG AAGCCCAGAA TGTCCAAGAG GTCATCACCC TCTTTTGGC	4140
AACCCTAGAG TTAATCAAAA CCCAGGAGTT GATCCTCGTG CAAGAGGAGA GTTTTGGAGA	4200
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CCAGTAGGAG AAAAGCAGAA GAGCTGATTA AGCAAGGCTT GGTGACGGTT AACGGCCAAG	4920
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GTATTTACCC TGTGGGTCGT TTGGACTGGG ATACATCAGG TGTCTTGATT TTGACCAATG	5160
ATGGGGACTT TACAGACGAG ATGATTCACC CTCGTAATGA GATTGACAAG GTTTATGTCG	5220
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ATCGCTCTGT GGTGCAGTTG ACCATCCATG AAGGGCGTAA CCATCAGGTT AAAAGATGT	5400



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TTGAAGCTGT TGGTCTCCAA GTAGATAAGT TGTCTCGGAC TCGTTTCGGA CACCTAGACT	5460
TGACAGGACT CCGTCCAGGA GAATCCCGTC GTCTTAATAA AAAAGAAATC AGCCAACTAC	5520
ACACCATGGC TGTAAC TAAG AAATAATGAA ACGAATTTTA ATAGCGCCTG TGCCTTTTA	5580
CCAACGTTTT ATCTCACCAG TCTTTCCACC CTCTGTGCGC TTTGAGCTGA CTTGTTCCAA	5640
CTACATGATT CAGGCTATTG AAAACATGG GTTTAAGGGG GTATTGATGG GCTTGGCTCG	5700
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CCTTAAACGA AATCAAGAAG GGGAAATGAGG TGGGGTAAAT AGATTTCAA ATGATAAAAA	5820
CGCATCCTAT CAGGTTTGAG TGAAC TTGAT AGGATGCGTT TTAGAATGTC AAAATTTTAT	5880
ACTCTTCGAA AATCTCTTCA AACCGCGTCA GCTTTCATCT GCAACCTCAA AACAGTGTTT	5940
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AAGTCCGCCT CCGCTTAGAT ACCAGAGGTC TGGTGTTAGT TGGATAATCT TACCATTTTT	6120
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TCCTTCATTA AGGAGGATCG CAAGGGCTTT TTTGTCAGAG CTTTCATTTT TAGTAGCGAC	6420
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GTTTGTACTA CATGCACCAA GTAGGAGCAA GAAGCTGGCC ACTAGGGCAG TGAAATAAAG	6960
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1062

CTGAGCAGGT CAGCCTGCAT GATTGATCG GTTCTTCCCT TGCTAAAGAC CTGGCCGTCC	7200
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AGTACCATAG CGATAAAGAC GCGCTGGAGT TGCCCCCCTG ACAGGCTATT GATGTAGCGG	7440
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AGCCTGCTCA TGATGGAGAG GAGAGTCGAT TTTCCAGCAC CATTTGGACC AATAAAGGCT	7740
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AGAAGCCACC CACACTCTCA ATGATCATACT TGATACGAAT TTCCAGTGCA AAGACTCGTT	7920
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GTAACCTGTG CTGATAGTCT TTGACAATCA GGTAGGTGAG GTTGGCCAGT ATAAAGCCGA	8040
AGAAGGCCAT AGGTCTACC AAGGCAGTGG CCGTTGAGGT CAAAAGCACG ATTCCCAGA	8100
GGAGCTCTTT CTGTTCTTTT TCAACATCGA GTCCCAATAT CTGAGCCGTT TCTCTTTGCA	8160
GGTGCAAGAC ATCTAGAACG ACTGCTTTTC GAAAGAAAAA GATTGTCAA GCGAGGATGA	8220
TCAGAGAACC GATGGCTAGG ATGGAAGTGT TGAGATGTTG AAAGGAGGCA AAAAGACTAT	8280
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GAAAGAGACT TCTGAGCGCT AGACAGATCA GCAGGACGAA GACCAGGTCT TGCTTCATCA	8400
GTGTCTTCAA GTAACCTTGT AAGGCGAGAA AGAAGAGGGA CTGGACAAGA AGTAAGACTA	8460
GGAATTCTAA GATAGGGGAT TTGCCAAGTT GAAGAACTT GCTTTCAAAA ACCAGTAGTA	8520
GGGTTTGTAG TAGGACGTAG AAGGATTCAA TTCCCAAAAT ACTAGGCGTC AGGAAGCGAT	3580
TTTCCGTCAG GGTTTGAAAA CTAATGGTCG AAATCCCAGT CGCGATGGCT ACCAAGAGAT	8640
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AAAAGTAGAG AAGACAAGCT CCGATGGCAA GAATAATGAG AATCCAGAAG AGCTTGGTAT	8760
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CTACCGATGA TTCCTAGCAA GAGACTGACA GACAATCAT AGGGCCTAAT CAGAACTCGG	8880
GATAGGATAT CGCAAGCCAG AACTAGATTG GCACCAACCA GTGCGACCAT GAGTTTGGTT	8940

1063

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ATGATGGTGA AGGTTTGGGA TAATTTCCAA ACGGTTATCA GGATGATGAG GCCTAAGAAG	9180
AGCCACTCAT ACTGATGGGT CTGAATCATG GAGAAGGAGC CCTGGGTCCA GGCAGTCATA	9240
CTCTGAACCA GATTGAAACG ATAGGCGATA ACTTCTGTGA CTGAGCCGAT AATCCCGCTA	9300
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GCTAGGAAGA AGAGGGTGAA TACGATGGAT GAAACAAAAG CGAAGAGCAT CTTGTGGGTC	9420
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GTTCCAACCTG TACTCGGTGC AGCAAACTGA TTTTGGGTAA TAGTCTGCAT GAGAAGGCCCT	9540
GCCATACTCA TACTAGAGGC AGTCAGGAGA ATACTGATAG TTCTTGGGAG ACGGGACTCT	9600
TGAAAGAGGA GCCAGGTCTG CTGGTCGAAA TCAAATAGCT TTCCCATGA AAAATCACTG	9660
GTCCCAATGC TAATAGAGAG AAAGACTAGG AGTAGAAGTA AGCCAGG	9707

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5910 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCGCAATTAT GCTTGAAAAG GAGTATACTT ATAAGTAACG CAAACGTTTG CGTCTGAAAA	60
ATACGCAACG TTCCATTATT TTAACACACG AGGTGCTATT ATGAAAAAAC GTCAAAGTGG	120
TGTGTTGATG CACATCTCTT CTCTTCCAGG AGCTTACGGA ATCGGATCAT TTGGTCAAAG	180
TGCTTACGAC TTCGTTGATT TCTTGGTCCG TACAAAACAA CGTTACTGGC AAATCCTTCC	240
ATTAGGAGCA ACTAGTTACG GGGATTCTCC TTACCAATCT TTCTCAGCCT TCGCAGGAAA	300
CACTCATTTT ATCGATTTAG ATATCTTGGT GGAGCAAGGT TTGTTGGAAG CAAGTGACCT	360
TGAAGGAGTT GACTTTGGTA GCGATGCGTC TGAAGTTGAC TATGCTAAAA TCTACTATGC	420
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TTTTGAGAAA TTTGCTCAAG ACAACCAATC ATGGCTTGAG CTCTTTGCTG AGTATATGGC	540
TATCAAAGAG TATTTTGACA ATCTTGCTTG GACTGAATGG CCAGATGCAG ATGCTCGTGC	600

1064

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GTGGGCAAAT CCACATCTCT TCAAAACAGA TGTCAATGGT AAGGCTACTT GTATCGCAGG	840
ATGCCCACCA GATGAGTTT CTGTAAGTGG TCAGCTTTGG GGTAATCCAA TCTATGACTG	900
GGAAGCAATG GACAAAGACG GCTACAAATG GTGGATTGAA CGCTTGCGTG AAAGCTTCAA	960
AATCTACGAT ATCGTTCGTA TCGACCACTT CCGTGGCTTC GAATCTTACT GGGAAATCCC	1020
TGCTGGTTCC GATACAGCAG CACCTGGTGA GTGGGTGAAA GGTCCAGGTT ACAAGCTTTT	1080
TGCAGCCGTT AAGGAAGAAC TTGGTGAGCT AAACATCATC GCAGAAGACC TTGGCTTCAT	1140
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CAGATATCGC TCGCAACTTA ACTCTCTTCC TTTACCCAGA TGATAGTGAC CGTCAAGGTG	2340
AATTGCTCCG TATCTTCCAA CAATACTTCA TGGTTTCAAA CCGTGCGCAA TTGATCATCG	2400

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ACGAAGCAAT CGAAAAAGGA AGCAACTTGC ATGACCTTGC TGA CTACGCA GTTGTCCAAA	2460
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CAATCCTTGC TGAAGCGCTT GAAAAATGGC CTCTTGAATT CTGCAAGAA GTGGTTCCTC	2640
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GATACAGTGT TAACGGGGTT GCAGCACTCC ATACTGAAAT CTTGAAAAAT TCTGAGTTGA	2820
AAGCCTTCTA CGACCTTTAC CCAGAAAAGT TCAACAACAA AACAAACGGT ATCACTTTCC	2880
GTCGTTGGCT TATGCATGCT AACCCAAGAT TGTCTCACTA CTTGGATGAG ATTCTTGGAG	2940
ATGGTTGGCA CCATGAAGCA GATGAGCTTG AAAA ACTTTT GTCTTATGAA GACAAAGCAG	3000
TTGTCAAAGA AAAATTGGAA AGCATCAAGG CTCACAACAA ACGTAAATTG GCTCGTCACT	3060
TGAAAGAACA CCAAGGTGTG GAAATCAATC CAAATCTAT CTTTGATATC CAAATCAAAC	3120
GTCTTCACGA GTACAAACGC CAACAAATGA ACGCTTTGTA CGTGATCCAC AAATACCTTG	3180
ACATCAAAGC TGGTAACATC CCTGCTCGTC CAATCACAAT CTTCTTTGGT GGTAAAGCAG	3240
CTCCAGCCTA CACAATCGCT CAAGACATTA TCCATTTAAT CCTTTGCATG TCAGAAGTTA	3300
TTGCTAACGA TCCAGCAGTA GCTCCACACT TGCAAGTAGT TATGGTTGAA AACTACAACG	3360
TTACTGCAGC AAGTTTCCTT ATCCCAGCAT GTGATATCTC AGAACAAATC TCACTTGCTT	3420
CTAAAGAAGC TTCAGGTACT GGTAACATGA AATTCATGTT GAACGGAGCT TTGACACTTG	3480
GTACTATGGA CGGTGCTAAC GTGGAAATCG CTGAGTTGGT TGGAGAAGAA AACATCTACA	3540
TCTTCGGTGA AGATT CAGAA ACTGTTATCG ACCTTTACGC AAAAGCAGCT TACAAATCAA	3600
GCGAATTCTA CGCTCGTGAA GCTATCAAAC CATTGTTGTA CTTCATCGTT AGTGATGCAG	3660
TTCTTG CAGC TGGAAACAAA GAGCGCTTGG AACGTTTTTA CAATGAATTG ATCAACAAAG	3720
ACTGGTTCAT GACTCTTCTT GATTTGGAAG ACTACATCAA AGTCAAAGAG CAAATGCTTG	3780
CTGACTACGA AGACCGTGAC GCATGGTTGG ATAAAGTCAT CGTTAACATT TCTAAAGCAG	3840
GATTCTTCTC ATCTGACCGT ACAATCGCTC AGTATAACGA AGACATCTGG CACTTGA ACT	3900
AATACTCTTC GAAAATCTCT TCAAACCACG TCAGCTTTAT CTGCAACCTC AAAGCAGTGC	3960
TTTGAGCAAC TGCGGCTAGC TTCCTAGTTT GCTCTTTGAT TTTCATTGAG TATAAGATAC	4020
AAATTTATAC TAATACATTT TGTAAAAAAG CGAGTTTCGA TTGAAATTCG CTTTTTTAAT	4080
GATGTAGATT TGGGTCAATC TTGTCTAAAA ATAGGGAAAT CCTAGATACA GTGAAGGCTT	4140

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TAAATGCTGG TTTTACTGT CCTCAGCCTT ATATTTTTTC GTAGTTGGTT ACCTCATATC	4200
TATTATATTC GCTTACATAA AGTATTATAA TATAATTGTA GGAAAGAAGG TGTTTTATG	4260
ATATACACAC TTAAATTGGT GTTGTTTATT ACCTTTCTTG TAATAAGCTT GTTACCTGAT	4320
AAGATTTTGG GAAAAATAA AAAAATTTGG AAAATAGTTT TTGCAATATT GACGGCAGTG	4380
GCAGCATTGT CATTTATGTA CTAAGTTATT TTAAGAATGT AGGGAAATAA ACCCTACATT	4440
CTTTTAGTT TTTCTGTTT TCTAAATTCT ATTTATCCAA GCGATTCAAC ATTTCTTGCT	4500
TCTTCGCTTC AAGTTCTGCA CGCTTTTCTT CGATTTCTGGC ATGTTTTTTC TCGAGTTCAG	4560
AACAACCTGC ACCATTGCTA AATTCCTTTC GCCATCAGGA GATAGGGTGA GTCGACATGT	4620
CTATTACTCA CCCAAAGCAG TCCTACAAAG CAGGAATTTT CTGTTACTTT TTTGGAAATA	4680
GTAACGTTTA TACAGCTTTG AACTTCTGTA TCAAAGCGCC AAACACACTC CGAGGGGTTT	4740
ACAGAAAGCA GAAAAGGAAT GATCTGGTAT AAGATCATTC CTTTTCyCTC TTTTCTTTA	4800
AGTAATTATA TACAATGTAC GACGAAGTCG TCATTGCAAT GCTGATCCAC CACCTAAAGG	4860
GAACTTTAAA CAACATTGAT AAGATAAAGA ATATAAACAA CGAAAATACG TTATACCCAA	4920
TTAATTTTAT TGTATATCTC ATGATTAAAA GTTAATCCTT CCGTTGTTAG GAATGGCATC	4980
ATTTTTATCC CATAATTGTG CTAAATAAGT CCCCAGTGAT AATAAATTCA TAGCGAATTC	5040
TAAAGCAACA TCATTTACAA ACCAACTACC TAGATATCTA GAAATTGCTG AACGAATAGC	5100
ACTTTTGGCT GCATGTTTTC CTTTACTTTT AATTAGATTT GCAAGGCCTG CAGTAGTTCC	5160
TCCTAATGCT AAAGCTATTG CAGTATCTAA TAGAGCACCC ATTTGATTAA CTGTAATACC	5220
TTGCCAAACT GCTCTAAATG GAGAGTATGT AGGTGGGATT GTATAATCGC CTTGTAATTG	5280
TCGGTTAATT ACTTCTTTGA TCCATTGTTG TGAGACGTCT GGATGAAAAG ATTGGATTTC	5340
GTTTGCAAGT GTATTGATTT GTTCTTCTGT TAGAGAAGTG ACAGGTTGAA GTTCCATATT	5400
TGTTTCAATT TGTGATACTT GTTCAGAAGC GTATACAGCT GAAACACTTG GAATCGCTGA	5460
TACAATTAAC ACAATTGACG TCAAAAAAAC CGAAATAAAT TTCATTAATT TGTTCATGAG	5520
CTTTCTCCT TTTTATTTGC ATCTGCTTAC ATTTTATCAT ATACTGTTAT TATAGTCAAA	5580
AAAATATGCT ATTATGTTAA AAAAATATTT TTCAAATAT AAATGGACGG ATTTATTTTG	5640
GATTTTATTT GTTATTTTGA CCTGCCTCTA TATTGGTAAC CATGATTTGT TTA CTCTCAA	5700
TCATCAAGAA TTCTCTTTTC GTGGTAGCGT TTGGGGTCTG GTACTGGCCT TATATCACTT	5760
ACTATTCATT GATAAGTTTG TTATATCGAA TCGAAAATAA AGATTAGAGC TATGCTTGAC	5820
TGTGTACTTT TAGGATTTAT TTTGGAGGAA GATTTTGTCT CTATTATTTA TTATTTTAAA	5880
TTTATTTATT TTGTATAAGA TCTATTCTTT	5910

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## (2) INFORMATION FOR SEQ ID NO: 166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

GGCATAGCGA CTCATTTTTT CAACTGTCCA GGCTGGATAC CAGACTAATT TAACCTCAGT	60
ATCCGTTACT TCTGGAACCT CTATCATAGC ATCATAAATC TGGTCTGTCA AAAGGTCTGC	120
TAAGGGACAA CCCATAGTTG TCAAAGTCAT GTCAATCTCT GTTTGCCCTG TGTCAACCGTC	180
AAAACGAATC TCATAGATCA AACCAAGATT GACAATATCG ATTCCCAACT CAGGGTCCGAT	240
GACTTCTTCC AAGGCTGTTA AAATCCGTGT TTTGATGTTT TCAATTTGCT CTTCTGTATA	300
AGCCATATTT TCCTCACTCT TAGTCTTCAA TAAATCAGC AAGCGGTTTG CTACGACTTG	360
GTTGGCGTAG TTTCTCAAA GCCTTTGCTT CAATCTGACG GATACGCTCA CGAGTTACGT	420
TAAAGACTTT CCCACATCT TCAAGTGTGC GCATTTTCC ATCATCTAGT CCAAAACGTA	480
GACGCAGAAC ATTTTCTTCA CGGTCTGTAA GAGTATCTAA GATTTTCATCC AATTGCTCAC	540
GCAAGACGAT ACGAGTCGTA TAATCCACTG GATTTTCAAT CACTTCATCT TCGATAAAGT	600
CTCCAAGGTG GCTATCGTCC TCTTCACCGA TAGGAGTTTC AAGAGATACT GGTTCCTGGG	660
CAATCTTCAA GATTTTCACG ACCTTATCAG GTGTCATATC CATTGCTTCA GCAATCTGTT	720
CTGGTGTCGG ATCTTGCCCC AATCTTGAA GGAGATTCCG CTGTTACGA ACCAATTTAT	780
TGATAGTTTC AACCATGTGA ACTGGGATAC GGATGGTACG AGCTTGGTCC GCAATAGCAC	840
GAGTGATAGC CTGACGAATC CACCAAGTTG CATAAGTTGA AAACCTGAAC CCTTTAGAAT	900
AGTCAAACCT GTCAACCGCC TTCATCAAGC CCATATTTCC TTCTTGAATC AAGTCAAGGA	960
ACTGCATACC ACGACCGACA TAGCGTTTGG CAATGGAAC AACCAAACGA AGATTGGCTT	1020
CCGCAAGACG TTGTTTGGCT TCGATATCAC CAGCTTCAAC AGCCAGTGCC AACTCTTTCT	1080
CCTCTTCATT GGTCAAGAGA GGAACGACCC CTATTTCTTT CAAGTACATA CGGACAGGGT	1140
CATTGACCTT AGCAGAAGTT GACCCAATCA AGTCCTCATC GCTGAGTTCT GGTCTTCTT	1200
CATTGCTGAG AACACGCGCA CTTGGATTTT CTTGTTATC TGTGATAGAA ATGCCTGCAT	1260
CCTGAATCCG TTGCAAGAGA TCTTCAATCC CATCAGCGTC CAAGGTAAAA GGAATAACCA	1320
GACTTGCAAT GATTTTCATCA TCTGTTGCTG TCCCTTTTGG CTTATGATTA CGGATAAATT	1380

1068

CTGCTACCTG	TACGTCAAAT	GTTGTTACTT	CTTTTGTGTT	TGTTGCCATT	ATTACTCCAT	1440
TCTTCTCTTT	TGGGAAATTA	AACGTTCCAA	TTCTTCTAGG	GCTGTATCTG	TATCTCCTAC	1500
ATGGCTAGCT	TCCTGCACCT	TCTTTTTGAT	TCTCATATTG	TCCTGATTCA	AGAGAGCCTT	1560
GTTTCGAGTC	ATCTCTACTT	CACTAAGTTC	CTGCGGCGAT	ATCTCAGCAG	GCAAATCCTG	1620
AGCTAAAACT	TGGTACCAAG	CTCTTTCAAC	TTCTCTGTCT	TGCTCTGCTA	AAACTTCTGG	1680
AGGAAGATTT	CCATACTGGC	CAAGCAAGTC	ATATAAGACC	TGAAATTCAG	GTGTAGCAAA	1740
TGCAAAGTCT	TCTCGCAAAC	GGTAATCGTT	CAAAACAAGA	GGGGATTCCA	TCATCCGATA	1800
GAGTAGATGG	GCTTCTGCCC	TCATAATAGC	CGATAACTGC	TTGGTGACAG	GCATGGTGAT	1860
TGGCGTCGGT	CTGGAAATTC	CTTCCATGCG	ATTCTGCCTT	TGCACCTGAC	GACTCTCATT	1920
AACAATCTGC	TCAATCTGGG	TATAATCAAA	GGACGCCAGA	CTGTCAGCTA	AAATATGAAT	1980
ATAGCTGTTT	TGAGCAGCGA	TGGACTTTTC	TTGAACAATC	AAGGGAGCTA	TTTTTTCAAG	2040
AAACTCAATC	TGAGCCTGCA	GATTTTCACT	GTTTTCAGGT	TTGTAATGAT	GAATGTAGAA	2100
CTCAATCGGA	CTAATACGAG	TTTTCGTTAA	TAGATAGGCC	AAGTCTTCTG	GACCATTTTT	2160
TTGTAGATAC	TCATCAGGAT	CCAAGTTATC	AGGCATGCTG	ACGATTGCA	CAGGCATATC	2220
ACCAATTTCA	TCCAATGCTT	TCAATGTGCG	GGCTTGCCCA	GCCTTATCTC	CATCGTAAAC	2280
AAGAACCAAT	TTCTTGGTTA	ACCTTTTCAG	ATGCTCAACA	TGCTCTCGAC	TCAAGGCTGT	2340
TCCCATCGAC	GCCACAGCAT	TTTCGATTCC	AGCCCGATAG	GCTGCAATAA	CATCCATGAA	2400
TCCTTCCATC	AGGTAAATCT	CACTAGCTTT	TCCAGAAGAT	CTTTTGGCCC	TATCCATATG	2460
ATATAATTCG	TAACTTTTGT	TAAAAATTGC	AGTCGATCGG	CTGTTTTTAT	ACTTAGAAGT	2520
TTGTGAATCC	GTTTTTTGCC	AGATACGACC	TGAGAAGGCA	ATGACCTTTC	CTTGGTCATT	2580
TGTCAGGGGA	AACATAATGC	GATTGTGAAA	GGTGTCTACA	AATTGATTGG	CATCCGAGAG	2640
ATAAACAGG	CCTGAATCCA	GTAAATCCTC	TTACGATAC	TGATCAGACA	AACGTTGATA	2700
GAGATAGTTT	CGTTCTGGAG	GTGCTAAACC	AATCCAAAAA	TGTTTAAGCA	CTTCATCTGT	2760
CAACCCCGC	TGATAAAGGT	AATTTCTGGC	CTCTTCGCCC	ATAGTCGTTG	TCATGAGAAT	2820
AGCATGGTAA	AATTTGGCTG	CATCTTCGTG	CATATCATAA	AGAGCTTGGT	GAGGTGAGGC	2880
TGACTTCTGC	TCACTATAAA	GCGGTTTTTC	AACCTCAATT	CCAACACGCT	GACCTAAGAT	2940
TTGGACTGCT	TCTATAAAGG	GAACCCCTTG	GTACTCCTCG	ATGAACTTAA	AGACATCACC	3000
TGAGCGACCA	CAACCGAAAC	AGTGATAAAA	CTGCTTGTCC	TCTACAACAT	TGAAAGATGG	3060
TGTTTTTTCA	CCATGAAAAG	GACAGAGCCC	TAGATAGTTC	CGTCCTGCCT	TTTGTAAAGA	3120
AATCACATCT	CCTATGACTT	CCACAATGTT	GGCATGTGTT	TTGATTTCTT	CAATGACTTG	3180



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TTTGTCAACC ATACACAATA CCTCCATGTT ATCATAGTTT ACTTTATATA GTATACTTTA	3240
TTTCAGAAAA AAAGTAAACC ATTTCACTCA TTTTCCCTAC TTTATTCAAA GAGTTGATAA	3300
TAATCAGAGA TTTTCATTTT TGCTTTTTCT TCTTGGTTTA AATCTTGGAT AATTCGTCCT	3360
TCTTTCATGA CAATCAAGCG ATTGCCGTAT TTGAGAGCAT CTTCCATATG ATGAGTAATC	3420
ATAAGGGCTG TTAGCTGATC TTTCTTAACA AATTCATCTG TCAATTCCAT CAAAGCAACA	3480
CTAGTCTTTG GATCCAGGGC AGCAGTATGC TCATCTAACA GGAGTAATTC AGGTCGCTTC	3540
AAGGTTGCCA TCAAGAGACT CAAAGCCTGT CTTTGTCCAC CTGATAAGAA CTCAATCGGT	3600
GTATTCAAGT GTTCTCAAG ACCATTTCTT ACTTTTTCAA TGGTTGCCTG AAATTCATCC	3660
TTATAGCTAG TCAAGCGTCG TGGTAACAAT CCACGCTTTT CACCACGAAA CTTGGCGATT	3720
AAAAGATTTT CAGCGACCGT CATACGGGGA GCTGTCCCA TCTTTGGATC TTGGAAGACA	3780
CGAGACAGGT ACTTGGCAGC CTTCTCGGT GAAACTTAG TGAGATCTTC ACCTAAAATA	3840
CGGATAGTTC CACTAGTTAG TGATAAGGTC CCTGCTATAG TGTAAAGAG AGTTGATTTT	3900
CCAGCACCAT TTCCGCCAA AATCGTGATA AAGTCCCGTT CAAAAATTTC TAAGGAAACA	3960
TCATTTAAAA TAATCTTTT TCCATCAAAG CCATTTTAA CGATTTTGGT TGCATTTTTT	4020
AATTCTACAA TTGCTGTCAT TTGCTTAACT TGGCTCCTTT CAAGATTGTT TGCTTAAATG	4080
TTGGAATCAT GAGGCAGACT GCTAAAATCA AGGCACTGTA TAAACGAAGG TAACTGTAT	4140
TAAAGCCAAG TGCATAACT GCCCACACTA AAAATTGATA AGCGATAGAA CCTACAACGA	4200
TAGTAACCAA ACGCTCTGCC AAGCTCAAAC TCTTGAAAAT AACTTCTCCA ATAATCAAAC	4260
TTGCAAGCCC CACAACGATA ACCCCGATCC CTCGAGACAC ATCGGCATAA CCTTCTTGCT	4320
GAGCAATGAG GGCACCTGCA AGGGCAATCA CACCATTGTA TAAGACCAAG CCCATGAGCT	4380
CCATGCGTCC AGTATGAATC CCGAACTTC TAGCCATATC AGGATTATCC CCTGTAGCAA	4440
TATAGGCTTG TCCGAGTTTA GTGTCCAAGA AAAAGAGCAT GAGAGCAATA ACAATACTCA	4500
CAAAGATGAG ACCTGTCAAG AGTTGATTCA AATCCGAATC AAAAGGCAAA ACATCCTGAA	4560
TTTGCTTGGT TCCAAGCAGG CCTAAATTCC CACGTCCCAT AATCAAGAGC ATGATTGAGT	4620
GACAAGAAGT CATCACCAA ATCCCTGAGA GCAAGGTTGG GATCTTCCCT TTTGTATAAA	4680
GAAGGCCTGC TGCCATTCCA GCCAAACAAC CTGCTCCTAC AGCAACAAGT GTCGCTAAAA	4740
ATGGGTTTAC GCCTTTGGTT ATCAAAGTGA CAGCAACAGC TCCCCAAGA GGAAGGAAC	4800
CTTCTGTCGT CATATCTGGA AAGTTTAAAA TCCTAAATGT CATAAAGATT CCCAGACCTA	4860
GAATAGCCCA GACAAATCCT TGAGAAATAA TGGAAACAAT CATATTTTAT TTAATCCTTT	4920

1070

CTATATTCAT CTTTTTAAAA AATGGGAAGA GTCTCCTCCT CCCTACCTTA TTTATTCGAT	4980
GACTTGTCCT GCTTCTTTGA GAACAGACTC AGGAATAGTA ATACCTAGTT CTTGTGCTAT	5040
TTTTTTATTG ATGACTGACT TACCAGTTGA AAAGACATTG ACTGGGGTAT CGGCTGGTTT	5100
TGCACCTTTC AAGACTTGCA CAATCATTTT ACCTGTTGCC ACACCAAGGT CATGTTGGTC	5160
AATTACAAC TATGCCAAAC CACCTACTTC TACCATAGCT GTCGCACTGG GATAAATTGG	5220
TTCTTTAGAA CTTTGATTGC TAGAGACAAC CGTTGGAAAT CCTGATGCAA TGGTGTATATC	5280
AATTGGAACC CAAATAGCAT CTACCTTGCT AGTCATAACA GTGACAGTTG AGGCAATTTT	5340
ATTGTTGAA GGAAGTCAA ATGTTTCCAC TGTCAGACCT GCCTTTTCAG CATAAGCCTT	5400
AAATTC	5406

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAGCTTGCTC TTACTATTAT AGCAGATGTT ATAGCTGGAA TTATCTTGTA TTTCGTCTGC	60
AAATGGCTAG ATGGTAAGAA GTAGACCGAA TGACTAGCCT ATAAACACCC GTTAAATCGC	120
TAAGATACGT CAAAAAGCC CTTAACTATG GCACTAGTTA GGGGCTTTGG TGTCTAATG	180
AACCTTATAC ACTAACTACA TTCTAGCATA TAAGCCCAGA TATTTCAAGA GTTTTATTTA	240
TTGTTTAAAG TTCTGAAAGG TCTATAATGA AGTTAGCCAT CTAGTATCAA AAAACCGACT	300
AGCTCTTATG AACTAGTCGA TTCTCATCA ATGCGCCAAC ATTTCTTGGG CGATTCTTG	360
GCCAGATAGG TTATCTGGGT AGTAGGTTGG CCAGTTGTCC ATTTCTTCAA AGAGGGCTTC	420
TTGGCTTG TG CCTCCAAAGA AGATATGGAA ATGTTCTGCC TTAAGTGGG CAACATTG.G	480
GTCACATAAC TGAACATACT TGAATTGTCC AGCGTCAGCA TCTGTGGCTT CAAAGAGGAA	540
ACGCACGCCA CGATTGCCTT TCTTGTAAGT CAAAATTTTC TTACCGACAT ACTTGTAAGT	600
GTATTTCTTG CTTTGTCAC CTTGAACAAA TTCCATAGTA TTATCAGTAA TGTTAATCTT	660
AGTCACATCT GTATGATAGC CTTTGTATA GTAAGCCTTG TACTCAGCCT GGGTCATCTT	720
ACCAGTCAAC TTAGCCTTGT AGTCAAAGAC TTGGTCAAAC GTGCCGTCTT CAAGGAAAGG	780
ATAAACTGAT TGCCAGTTAC CTGCATAGTC ACTCAAGGTG CGGTCCTTGA CAGCTGCATC	840
CTCGAAGTAA CCATTTTGA CTGTCTTGGT ATCCTCTGCC TTTTCAGGT CAATTGCTGG	900

1071

GCCTTCTTGG TCTGTTGTTT GTTTCAAAGC CTTGAGGTTT TTCTCCATCA CGGAAATGTA	960
GTTTTCTCCA GCCTTGGTGT CCTCTTCTGT CAGACTTTCT AAAGGATTGA GGACATCAGT	1020
TTTGACACCT GCTTCTTTTG AAAGTGTGTT AGCAAGGGCT TGTGAGGCAT TTCTTCAAAA	1080
TAGATATAGG CGATTTTATT TTTCTTGACA TACTCTGTCA ATTCTGCCAA GCGAGCAGCT	1140
GATGGCTCTG CATCTGGAGA AAGTCCTGAG ATTGCGACTT GTTTGAGTCC ATAGTCCAAG	1200
GCAAGATAGT TAAAGGCTGC GTGTTGAGTC ACAAAGCTCT TTTGTTTTGC TTGAGACAAA	1260
CCTTCTGCGT AAGCCTTATC CAAGGCTTGC AATTTTTCGA TATAGGCAGC TGCATTCTTC	1320
TCAAAGGTCT CTTTTTTATC AGGATAATCT GCTGACAAGC TGTGCGGGAT GTGCTCTACT	1380
AGTTTAATGG CACGAACTGG TGATAACCAA ACATGGGGGT CAAACTCATG GTGATGACCT	1440
TCTTCTCCAT GGTCTGGTC TCCCTCTTCT TCCTCGCCAC CTGGCAAGAG CAACATATCG	1500
CCTGTCGCCT TGATGGTTT CACTTTTTTC TTATCCAAGG TATCTAGCAA TTTAGGTACC	1560
CATGTTTCCA TGTTTTCATT TTCATAAAGC AAGGTATCTG CATCTTGGAT TTTGGCAACT	1620
GCCTTGGCAG ATGGTTCGTA TTCATGAGGT TCTGTCCCAG CACCGATTAG GAGTTCTACA	1680
TTAGCCGTAT CTCCTGCGAC TTGCTTGGTA AATTCATAGA CAGGGTAAAA GGTGTGCACG	1740
ATATTGAGTT TACCATCTGC CTGTTTTTGA TTGGAACAAG CCACTAAAA CAAGGCACAT	1800
AGACTGGCTA GTAATAAGCT AATTTTTTTC ACGTTCGTCT CCTATTGAT AAAACGTCTT	1860
ACTAACTGA TTAGTATAAA GACAGTTACA AAAATAATGG TAATACTTGC ACTTGCAGGT	1920
GTTTCTGCAT AGTAGGAAAT GTAAAGTCCT GCTACCATTC CCAAAAAGCC AATCGCACTG	1980
GCAAGCAGCA TAACCGATTT AAAGTTTTTC CCCAGACGCA GGGCAATACT AGCTGGCAAG	2040
ACCATAATGG TCGATACCAG AAGAGCTCCT GCTGCAGGAA TCATAAGGGC AATAGCCACC	2100
CCTGTCACCA TGTAAAAAG AATGGACATG GTACGAACTG GCAAGCCATC CACAAAGGCC	2160
GTATCTTCGT CAAAAGTTAA GATATACATA GGACGAAGAA AGAGAAAGGT CAAAATCAAA	2220
ACAACCGCCG CAATGACAAA GAGGGAAATG ACCTGTTCTT CACTGATAGT CACGATCGAA	2280
CCAAAGAGAT ATTGGTCCAA ACTCATTGAA CTCGAGCTTT TACCCTTGCT CATGACAATC	2340
AGAGAAACAG CCAGACCTGT TGACATGAGG ATAGCTGTCC CGATTTCCAT AAAGCTCTTG	2400
TAAACCGTAC GGAGATACTC CAGAAAGACC GCCGCAATCA AGACAATGGC AATAGTAGAA	2460
ACAGTTGGAG AAATCCCCAA AACCAGACCA AAGGCTACAC CTGAAAGTGA GACGTGGCTA	2520
AGGGTATCAC TCATCAAAT CTGACGACGC AAGATGAGGA AGGTTCCCAA TACCGGTGAG	2580
AAAAGACTCA TAGCAATAAC CGCCAAAAAG GCGCGTTGTA TAAAGTCGTA AGATAATAAA	2640

1072

CTAAGCATGG CCCACCTCCT GGCCATTCTC ATGAACATTG AAACAACGCC ATGGCGAGTC	2700
TTGGTTACGG ACTAGATGAA TATTGCGATC CGCATAATCC TTAACCTCTT CAGGGTCATG	2760
GGTAATCATC AAAACAGCCT TGCCATGATG ATGGGCGCTG TGGTGCATGA GTTCGTAAAA	2820
TTCATTTTFA CTTCTGTCAT CCATCCCCGT TGTCGGCTCG TCTAGGATAA ACACATCAGG	2880
GTCAGAAGCA AACATACGCG CAATTACCGC TCGCTGCTTT TGTCCCCCAG ATAGAGACCC	2940
CAAGCGTTTG TCTCGATGTT CCCACATGCC AACTGAGTCC AGACTAGCCT TGATATGCTC	3000
CTCATCATGA GCATTCAAAC GACGGAACCA GCCTTTTCTC GGATAGCGAC CCGACTTGAC	3060
AAATTCATAG ACCGTACTTG GAAAACCAGC ATTAATACTG GCAATTTGTT GAGGAAGATA	3120
GGCTATTCTC AATTTCTTAC CTTGCGTATT TGTCTTTGAA ATAGCCACCT TTCCAATGCG	3180
TGGTTGCAGA ATTCCAAGAC TAGCCTTGAT GAGCGTCGTC TTAGCCGCTC CATTTTCCCC	3240
AGTCAAGGTA ACAAATTCCC CACTATCAAC ACAATAATTG ATATGTTCAA GAACAGGCTC	3300
CTTATCATAA TAGAAGGACA AATCCTCTAC CGTAATATAT CTCATTATTT GATTTCTCCT	3360
ACTAAAGCAG TCAAAAACCG CTGAATCACT TTTTGTTTAT TTGGAGTAAA CTGAGTCGCC	3420
ACTTGTTTAT AGGTTAAAAG TGTATGCTCA TGGTGATGGT GGTGCTCCTC AGCGATTGGA	3480
CGAGCCAAGT CAGTCAACTG ATAAAAATC ACACGCGCAT CTTTAGAATC TTTAGATGTT	3540
TCCAACATCC CTTCTTGAC CAAAGACTTA ATGGCCTTGG TAACTGCCGC CTGACTGACA	3600
TTGAGACGAC GGGCCAATTC TGAATTTGTT AAAGATTCTT CTGACAAGAG CATAAGGATA	3660
TGCTCCTGAG TATTGGTCAG GGCCACCTCG CTAGTGCAAT GACCTATTAG GATTTTCATG	3720
TGATTTTCCG CCTGCAAAAT CACCTCATTC AAAAAAGCAT TGATATCCTT TGCTAGCTGT	3780
CTCATATCTG ACTCCTTTCC TTTTAGACTT CTCTTTTTTA AGAGAAAAAT ACTATTCTTT	3840
GACATTTTGT TTACCAGTTA ATTATATCAC AAGCAAAAAA AGAGTCAAGA AAAAACGTGA	3900
AAACTAGTTT CATTCCTGAA CTCTTCTATA TTATATTATC TATTGAAATT CTTTGACATC	3960
TCCATCATAA GTCGCCAAT CTTTGCTGAA AAAGCGCTCA TTCAGATGGT AAGTCGGAGC	4020
TGGTGTGGGA TTGGATAGGA AAGGATCAAC TGCCTTGTC AAGCCAACC AACCCAACCA	4080
ACCAAGGTGA ATGGTGTCTT TCATAAAGAA AGGCTCCCCG CCGTCTTAG AAAAATCTGC	4140
TATATTGGTA AAACCTTGAC TTTCTAACTG GTAGCGAATC TTCTGCACCG TTTGTTGGTA	4200
CATATCCTCT CGTAGACCAG CATAGTTCAT CCATTTTTTA TTAACAGGTG GAATGATAAA	4260
AATCGGGTTT ACCTTAGATT TAGAAAACCTG TGTAAAACC AACTGCAAGT CATTATACTC	4320
TGGCGACTTG AGATAGGTAA AGCTTTTCTG AGAATCCTTT AATTTCTTCA AATCCTTCTT	4380
GATCTGCTCA TTATAGAAAT AATTTTCCAT TCCCATCTCA TTATTGGAAG TATTTTTTTC	4440

1073

AGCATCTGCT TTGACAACAT CTTCTATTGC CTGATAAGAA AACTGGTCTG GCAAGATTTT	4500
TAAATACTTA GCTACATGCT TATCGTAGTT AACATAGCCT CTAACCGAAA ACTGACCAAA	4560
AAAGGAAGCT TGGCGTTCAT TAAAACGAGC CAATAATTCA ATCATTTCAT TGTCTGCTGT	4620
CGACAATTCT TCTTTACTTG CCAACTTCTG AACCAGGTCC TTCATAGCTA CGTTTGGGAA	4680
CTGTTGCAGT AAGCGAGTCG CTGCATATTG ACTAGCCTGA TCCCCAGATT GATGTTTCAG	4740
AAAAGTAGTC AACTGGTCTC CATTAAAATA CTGCTGGAAG GCTGCTGGAT CATAGCCATT	4800
TTTACTGAAC CACTGAGGTG AGATAACATA CACAACCTGT TTATTCTCCA GCTGTGGTAA	4860
CATCTGTTGC ATTCCAAAAT ATTGGTTAAG CGATGCAGCT CCCCCCTGTC CTAAAAGATA	4920
AGGACGGTAG GAACGATTGT ATTTCTCAGC TAATACCGCA GGATGAGCAC CGTCAAACG	4980
AAGCCATTCA CTAGAGCCAA AGAAGGGAAC AAAACGCACA TTTGGATCAG ATAGTGCTCT	5040
GACTTTTTGA CTTGCTCCT TAAACTATC GATAGTAGTA GCCACTGCTG AACGCTTTTC	5100
AGCTCCTAGA TTATGATGCA TCTCAGTAGG ATAAAAGAAA ATGAGCAGAA AAACCAACAA	5160
ACCAGCGATC AAGACCGGTC CGAAGATCAT CCATAAGCGT TTAAGCATT TGTAGCTCCA	5220
CAATACCAGC TATGATTTTA TTAGCTGTAT TCCAGTCGTC ACGACCAAAC TCTGTTACAG	5280
GGACACGAAT GTCAAAACG TTCTCAATCT CCACAATCAA CTCAACCGTT CCCATACTAT	5340
CCAAGACACC TGCATCAAAA AGATCTTCAT CCATCATGTC AGAAACATCT TCCATAAACA	5400
ACTCATCAAT AATTCAATA ACTTCTGATT TGATATCCAT ATTTTATTTT CTTTATTTT	5460
TTAAACCATA GATTATTCAA GAATCCAGAA AAGATTAAGA ATGACAACAT GACAACATGG	5520
AAAGTGACAA CCATGCCAAG CAACTGAATC CAGCGATTCT CAGGTAGGGC AGCCTTCCCT	5580
GCTTTTTTCC GTTCCTTATT GAGCGTTTTT TTCTTGCAG CCCAGGCATC ATTGATGACC	5640
AAGCCTAGTC CATGAAAGAG TCCATAGGCG ATATAGTACC AGGTCACACC ATGCCAAAAT	5700
CCCATAATCA GCATATTTAC AATGTAGGCC ATGCTTGAGG TTACATTACG ATTTTAAAG	5760
ACTTCTTTT TGGTTAACAC CATCACCATT CGCATAAAGA CAAAGTCACG GAACCAGAAG	5820
GACAGACTCA TATGCCAGCG ATTCCAAAAC TCCTTTAAAT CCCTTGATAA AAAGGGCTTG	5880
TTAAAGTTGA TAGGGCTACG GATCCCATC AAGTTTGAGA TGGCCAAAGC AACATAGAA	5940
TAACCTGCAA AGTCAAAGAA GAGTTCAGA CCAAAGTAT ACATAACTGC CAAGGCATAG	6000
AGATTAAAGA AGCCACCTGA CTGCAAGGCT AAATTCTTCA GAGGAGGTAG TAAGGTCTCT	6060
CCTAAACAT GAGCTAGGAT AACTTATAC AAAAGCCCC ACATGATATA GCGGACAGAT	6120
TCATCCAGCA TATCCATCAA CTCATCTCGC TCAGGAATAG CCTGATAATT TTCATTAAAT	6180

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CGCTTAAAGC GATCGATTGG ACCACTCGAG AAAGTTGGCA TGAAGAGAAG GAAACGGAGG	6240
AATTCCCAGA GGGTAAAATC CTTAATCACT CCATCTCTCA GCTCGATGAC AATTCCAACC	6300
GAACGAAAGG TCAGGTAAGA AATTCCCAAG AACCCAAGCA AAGACTGCGT TCCATTGATA	6360
GCTGGTTGCA CCTTGACAAA GATAATCGGA AGTAGGGACA GAAAACTAAC TAAGTAGAAG	6420
ACCCACTTGC CATCCTTGCT TTTTCGATAA TGCTTGTAAG AAAGCAGGAG CAATATTTCC	6480
CAGCAAAGGT AAATACCCAA GGCAGCTAGT TGATTGGTCT TTCCACCCAC CAACATGGTG	6540
ACAATAAAGA AGAGACTTAC CAACACTTCA TACCAGGCAA AGCGTTTCTT GAAAAAGAGA	6600
CCTATAAAGA TGGGCAAGGT TGCAGCAATC ACATAAACAA AATACTGAGG ATTGCCATAT	6660
GGCTCTAAAT GAGGAAGCTG TTGAAAAAC TCCATCATCT CTTATTCACC TCGTTAATCA	6720
ATCCTTTGAT GTCAATCTTT CCATTTGGAG TTAGTGGCAA ACTGTCTCGG TAAAGGAATT	6780
TAGATGGCAT CATATAGGAC ATCATGATGT CTGTCAGGTC TTCTTGATG GCCTTGGTAA	6840
TATCGATATC TCGCTCAAAC TGCTCAGGAA CACCGTCTTT TAAGATGACA TAAGCCAATA	6900
GATTTTGTAC CTTGTGGTCC TTGTTATAGC GCGGTACTGC GACAGCAGAT TCGATAAAGC	6960
GAGACTTGTT GAGGTTTTGA GAGACATCTT CTAACCTCAAT GCGGTAACCG TTAAACTTAA	7020
TCTGGAAGTC CATGCGTCCG CCGTAGAGAA GCAAGCCCTC ATCTGTCATG GTTCCCACAT	7080
CGCCTGTGTG ATAGGCTGGC AGATCTTCAA ACTCAAAGAA GGCTTCTGCT GTTTTTTCAG	7140
GATTGTTTAT ATAACCTTTT GAAACAGCTG GCCCAGAAAC AATGATTTCT CCCTGCTCAC	7200
CATTTGGCAG TTTATTTCTT TCCTCGTCAA TGATAAAGGT TGGAGAATCA GCCTTGGTAT	7260
AGCCGATTGG TAGGCGTTTG AGAGTCGCTA ACATCTCGTC TGTCACGGCA ACTGCTGACA	7320
GAGCTACTGT CGCTTCTGTT GGGCCGTAAG CATTGATGAT ACGGGCATT TGGGAAACGCT	7380
CGCGCAGTTT TTGAGCTGTT TTGACCGTCA ATTCTTCACC ATCAAAGTAG AAATGCGTGA	7440
TTCCAGGCAT TTTCTCACTG TTGAAGTATT CAGACAACAT GGCCATATCT GCAAAGGATG	7500
GTGTTGATGT CCAGATAGCG ATTGGCAATG AAAAGATAGC CGCAAAGAGT TGCTTAAAT	7560
CCTGAGTGAT GACTGAAGGA AGAGTGAAAA GCGTACCACC AAGTGCCAAG GTCGGTGCCC	7620
AATACATGAC AGACAAGTCA AAAGAATAAG GTGGCTGTGC CAGCATTTGC GGACGACTCG	7680
GTGTCGCAAA TTCCTTATCC GTAATCATCC AGTTTGTAAG GCTGAGGAGA TTATCATGTG	7740
AAATCTGCAC TCCCTTAGGC TTACCAGTCG TACCAGAAGT AAAGATAATG TAGTAATTAT	7800
CATCTCCCTT GACTGGATGC GTGATTTTAT AGTTATTTCC TTGGGCAAAG GCTTCTTGAA	7860
CCTGAGCTAG ATTTATCATT GGTGTAGAAA CCTGCTCCAA GGGAAAGGCT GAAATGGCAA	7920
TAATCAAGCT TGGCTCTGCT ACTTCTAAAA TAGCTGAAAC TCGCTCCAAG GCCGAATGGC	7980

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TATCAATTGG AATGTAGGCA TGACCTGACT TAGTCAGCGC TACAAAGGTT GCCAACATTT	8040
CATATTCTTG GCCACCAAAA ACAACCACAG GAGACTTCTC AGGCAAGCCT AGTTGGTCAA	8100
TGACTGCAGC CAAACTATCC GAATCAGCCT TTAAATCGCC ATAAGTGTGT TCCTGCCCCA	8160
AAACATTATA GACAGGATAG CTAGGCTGTG TCTGAGCAAA ATGCTCAATG GTTTCATCA	8220
TATCTGCTAT TGGTTTATTT GACACAATAG GGATTCTCCT TCAAGTTAAA ATTCATTATA	8280
GATAAAGCTT CCTTGACCCT GACCAAGATA GCTAAAGAAG TAAAGCAGCC CTAGAAAGAT	8340
AAGAAAATAC AAGGCTGTCC GACCAAGAAA GAGGTACAAT TCTTTTCTCT GTTTCATCAA	8400
GAAAAACCAT TCATTTCTGT AATTTTTCGC TAAAATAAGA GTGATTCTTA CTAGCTTATT	8460
TTTCTACCAT TGTACCACTT TATATAGTAT CTTTTCATTT GTTTACCGTA TGTTCCTAAT	8520
AGATTTTCAGC TTATTTTAAG GATTATACAG TTTTCTATG TATATTTTCA AATAGAGTGA	8580
TCCTGCTTCA AAACCTCATT TCAGGAGACA ATGAAGTAAA TCTTCCATA ATAAAACACA	8640
CAATATCAAG TTTTTTCAAC ACCTGATACT ATGCGCTTTT CTGATTTTAA AAGACTTTTT	8700
AACCACTCTC TCATTTAAAA TAATCTCGTC TGATATAAAT TAAAATAGCT TCTATCATCA	8760
GACAAATGGC TGATAGCCAA AAACCTGATG TAATACCAAA ACTCTCAGTA ATATAGCTCA	8820
TTAGCAAAAC AAATACTGAA AATGCTAATG TAGAAATCAC TTCAAGAACG GAATAGACAT	8880
TAACTAAATG ATTTTCTCTT ACTGTTTCCT GAAGAAATAC ACTTTCAGGA ACTTCTTTTA	8940
GTTGCGATAA CATAACCACT AAAGCTGAAA ATAATAAAAA CATCTGTGCG TTTGGAAAAT	9000
ATAGAATAGT CAGTGTCACT ATTTCCATAG CTACAAGAGG AAAAGAATA CTTTCCCCC	9060
AAATCATTCA TACCTCTCTC AACTAGATGT AACTTACAAA ACCCCTGACC TCATGAGCCA	9120
CTTCTTCTCT CCTCATGAGG TCAGTTTAC TTTCTGCTGT TCCAGTATCG TTTTCTCTCG	9180
CTAGATTTCC TCAAAAGGGC AGACTCCTCC CTTGGTGCGT CACACGATTT TTTTCATCTCG	9240
ACTGTTCTTT AATGCATCAT TAACGACGCT TTTCTTCTAG GTGGTTCATA AGGAACAGGA	9300
AGATTCAGGT TGACTTTTCT AATCCTAGAA TAAAGTGCTG AAAACAATTC GGAATAGGCA	9360
TAGAGACTAG ACAATTTGAG GAGCTGCTTG CGTCCTGTTT GAACACATTT TCCCACCACG	9420
TGAAGAAAAA GATGGCGGAA GCGTTTGATT GTTAAAGTTT GGAAGTCACC TCCAGCTAGA	9480
TGTTTGAGAA AAAGATAGAG ATTGTAGGCG ATACAGCTCA TCATCATACG AACTTCGTTT	9540
TTGATTAAGG TTGAACTATC CGTTTATCG CCAAAAAATC CCTCCTTCAT CTCCTTGATG	9600
AAATTCTCGG CTTGACCACG TCCACGATAA AGCTGAAACT GGTCTTGGCT GTTCCACTCG	9660
TCATATTTGT AACGAGAGAA ATAACATCGT AGAACAAGTA TCCTTCTTTT C	9711

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(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3025 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CCCCCTTGTC AAAACTGTAA AATTAACGAC TCAACAATTC ATCTTTACAC CAATCTCAAT	60
GGAAAACAAA AACAAATTGA CCTCTGTCAA AACTGCTATA AGATTATCAA AACAGATCCT	120
AACAATAGCC TCTTCAAAGG TATGACGGAT CTGAACAATC GTGACTTCGA TCCCTTTGGT	180
GATTTCTTCA ATGATCTAAA CAATTCAGA CCTTCTAGCA ATACTCCTCC TATTCCCCCA	240
ACCCAATCAG GTGGAGGTTA CGGTGGAAAC GGCGGTTATG GTTCCCAAAA TCGTGGATCT	300
GCTCAAATC CGCCACCTAG CCAAGAAAAA GGCTGCTGG AAGAATTTGG TATTAATGTA	360
ACTGAAATTG CCCGTCGTGG AGACATTGAC CCCGTTATTG GGCGCGACGA TGAGATTATC	420
CGTGTCATCG AGATTCTCAA TCGTAGAACC AAGAATAATC CTGTCCTTAT CGGTGAACCT	480
GGTGTCGGAA AAACGGCCGT TGTCGAAGGT CTAGCTCAGA AAATTGTCGA TGGCGATGTG	540
CCACATAAAC TCCAAGGTAA ACAAGTCATC CGTCTGGATG TGGTTAGCTT AGTTCAAGGA	600
ACGGGGATTG GAGGACAATT TGAAGAACGC ATGCAAAAAC TCATGGAAGA AATTCGCAAA	660
CGTGAAGACA TCATCCTCTT TATCGATGAA ATCCATGAAA TTGTTGGTGC TGGTCTGCG	720
AGTGATGGTA ATATGGACGC AGGAAATATC CTCAAGCCAG CCCTTGCTCG TGGAGAACTG	780
CAACTAGTCG GTGCTACTAC CCTCAATGAA TACCGTATCA TTGAAAAGGA TGCTGCCCTC	840
GAGCGTCGTA TGCAGCCTGT TAAAGTCGAT GAACCAACGG TGGACGAAAC AATCACTATT	900
CTCAAAGGGA TTCAAAGAA ATACGAAGAT TACCACCACG TTCAATATAC AGATGCTGCG	960
ATTGAAGCAG CTGCAACTCT TTCCAATCGC TACATCCAAG ATCGCTTCTT GCCTGACAAG	1020
GCCATTGACC TCCTAGATGA AGCTGGTTCT AAGATGAACT TGACCTTGAA TTTGTGGAT	1080
CCTAAAGTAA TTGATCAGCG CTTGATTGAG GCTGAAAATC TCAAGTCTCA AGCTACACGA	1140
GAAGAAGATT TTGAGAAGGC GGCCTACTTC CGCGACCAGA TTGCCAAGTA TAAGGAAATG	1200
CAAAGAAAA AGATCACAGA CCAGGATACT CCTAGCATCA GCGAGAAAAC TATTGAGCAC	1260
ATTATCGAGC AGAAAACCA TATCCCTGTT GGTGATTTGA AAGAGAAAGA ACAATCTCAA	1320
CTCATCCATC TAGCCGAAGA TCTCAAGTCT CATGTTATTG GTCAAGATGA TGCAGTCGAT	1380
AAGATTGCCA AGGCTATTCT CCGTAATCGT GTCGGACTTG GTACCCCTAA CCGCCCAATC	1440



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GGAAGCTTCC TCTTCGTTGG GCCAACTGGT GTCGGTAAGA CAGAACTTTC CAAACAACTG	1500
GCTATCGAAC TTTTGGTTC TGCTGATAGT ATGATTGCTT TTGATATGAG TGAATACATG	1560
GAAAAACATA GTGTGGCTAA GTTGGTCGGC GCTCCTCCAG GTTATGTTGG CTATGATGAG	1620
GCTGGTCAAT TAACTGAAAA AGTTCGCCAC AATCCATATT CTCTCATCCT TCTCGATGAA	1680
GTGGAAAAAG CTCACCCAGA TGTTATGCAC ATGTTTCTTC AAGTCTTGGA CGATGGTCGT	1740
TTGACAGACG GGCAAGGACG CACCGTTAGC TTCAAGGATG CCATCATTAT CATGACCTCA	1800
AATGCAGGTA CAGGAAAGAC CGAAGCTAGC GTTGGATTG GTGCTGCTAG AGAAGGACGT	1860
ACCAATTCTG TCCTCGGTGA ACTCGGTAAC TTCTTTAGCC CAGAGTTTAT GAACCGTTTT	1920
GATGGCATTG TCGAATTTAA GGCTCTCAGC AAGGATAACC TCCTTCAGAT TGTGAGCTC	1980
ATGCTAGCAG ATGTTAACAA GCGCCTCTCT AGCAACAACA TTCGTTTGGA TGTAAGTATG	2040
AAGGTCAAGG AAAAGTTGGT TGACCTAGGT TATGATCCAA AAATGGGAGC ACGCCCACTT	2100
CGTCGGACTA TTCAAGACTA TATTGAGGAC ACAATCACTG ACTACTACCT TGAAAATCCA	2160
AGCGAAAAAG ATCTCAAAGC AGTTATGACT AGCAAGGGAA ACATTCAGAT TAAATCTGCC	2220
AAAAAAGCTG AAGTTAAAAG TTCTGAAAAA GAAAAATAAA TCCTATAAAA AAGGAGTAGA	2280
AAATGAAATT TTTCTGCTTC TTTTTTACT AAAATAACTG TAATTTCTTG ACAGCTTGCC	2340
CTTTGTCCAT TATGATATAT AGTAGACTGA ATCTGAAATA GTACGAAACA ATTGCTAAAA	2400
CATTTATAGA AATTAATTTT ACTTTCCCAA TCGATTTGTT CTCATCTTAT TTCAATCTGC	2460
TATAGTCAAT TGAAACAAGA ACAAGACAAA AGAGCCTCAT AAAAGGTATT GCAACTTGGT	2520
AATACCTTTT TGAGGTGCTT TTTGATATGA GCCCATGTTT TCTCAATAGG ATTGTAATCA	2580
GGTGAGTAGG GAGGAAGAGG TAAAAGTTTA TACCCAAACT CTTACACAAA GAGTTCTAAC	2640
TTACCCATTC TATGGAATCT TGCAATTATC ATAATAATAA CCGATGGTGT GGTAAATGTT	2700
GGTAAGAGAA ACTTCTGAAA CCAAGCTTCA AAAAAGTCGC TCGTCATCGT CTCTTCGTAA	2760
GTCATTGGAG CGATTAACTC ACCATTCAAT TGTTAGACCT GCAACCAAAG AAATCTCTG	2820
ATATCTTCTT CCAGATACTT TGCCTCTTCT TAACTGACCT TTTAATGAGC GACCATATTC	2880
TCGATAAAAA TAAGTATCGA ATCCTGTTTC GTCAATCTAA ACAGGTGCTA GGTGCTTTAA	2940
ACTATTAAAA TTCTTAAGAA ATAAGGCTAC TTTTCTGGG TCTTGTTTAT AGTAGGTGTA	3000
GTTCTTTTTT TTTTCGAGTG TAGCC	3025

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4104 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TTTAAGGTTT TAAAAAAGT TTTGAAAGG TTTCTTCTTT ATTTTAAAG CGAGAGATAA	60
CGTTGATATC TAAATCGTGG TCAAAGCCGG CAATTTTCC TTTAGATGTG TATTGGTGAA	120
TATCATAATC TAAATCAGTT TTAGGACTGC TCTCCAAAA TCCTGAGTCT GAGCCGTAGA	180
CGGAATCCAA ACAGAGGTAA ACTTGCCTGT ATCAATACTG TGTCTTCCA TGAAGTAGAC	240
ACCAACGTAG ATGCCGATGT TTTTAGCACC CAGTGATGCT AGTTTGTCTC GAAAGTTTTC	300
GACACCTTCG TTCATATTAG ACATGGTTTT GTCTTCCACG TCAAGCCAAT AGTAACTAGG	360
GCTGTAAGGA GAGGCAGCAT TGTAGAAAAC TTCGGCAGCC TTTCCATTT CTTGGACACT	420
TTTTCCAGCT ACATAAGCGT AGACAGCAAC TGGGACATTC CGCTTTTGAA GTTCAGTGAT	480
ATGACTCTTA TAGGCCTTGT CTATTCCATT GATAAATGAA GCATCATTTT CTTTGTCTGT	540
TTGAGCACCA CTGTGAACAC GAACAATAGC ACCTGAAATA TTTGTGAGA GGGCATCGTA	600
GTTGATTTCC TCAGGACGCT GCCAGCCAGA GAGGTCAATA ATCGGTTTGT CTAAGTGTTT	660
CAAAGCCTGT GCTTCAATCT GTGCTATATT GGATTTTGT TTAACGATT GGCTGTCATT	720
AAGTGGCGA TTGATGATTA AAATGAACAT CATAATCCCA AAAAACTAA ATAAATAAG	780
TGGATGAATT TGTTTTCTCA TATCTTATAA TTCTACCCTA AAAATCAAAA AAAATCAAAA	840
AAATGGGTTA AGGAAGAGAC TTTAGAGCAT TTTTTCATTC AAGAGTGCGG AATGATTTGA	900
AATATGGTAT AATAAAAGG AATTCTACA GAAAAGAGAA GATTATGTCA AATTTTGCCA	960
TTATTTTAGC AGCGGGTAAA GGGACTCGCA TGAAATCTGA TTTGCCAAAA GTTTTGACAC	1020
AGGTTGCGGG TATTTCTATG TTGGAACATG TTTTCCGTAG TGTGGGAGCT ATCCAACCTG	1080
AAAAGACAGT AACAGTTGTA GGACACAAGG CAGAATTGGT TGAGGAGGTC TTGGCTGGAC	1140
AGACAGAATT TGTGACTCAA TCTGAACAGT TGGGAACCTG TCATGCAGTT ATGATGACAG	1200
AGCCTATCTT AGAAGGTTTG TCAGGACACA CCTTGGTCAT TGCAGGAGAT ACTCCTTTAA	1260
TCACTGGTGA AAGCTTGAAA AACTTGATTG ATTTCCATAT CAATCATAAA AATGTGGCCA	1320
CTATCTTGAC TGCTGAAACG GATAATCCTT TTGGTTATGG ACGAATTGTT CGTAATGACA	1380
ATGCTGAGGT TCTTCGTATT GTTGAGCAGA AGGATGCTAC AGATTTTGAA AAGCAAATCA	1440
AGGAAATCAA CACTGGAACA TACGTCTTTG ACAACGAGCG TTTGTTTGAG GCTTTGAAAA	1500
ATATCAATAC CAATAACGCT CAAGGCGAAT ACTATATTAC AGACGTCATT GGTATTTTCC	1560

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GTGAACTGG TGAAAAAGTT GCGCTTATA CTTTGAAAGA TTTTGATGAA AGTCTTGGGG	1620
TAAATGACCG TGTGGCGCTT GCGACAGCTG AGTCAGTTAT GCGTCGTCGC ATCAATCATA	1680
AACACATGGT CAACGGTGTT AGCTTTGTCA ATCCAGAAGC AACTTATATC GATATTGATG	1740
TTGAGATTGC TTCGGAAGTT CAAATCGAAG CCAATGTTAC CTTGAAAGGG CAAACGAAAA	1800
TTGGTGCTGA GACTGTTTTG ACAAACGGTA CTTATGTAGT GGACAGCACT ATCGGAGCAG	1860
GAGCGGTCAT TACCAATTCT ATGATTGAGG AAAGTAGTGT TGCAGACGGT GTGATAGTCG	1920
GTCCTTATGC TCACATTCTG CCAAATTCAA GTCTGGGTGC CCAAGTTCAT ATTGGTAACT	1980
TTGTTGAGGT GAAAGGATCT TCAATCGGTG AGAATACCAA GGCTGGTCAT TTGACTTATA	2040
TCGGAACTG TGAAGTGGGA AGCAACGTTA ATTTCCGGTG TGGAACTATT ACAGTCAACT	2100
ATGACGGCAA AAACAAATAC AAGACAGTCA TTGGAAACAA TGTCTTTGTT GGTTCAAATT	2160
CAACCATTAT TGCACCAGTA GAACTTGGTG ACAATTCCCT CGTTGGTGCT GGTTCAACTA	2220
TTACTAAAGA CGTGCCAGCA GATGCTATTG CTATTGGTCG CGGTCGTCAG ATCAATAAAG	2280
ACGAATATGC AACACGTCTT CCTCATCATC CTAAGAACCA GTAGGAGCCT ATCATGGAGT	2340
TTGAAGAAAA AACGCTTAGC CGAAAAGAAA TCTATCAAGG ACCAATATTT AACTGGTCC	2400
AAGATCAGGT TGAATTACCA GAAGGCAAGG GAACTGCCCA ACGGGATTTG ATTTTCCACA	2460
ATGGGGCTGT CTGTGTTTTA GCAGTAACGG ATGAACAAAA ACTTATCTTG GTCAAGCAGT	2520
ACCGCAAAGC TATCGAGGCT GTCTCTTACG AAATTCCAGC CGGAAAATTG GAAGTAGGAG	2580
AAAACACAGC CCCTGTGGCA GCTGCCCTTC GTGAATTAGA GGAAGAAACA GCCTATACAG	2640
GGAAATTAGA ACTCTTGTA CATTMTTATT CAGCTATTGG CTTTTGTAAT GAGAAGTTAA	2700
AACTATATTT AGCAAGCGAT TTGACAAAAG TGGAAAATCC GCGTCCGCAG GATGAGGATG	2760
AAACCTTGGA AGTCCTTGAA GTGAGCTTAG AAGAAGCGAA AGAATTAATC CAATCAGGTC	2820
ATATCTGTGA TGCCAAGACA ATTATGGCTG TTCAGTATTG GGAGTTGCAG AAAAAATAGA	2880
GGAGGTCAGT ATGGGTAAAT CTTTATTAA C GATGAAATG ATTGAAAGAG CTAATAGAGG	2940
CGAAAAAATT TCAGGTCCTC CTTTGCTAGA TGATAATGAG GAACTAAGA TTTTACCAAC	3000
CTCTTCTTCC CGTTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC AGGAAACCTT	3060
GAAGATTCAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA CCAAGAGAAA	3120
TGTCTTCAAT TCTAAGTTGA ATAAAATCTT ATTTGCGGTC ATCTTTCTCT TGATTTTGCT	3180
TGTTTTAGCA ATGAACTTT TGTAATAGAA AAGGAATTGA AATGAAAATA GGAATTATTG	3240
CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATTT AGATAATGCC CAGGAGCAAG	3300

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TTGTTTTTGG GAATACCTAT CATACAGGAA CCATTGCTTC TCATGAAGTC GTTCTTGTAG	3360
AAAGTGGAAT TGGTAAGGTC ATGTCTGCTA TGAGTGTGGC GATTTTGGCT GATCATTTCC	3420
AGGTGGATGC CTTATTAAT ACGGGTTCAG CTGGGGCAGT AGCAGAAGGT ATCGCTGTTG	3480
GGGATGTCGT GATTGCTGAC AAATTAGCCT ATCATGACGT GGATGTCACA GCTTTTGGCT	3540
ATGCTTATGG ACAAATGGCG CAACAACCGC TTTATTTTGA ATCAGACAAA ACCTTTGTTG	3600
CTCAAATCCA AAAGAGTTTA TCTCAATTGG ACCAAAACCTG GCATCTTGGT TTGATTGCTA	3660
CAGGAGATAG TTTTGTGCA GGAAATGACA AGATAGAAGC GATTAAGTCC CATTTCCAG	3720
AAGTTTTAGC CGTGGAGATG GAGGGGGCAG CTATTGCTCA AGCAGCGCAT GCCCTCAATC	3780
TCCCAGTCTT AGTCATCCGA GCTATGAGTG ACAATGCCAA CCATGAAGCA AACATCTTTT	3840
TTGATGAGTT TATTATCGAA GCTGGACGTC GCTCTGCCCA AGTCTTGTG ACCTTTTGA	3900
AGGCTTTAGA TTAAGCGGAA ATTTGACAGT TTTCTAGCT TATGATAAGA TTTAAGTAAA	3960
GAAAAGCTAG AAAACGTTTC AGAGGATATT ATGAGTATTG AAATGACCGT CAGTGAGATT	4020
GCAGAGGTCT TAGGATTATC TCGCCAAGCA ATCAATAACC GTGTCAAAGA ATTACCAGAA	4080
GAAGACACAG ATAAAAATGA CAAG	4104

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CACGGATAGG CTCGGCTTTC ATCAGTCCTC AGGCTGATTT ACTAATAGCA ACTTTCCTCG	60
ACAAAGTCCA CAGCGATACG TnTGGGTATC AATCCTACGC TTACGCTGAT ACCTTTGCTG	120
GCAGGATTGG CAACGATAGA GCTTGATTGG CTTGGAGTTA CTATTGGGCA AGGATGGTAC	180
AAACCGTAAT CCATCCACTG CTTTCAACAG TTCTTAAAA TCCCGATCCT TGTGTTGATA	240
GCCTTTCCTT TGAAAATAGA GGTGATAATG ACAGAGTTCA TGTCGGACAA TTTTCCTAAA	300
AACGTCCAAC CCCAGTTCCT GATAAACCTT GGGATTAAAA TCCAAATGCC CATCTTTGGG	360
GAAAAATCGC CCACCTGTG AACGTAGACG CCTATTCCAC TGGACATGAT GGATAAAAGG	420
TCTGCCGAAG TCTTCTAGTG AAACCTGCTT GACGTAATCA GTCAGTTTCA TTTGGAGCTA	480
GGAGAGACAG ATTAACTTTT TCACGTTTCA TATCAATTTT CTTAACCCAA ACGCTCACCA	540
AATCTCCAAC TGCCACCACT TGACTAGGGT GTTTGATAAA CTTGCGACTC ATATGGGAAA	600

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TATGGATGAG ACCGTCCTCA TGAATTCCGA TATCAACAAA AGCACCGAAA TCAACAACGT	660
TACGCACCAC TCCTTCTAGC TTTTGTCCAA CCACCTAAGTC CTTGATATCT AGGACATCTT	720
GGCGAaCACA GGTGCGTCAA AGGAATCACG GAAATCTCGA CCTGGTTTGA GAAGATCTGC	780
AATGATATCT TTAAGAGTTT CTGGACCAAG GTCTAACTCT TCGGCCATTT CCTTGACTGA	840
AAGCGACTTG AGTTTGCTTT GGGCTTCTTC GTTTAGGTCT TTAATATCTA AACGTTTGAA	900
GAGTTCCTTA ACTGCAGTGT AATTCTCTGG GTGAACTCCT GTATTATCAA GGATATTGCT	960
ACTTTCAGGG ATACGAAGGA AACCAGCAGC CTGCTCAAAG GCCTTGGCTC CCAGACGAGG	1020
AACTTTCTTG ATTTGGGCGC GTGAAGTGAT TTTTCTTCT TCCTCGCGGT ATTTGACAAT	1080
ATTTTCAGAG ATAGTTTGTG TGAGTCCAGC TACGTGTGAA AGAAGAGCTG GGCTAGCTGT	1140
ATTGACATTG ACACCAACTT GGTAAACCAC TGTATCGACA ACAAAGTCCA GACTCTCAGA	1200
TAGTTTCTTC TGACTGACAT CGTGTGGTA TTGACCGACA CCAATTGACT TAGGATCGAT	1260
TTTGACCAAT TCCGCAAGAG GATCTTGCAA ACGACGGGCG ATAGAAATGG CAGAGCGTTT	1320
TTCAACGGTC AAGTCTGGAA ACTCCTGACG AGCAAGTTCT CTGGCAGAAAT AGACAGAAGC	1380
ACCACTTTCA TTAACGATAA CATAGCTGAC TTCAGGGAAA TCTTTCAGAA CTTCCGCTAC	1440
AAAAGCTTCA CTTTCACGAC TGGCCGTTCC ATTTCCAATG GCAATAATCT CTACACCGTA	1500
TTGACCAATT AAATCTGCTA AATCTTCTT GGCTTCTTCG ATTTGACGAG CTGATGCTGG	1560
TTTAACAGGA TAAATAACCT GAGTTGTCAG CATTTTCTCT GTTGATCCA CGACAGCTAG	1620
CTTGGCACCT GTACGAAAGG CTGGGTCAA TCCAAGAACC ACGCGCCCTT TCAGTGGAGC	1680
AACCAAGAGG AGATTGCGCA GATTGTCAGA AAAAAGTTGG ATAGCTCCTT CTTAGCTTTT	1740
CTCAGTTAAT TCTGTCCGAA TACGACGCTC GATAGCAGGC AAGACCTTTT TCTTAACGGA	1800
TTGCTGAACA ACTTCATCAA TATAAGCATT TTTCACCTTG AAACGAGTAG CAAAGAAGGC	1860
AAGAATACGG TCCGTGCGAT GTTCAAAACC GATCTTCAAG ACACCAAGTT TCTCCCCACG	1920
ATTGAGAGCC AAGGTACGAT AGCCTTGAT AGTTCCAAT GTCTCTGAAA AATCATAATA	1980
AATCTGAAAA ACCTGCTTTT CATCAAGACT TTCATCCTTG GCTTGAGAAG TAAGTTTAGA	2040
GTGTCTCAGC ACTTCTGAT AAGTCATAGA ACGCAAGGTC ACATCTTCCG ATAAGGCTTC	2100
GACCAAAATA TCAACTGCAC CGGTCAAGGC TTCCTTGCCA GTCGCAAATC CTTACAGAC	2160
GAACTTTCA GCTTCTTTCT CTAAGTCAAC TATATTCTGC AAAATCAAGC GAGCAAGAGG	2220
AAAGAGTCCA GCTTCACGGG CAATGGTTGC CTTGGTACGA CGCTTTTCTT TATAAGGAAG	2280
ATAGAGTTCT TCAACGTCTG CTAATTTTTC GGCAACTAAG ATAGCTTCTT CCAATTCCTT	2340

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GGTCAACTTA CCTTGTTCTT GAATCTTAGC TAAGACAGCT TCCTTACGGT CATTGAGATT	2400
TGTCAGACTT TTATCCAAAT CAATAATAGC CTTAATCGCC ACCTCATCCA GACTACCAGT	2460
CATGTCCTTG CGATAACGCG CGATAAAGGG AATAGTCGCC CCTTCAGCTG TCAAACCTAG	2520
AACGGTATCA ATTTGCTTTA ACGTCACTCC CAAATCCTGA GAGATTTTTT CATATTTTTT	2580
ATCCATAAAT CTATTATACC ACAAGCTAAA CGTTTCAAAT TAACTCGTAG AACATTTAAA	2640
AAATATGTAG GAAATAGATT TATATGCTAC AGCGCAATAA CTGCACTTA AAGAGCATTG	2700
CCACCTTTTT TTAACCAAGC CATGATATCA AAAGTATTTA ATGGATCAGA CATAATAGCC	2760
AGTTCTGGAA GATGTTCCCTG ACCTGGAATA ACACATTGAC TTTTCAAATT TTTATATGGA	2820
CGATTGACTA AAATTAATTT ATTAGAATAA GGAAGATTAT CCATCTTATT TAAAATTTCT	2880
TCACTAGCTG AATCTTTATT ATCAAATTTA AAATAAAGAT TATTCCAATT TATGCGTTTT	2940
TTTCTTTTTT CCCACTTAGT TCGTGCTTCT TCAATACTAG AATAATGTAG AAAATGAATA	3000
TCTATATCTC CTAAGTGCCC CAAAGGATAA ACTTCATGAG TCCAGCTCGG TGAAATAAGT	3060
TCCTCTTCGA AAACAAGTTC TTGTTCCATA TAATAACGAA AATGCTTTGT AAGTTTATAA	3120
TAATCATCAG GAAGAATRAA TAAACCAACA AAAGGTGTTT TATATTGAAA ACCAAGCTGT	3180
TTATAAATTA ATCCTCCAAC ACAATTATTA CTTATAATCG TAAAATCTAA TCTATCAAGC	3240
TCAAGAAAAG GGAAAATTCC TTTCTCTGCA GCTATTAACT TATGATAAAC AATATCAGAA	3300
TCTAAATATT CACCGTCATT TTTTAACCAA GCACTAAAAT TTGCCAATTC TTGAATATAT	3360
TGTTTTTTTCG CTCTTTCTAT ATCATAGTTT TCTAAGACGG CGCAATCTTT GATTCTATTT	3420
TCATAATTTT CTAATATGAT TTTGTAGGAG TCTTTTAGAG GTTTAGCATC TATAACAGGT	3480
TTATAGATAT ATGTCGGGAA ATTAATATAG GTTGCAGTTT TAGAGTGAAT ATAAAGTCTC	3540
CAAATAAGGT TGTTTATATC AAATTGATTT ATTTTTCGTA AAAGCTTACT ATTGAATAAT	3600
TTTCCAAATA ATGAGCGATA TTGTTTTCTA ATTCGATGAT CTGTATCATC CATCTTTTGT	3660
AAAACCTGAA CATTCGTTAA ATTTTCTGTC AACCAATTAT CCCCCAAAA AGGATAAAAG	3720
TAAAATACTC CATCAACCAA ATCAGCAAAA TGACCAAGAA CAACATCAGA ATCGGATAAT	3780
TTTATCGCAT GATACATCTT TTCAAATGTC CAATCAAATA ATGAATCATT TGAAGATAGA	3840
AACGTAATAT AATCTCCTGT AATCATATCA GACAACTCAG CAAAAGAATT CTCATCTATA	3900
ATCTTAATAT TAAATGATAG ATTCATCTGT TGGCTAATGG AAGCTATCTC CTCTGTAGAT	3960
TGATTTACAA TAATAACTTC TATATCTTTT AATGTTTGTC TCTCCACTAT TGACAAAGAC	4020
TCTAATAAAC TATTTTATC TCCTTGATGT AACAAAACAA CACTAATTGA GTAAGTCAGT	4080
TTGACTACCT CCCATAATTT TCTGATAATG ATTTTCTTTT TATTTAATTA TAGCACAATT	4140

1083

ATGATATATA TCAGGTAATA TCAAGCTATA TTATCTCTTA GCTACTCAAT TTGAAATTTT	4200
AACTTTTCCC TTTTCCGCAA AATAATAGTA TAATAGAGGT AGAATCTAGA ATCGAGGTAC	4260
ACCTATGGCT GTCAAATTTA CAAAACGAGA CGACTTGGAC AAGATGTTTG AAGAGTTTGC	4320
TAAACTCCCT GATTTGAAAC AAGTTACTTT CCCTGATGAC AAAGAGAAAA AAGTCAAAGC	4380
AGAAAAGAAA AACTAGATGA CTGCTTTTCA ACAACTCCCA TCTAGTGTAC TTCAAAC TGG	4440
AGCCATTTTT CTCTCCATTA TCATTGAAGC CCTTCCCTTC GTTCTGATAG GAAGCATTGT	4500
CTCAGGGCTG ATTGAAGTTT ATATCACACC TGACAAGGTT TATCATTTTC TCCCTCGAAA	4560
TCGTTGGGGG AGAATCTTTT TTGGGACCTT TGTCGGTATA CTTTTCCCTT CTTGTGAATG	4620
TGGAATCGTC CCCATCATCA ATCGTTTCTT GGAAAAAAG GTTCCAAGTT ACACGGCCGT	4680
TCCTTTTCTT GTGACAGCAC CTGTTATCAA TCCCATTGTT CTTTTGCGA CCTATTCTGC	4740
CTTTGGCAAC TCCTCCATG TCGCCCTATT ACGAGCTCTG GGTTCCATTC TTGTGGCTGT	4800
AATACTAGGA ATTTTCTAG GATTTTCTG GCAAGAACCG ATTCAGAAAG AAAATCGTCT	4860
GGCTTGTCAT GAGCATGATT TTTCTTACTT GAGTTCTGCA AAAAAAGTTT TTCAAGTCTT	4920
TGTGCAGGCC ATTGATGAAT TTTTGTATAC GGGGCGTTAT TTGGTATTTG GCTGCCTCTT	4980
TGCTTCTATA ATACAGGTCT ACGTTCCGAC TCGGATTCTG ACCTCTATCA GTCCGACCCC	5040
TCTTTTGGC ATCCTGCTCT TGATGATTTT AGCCTTTCTT CTTTCGCTCT GTAGTGAGGC	5100
GGATGCCTTT ATAGGTGCTT CTCTTCTCTC GAGTTTCGGT TTGGCACCAG TTCTGGCCTT	5160
TCTCGTCATT GGTCCAATGC TGGATATCAA AAATATTCTC ATGATGAAAA ATTACTTGAA	5220
AGCACGATTT ATCAGTCACT TCATAACAAT TGTAACCTCT GTCGTCTTAG TCTATTCTCT	5280
CTTGATTGGA GTTATCCTAT GATTTCGATT TTAGTTTATG CTGGCTATTT TGAAC TGA	5340
ATTACCTCC ATCTGTGGG CAACTAAAC CAGTACATCA ACATGCACTA TTCCTATCTG	5400
GCCTATATCT CCATGGTGCT TTCTTTTATC TTGGCTATCG TTCAATTGTA TATCTGGATG	5460
AAGCAAGTCA AAACCCACAG TCATCTGAAC AGCCGATTAG CCAAGATAAC GAGTATTTCT	5520
CTTCTGGCTA TTCCACTTGT CATCGGCTTA ACTTTCCCAA CTGTTAGCTT GGATTCTCAG	5580
ACTGTTTCTG CTAAAGGTTA TCATTTCCCC CTATCGGAAG GAACGGATCT AGCCATT CAG	5640
ACAAGCGAAG GGACGACAAG CCAATATTTG AAACCAGATA CCAGTTCTTA TTTTCAAAA	5700
TCAGCCTATG AAAAGGAAAT GCGAACGGCG GCGGATAAAT ACTTATCCCA AGATAGTATT	5760
CAGATCACTA ATGAAAATA TATGGAAGTC ATGGAGGCTA TCTACGACTA TCCAGATGAG	5820
TTTGAGGGCA AGACAATCCA GTTTACAGGC TTTGTCTATA ACGACCCAG TCATGCCAAT	5880

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AGTCAATTTTC TGTTCGATT CGGCATTATC CACTGTATCG CAGATTCTGG TGTCTATGGA	5940
TTGCTGACCA AGGGCAATAC CCGGCAGTAT GAAAACAACA CTTGGATAAC AGCCAAAGGA	6000
AAACTGGTCA ATCACTACCA TAAAGAACTC AAACAAAACC TTCCAACCTT GGAAATCGAC	6060
AGCTTTACCA AAGTCGATAA ACCAGAAAAT CCCTATGTAT ATAGAGCTTT TTAAGAAAAT	6120
CAAGATAAAA ACGAACAAGT TCTCTTCTGA ATAACAGAAA AAGAGCCTGT TCGTTTTTTG	6180
TTATATGAAA ATTAGTGAAT TGTAGATTTT CATCTTATAC CATTCCCAGC AATACAAGTA	6240
GCTCATAGAA AATAAGCGAG CCACTCATTC ATTAGACTAG CGATTTCTTT AGGTGCTTGA	6300
GTATAAAGCT CATGGCCAAA GTTTTCTAAA AAAATAGTAT CAAAATAGTC TGGCAATTCT	6360
TTTAGGGCTT CCTCTCTCCA TGTAGCTTCA TTAGGATAGC GAGGACTAAT AAACAAGGTA	6420
TCTCCCACTT CTCTCTTAAA AGCTTGATTT TTTCTCCGTA GCGGAGTATC GCTTCTATAT	6480
TTTCATAATT TATAGCCAAC TCATATCTAT TATACTCAAC ATTCCAGTGA TAAGACTGTC	6540
TTACAGCTTT CTCCATATTT TCTGACCAAT GCTTTGCTTC AGATTTTCTT TTAGAAGTAA	6600
GAACATCTAA GTCCGAAACA ATTTGAGATT TGATATAATT TTTAGTTTCC TCTAACTCTG	6660
TATCCAAAGG TAAAATCTTA TCTAAATCTA GATAGCCACC ATCCAAAAGA ATCAGTTTCT	6720
TTACTTCTTC AAATTCGGAT GCGAAATAAC GAGCTAAATC TCCTCCAAGA GAATGGCCTA	6780
TCAGACAGAT AGATTCTTCC TCTACAATTT CATTTTTAAA CCATGATTTT AATTCTGTTT	6840
CATCTCGAAG ATGCTTTTCA TATGGATTTA GAAAATAGAC CTGCGAATCT AGTTCTTGAA	6900
GAAAATCCTT GCTATGATAG GCATTGCTTC CCAAACCGCC AATAAAATAT TTTTTCATTC	6960
TCTACTTAAT ACTATGCTTA TTCATCTTTT GTTCAAAGAT AGTTGTGATA ATCTGACGCA	7020
ATTCTTCGCG TTTTPTTCTT GGAATCTCAC CACTTGTGTT AGCTACAGCG TAGAGTTCAG	7080
GGTATTCAAT TGAAATGCGT TTAATCGTAC GTGTTGTAGC ATGTTTTCTG ACAAAAAACG	7140
GGATTGCTT AATCAAGTCT TGTGGGACTA GCGCCAGAAT CTCTCAGTA GTTCTTTGT	7200
CACTAATATT AGACATTGTA AGCCTTTTCT TAATCATTTT CTGTTCTTTT TCTGTAAAAT	7260
CTTTTAATTC CATTCGATTA GTCCTCTAT TTTCTCTAAG TTAAATTATG TACTAATACA	7320
GATGAACTA CAAAGAATAA ACTTTAAGAA ATCTTCTCAC TGATAAGATT TTAGCATTAG	7380
ACTTCCTGCG AAACAAAATA TGGTATAGTA GTTCTATGAA TTATGAAGCA AGTAAACAAC	7440
TAACTGATGC ACGATTAAA CGTCTTGTG GTGTTGAGC CACGACTTTT GAAGAGATAT	7500
TAGCTGTATT AAAACAGCT TATCAACTTA AACACGCAA AGGTGGACGA AAACCTAAAT	7560
TAAGCCTAGA AGACCTTCTT ATGGCCACTC TTCAATATGT GCGAGAATAC CGCACTTATG	7620
AAGAAATTGC GGCTGATTTT GGTATTCACG AAAGCAACTT AATCCGTCGG AGCCAATGGG	7680



1085

TTTAAGTAAC TCTTGTTCAA AGTGGTGTTA CGATTTCAAG AACTCCTCTC AGTTCTGAGG	7740
ACACGGTAAT GATTGATAGC CATTCCCATC AATATCGTAT CTTTGGACAT AGCCAATAAA	7800
TGTTTCATTT TTGCGTGGTT TCTGGCTATT AACGATTGAA ATAACCCACC AACTTATCAA	7860
AAATAGAAAT AAAATCCTA AGATTACTGT CATATCATAA CACTATTAAA GTTTAACCCA	7920
CTTATCATT TCCATGATAA AAGGCTTAGC CAGTCCCTCG CCTGTATAAT CCGCATACTT	7980
GGTGCCCAA TACTTGTAGC AATCTTCCTT ACTAGCAAAT TTAATCGCTT GGTAGGGCTC	8040
TTCGAAAGTC AATTTCTCTA CAAATAAGAA ACCGTCATCA GCAGGTACTA AGACCCCAAC	8100
GTGGCCTACA AACAGATACT CGCCATCCAA ATTGTCTGTC AAGACTACAG ACAGCATTCG	8160
AGCTTTTTC TGAATTGAA ATTGTGAGAA GAATGCTTCC ATCTTTTCAG CGTGAACCTT	8220
GACATCTGTA GTTGACTCAG TTGGAACCTC CGAAAATAGA ATATCAAACCT CTCCTTATC	8280
TTGTGAATCA AAGACCTTTC CTTTATCAAT CGCATCATT TCTAGGAAAA GCAACTGGTC	8340
ATTCTTTTCA AGCTTTGGAA TGGTGACTGA ATTTTTCAAA AGACAATAAC TATTGATACG	8400
GCAGTTGGTC CCAACAAAAT CGCCCTTCTT TTGATTCCAG AGATGACTGA TTTTCTCAAC	8460
ATCGTATTCG GTGTGAGTAA AGGAAGTGAA ATCTCCTGAT AAGCCAGTTG AGCCGACAAT	8520
GGTATTATAG TCATTAACGA GATTAAAAAA TGCATCAACA CTATTTGGAT CCAAGTGAGC	8580
TGATAAGAGA GATTGACCT CTTCTGTACT TACCTGGTTG TTTAGGTTGG TGTATGAAGC	8640
TTTCCATGGA ACTTTCGCTG AACTGCTTTG CCTTTGATTC GTCCCTCAG AAGTAGCATG	8700
TTGTTGTTGA CAAGCAGCCA AGCCTAAAAA CAAGGCTGAA CAGATTCCTA ATGTGGCTAA	8760
TTTTCTTGAT TTCTTCATTT CTTTCTCCTA AATGTCTTGG ATTAAAGTTT CTTTAACTAT	8820
TGCTTTACAG ATATTGATTA CTTTCTCATT TAATGTGTTT ATCGTCTTTC CTCCGG	8876

## (2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14736 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

CGCAAACCTT CGCGGTCGGA AGGTAGTTTT ATGACACGAT TTGAGATACG AGATGATTTT	60
TATCTCGATG GAAAATCATT TAAGATTTTA TCTGGTGCCA TTCATTATTT TAGGGTTCCT	120
CCAGAGGATT GGTATCATTC GCTCTATAAC TTGAAGGCTC TTGGTTTAA TACGGTAGAG	180

1086

ACTTATGTTG CTTGGAATTT ACACGAGCCT TGTGAAGGTG AGTTTCATTT TGAAGGTGAT	240
CTGGATTAG AGAAATTTCT CCAAATAGCG CAGGATTTGG GTCTCTACGC AATTGTGCGT	300
CCGTCTCCAT TTATCTGTGC GGAATGGGAA TTCGGTGGCT TACCAGCTTG GCTCTTGACC	360
AAGAACATGC GAATTCGCTC ATCCGACCCA GCATATATCG AGGCAGTTGG TCGCTACTAT	420
GATCAGTTAT TGCCAAGACT GGTGCCTCGT TTGTTGGACA ATGGTGGCAA TATTCTCATG	480
ATGCAGGTTG AAAATGAGTA TGGTTCTTAC GGAGAAGATA AGGCTTACCT GAGAGCGATT	540
CGACAGCTAA TGGAAGAGTG TGGCGTAACC TGTCCCCTCT TTACATCAGA TGGTCCATGG	600
CGAGCTACTC TGAAAGCTGG AACCTTAATT GAAGAGGACC TCTTTGTAAC AGGAAACTTT	660
GGTTCTAAGG CACCTTACAA CTTTTCGCAG ATGCAGGAAT TCTTTGATGA ACATGGTAAG	720
AAATGGCCAC TCATGTGTAT GGAGTTCTGG GATGGTTGGT TCAATCGCTG GAAAGAACCG	780
ATTATCACAC GGGATCCTAA GGAATTGGCA GATGCAGTTC GAGAGGTTTT GGAACAAGGC	840
TCTATCAATC TTTACATGTT CCACGGTGGT ACAAACCTTG GTTTCATGAA TGGTTGCTCA	900
GCTCGAGGAA CTTTGGACCT GCCACAAGTT ACGTCTTATG ATTACGATGC CCTTCTGGAT	960
GAAGAAGGAA ATCCAACTGC TAAATATCTT GCAGTCAAGA AGATGATGGC AACACATTTT	1020
TCAGAGTATC CGCAGTTGGA ACCACTCTAC AAAGAGAGTA TGGAGTTGGA TGCTATTCCA	1080
CTAGTTGAAA AAGTTTCTTT GTTTGAAACC TTAGATAGCT TGTCAAGTCC TGTAGAAAGT	1140
CTCTATCCTC AAAAGATGGA GGAGCTGGGA CAAAGTTATG GCTACCTACT TTATCGAACA	1200
GAAACAACT GGGATGCAGA AGAAGAAAGA CTTCTGATCA TTGATGGTCG AGATAGGGCC	1260
CAGCTGTATG TCGATGGTCA GTGGGTAAAA ACTCAATATC AGACAGAGAT TGGGGAAGAT	1320
ATTTTTTATC AAGGTAAAAA GAAAGGGCTA TCTAGGTTAG ATATCTTGAT AGAAAATATG	1380
GGGCGTGTCA ACTATGGGCA TAAGTTCTTA GCGGATACGC AACGTAAGGG AATTGGGACA	1440
GGGGTCTGTA AGGATCTGCA TTTCTTACTA AACTGGAAAC ACTATCCACT CCCACTAGAC	1500
AATCCTGAGA AAATTGATTT TTCAAAAGGA TGGACTCAAG GACAACCAGC CTTTTACGCT	1560
TATGACTTTA CAGTCGAAGA GCCAAAAGAT ACTTACCTAG ACTTGTCTGA GTTTGGTAAG	1620
GGGGTTGCCT TTGTCAATGG GCAGAATCTA GGACGTTTTT GGAACGTTGG CCCAACTCTC	1680
TCACTTTATA TCCCTCATAG CTATCTCAAG GAAGGTGCCA ACCGCATCAT TATCTTTGAA	1740
ACAGAAGGTC AATATAAAGA AGAGATTCAT TTAACCTGTA AACCTACACT AAAACATATA	1800
AAGGGGAAA ACTTATGACA ATTGTAGGAT GCCGTATTGA TGGACGTTTG ATCCACGGAC	1860
AAGTAGCCAA TCTTTGGGCT GGAAACTAA ATGTTTCACG CATTATGGTT GTAGACGACG	1920
AAGTTGTCAA CAACGATATT GAAAAGAGTG GTTTGAAACT TGCGACACCA CCAGGTGTGA	1980

1087

AATTGAGTAT TTTGCCAGTT GAGAAAGCTG CAGCCAATAT TCTTGGTGGC AAATACGATA	2040
GCCAACGTCT CTTTATCGTG GCTCGTAAAC CAGACCGCTT CCTTGGTTTG GTAGAAGCAG	2100
GTGTACCACT TGAAACCCTT AATGTTGGGA ATATGTCTCA AACACCAGAA ACTCGTTCTA	2160
TTACACGTTT TATCAACGTA GTAGACAAGG ATGTGGAAGA CTTCCACAAA CTGGCAGAAA	2220
AAGGTGTTAA ACTTACTGCT CAGATGGTTC CAAATGATCC AATTTAGAC TTTTGTAGCT	2280
TATTAATAA GGAAAAAAT TTTTAGGAGG TCATTGTTAT GATACAATGG TGGCAAATTT	2340
TACTTCTCAC TTTGTACTCA GCTTATCAAA TCTGTGATGA GTTGACGATC GTTTCATCTG	2400
CAGGTTCCTT TGTATTTGCT GGTTCATTA CTGGTTTAAT CATGGGAGAT GTGACTACTG	2460
GTTTACTTAT CGGTGGTAAC TTGCAACTGT TCGTTCTTGG GGTGGTACC TTCGGTGGTG	2520
CTTCTCGTAT CGACGCAACT TCTGGTGCGG TTCTTGCGAC ACCTTCTCTG TTTTACAAGG	2580
AATTGATGCA CCGCTTGCCA TTAACAAT CGCTGTACCA GTAGCAGCTC TCTTGACTTA	2640
CTTCGACGTT CTTGGTCGTA TGAATACTAC CTCTTCGCT CACCGTGTGG ATGCTGCAAT	2700
CGAACGCTTT GACTATAAAG GTATTGAACG CAACTACTTG CTTGGTGCGA TTCCGTGGGC	2760
TCTATCTCGT GCCCTTCCAG TCTTCTTTGC CTTGCTTTT GGTGGTGCCT TTGTACAATC	2820
AGTAGTAGAC TTCGTTGAAG CCTACAAATG GGTGCAGAT GGCTTGACAC TTGCAGGACG	2880
TATGCTTCCA GGTCTTGAT TTGCAATCTT GCTTCGTTAC CTTCCAGTTA AACGTAACCT	2940
TCACTACCTT GCTATGGGAT TTGGTTTGAC AGCTATGTTG ACTGTTCTTT ACTCATATGT	3000
AACAGGTCTT GGTGGCGCTG TTGCTGGTAT CGTAGGTACT CTTCTGCTG AAGTTGCTGA	3060
AAAAATTGGT TTCGTGAACA ACTTCAAAGG TTTGTCTATG ATTGGTATTT CTATCGTAGG	3120
TATTTTCTT GCAGTGCTTC ACTTCAAAAA TAGCCAAAAA GTAGCTGTAG CAGCACCTTC	3180
TACACCATCA GAAAGTGGGG AAATCGAAGA TGACGAATTC TAATTACAAA CTTACAAAAG	3240
AAGATTTTAA TCAAATCAAC AAACGTAGCT TGTTTACTTT CCAATTAGGT TGGAACCTACG	3300
AACGTATGCA AGCTTCTGGT TACCTTTACA TGATCTTGCC TCAGTTGCGT AAAATGTATG	3360
GTGATGGAAC TCCTGAATTG AAAGAAATGA TGAAAGTTCA TACTCAATTC TTCAATACTT	3420
CACCATCTT CCATACCATT ATCGCTGGTT TTGACCTTGC CATGGAAGAA AAAGATGGTG	3480
TAGGTTCAAA AGACGCCGTT AACGGTATCA AGACAGGTTT GATGGGACCA TTCGCTCCTC	3540
TTGGGGATAC AATCTTTGGT TCACTTGATC CTGCTATCAT GGGGTCAGTC GCAGCAACTA	3600
TGGCTATCGC TGGCCAACCT TGGGGGATCT TCCTTTGGAT TGCAGTTGCA GTAGCGTATG	3660
ACATCTTCCG TTGGAACAG TTGGAATTTG CTTACAAAGA AGGGGTTAAC CTTATCAACA	3720

1088

ACATGCAAAG	TACCTTGACA	GCTTTGATTG	ACGCTGCATC	TGTACTTGGT	GTCTTCATGA	3780
TGGGTGCTCT	TGTAGCAACA	GTGATTAACT	TTGAAATTTT	TTACAAGTTG	CCAATCGGTG	3840
AAAAGATGAT	TGATTTCCAA	GACATCTTGA	ACCAAATCTT	CCCACGTTTG	CTTCCAGCAA	3900
TCTTTACTGC	CTTTATCTTC	TGGTTGCTTG	GTAAGAAAGG	TATGAACTCT	ACTAAAGCTA	3960
TCGGTATTAT	TATCGTACTT	GCTTTGGCTC	TTTCTGCCCT	TGGTCACTTT	GCACTTGGAA	4020
TGTAATTCCT	TATGACTAAA	TCATTAATTT	TGGTGAGCCA	TGGTCGCTTC	TGTGAGGAGC	4080
TTAGAGGTAG	CACAGAAATG	ATTATGGGCC	CACAAGACAA	CATTTACACA	GTAGCTCTTC	4140
TTCCAGAAGA	TGGCCCAGAA	GAATTTACTG	CTAAATTTGA	AGCTGTTATT	GAAGGATTGG	4200
ATGATTTTCCT	AGTCTTTGCG	GATCTTCTCG	GTGGGACACC	TTGTAATGTG	GTGAGTCGCT	4260
TGATCATGGA	AGGTCGTGAT	ATTGACCTTT	ACGCAGGGAT	GAATCTTCCA	ATGGTGATTG	4320
AATTTATCAA	TGCGAGCCTT	ACAGGCGCAG	ATGCGGACTA	CAAGAGCCGT	GCTGCAGAAA	4380
GCATTGTGAA	AGTTAATGAC	CTGTTAGCGG	GCTTCGATGA	TGACGAAGAT	GAATAATACT	4440
CTTCGAAAAT	CTCTTCAAAC	TACGTCAACG	TCGCCTTGCC	GTAGGTATAT	GTTACTGACT	4500
TCGTCAGTCT	TATCCGGCAA	CCTCAAAACG	GTGTTTTGAG	CTGACTTCGT	CAGTCTTATC	4560
CGGCAACCTC	AAAGCAGTGC	TTTGAGCAGC	CTGCGGCTAG	TTTCTACAG	ATTTTAGTTG	4620
GAATCGATT	CAATTCATGT	GACAACGTGA	AAATCGTTAG	AGCATTTTAT	ATAGAATATA	4680
CATGGGAATG	TAGCTTACTC	CCATTCCCAT	ATTTAATAGA	AAAAGAGGAA	CTCAATGCTA	4740
CATTATACAA	AAGAAGACTT	GCTCGAATTG	GGTGACAGAA	TCACTACCGG	TGAAATCTAC	4800
CAACAGCCTG	ATGTATGGAG	AGAAGCTTTT	GAATTTTATC	AAGCAAAACG	TGAAGAAATT	4860
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GCTGGGACTT	CTGCTTATGT	GGGAGATACC	TTGCTACCTT	ATTTTAAGGA	AGTCTATGAC	4980
GAACGCAAAT	GGAATTTCAA	TGCTATTGCG	ACAACAGATA	TCGTTGCCAA	TCCAGCAACC	5040
TATTTGAAAA	AAGATGTGGC	AACTGTCCTT	GTGTCTTTTG	CTCGTAGTGG	GAATTCGCCT	5100
GAAAGTTTGG	CGACTGTTGA	TTGGGCCAAA	TCCTTGGTGG	ATGAGCTTTA	TCAAGTGACG	5160
ATTACTTGTG	CAGCAGATGG	TAAATTGGCT	CTTCAAGCTC	ACGGTGATGA	TCGTAATCTC	5220
TTGCTCTTGC	AACCAGCTGT	CTCTAATGAT	GCTGGATTTG	CCATGACTTC	TAGCTTTACG	5280
TCTATGATGT	TGACAACTCT	CTTGGTCTTT	GATCCTACAG	AATTTGCTGT	TAAGTCTGAA	5340
CGTTTGAAG	TTGTATCTAG	TCTTGCCCGT	AAAGTTTGTG	ACAAGGCAGA	AGATGTCAAA	5400
GAGCTCGTTG	ATTTAGACTT	TAACCGTGTC	ATCTATCTAG	GCGCTGGTCC	TTTCTTTGGA	5460
CTTGCTCATG	AAGCTCAGCT	CAAGATTTTG	GAATTAAGTG	CTGGTCAAGT	TGCGACCATG	5520

1089

TATGAAAGCC CAGTTGGCTT CCGTCACGGT CCAAAATCTC TTATCAACGA CAATACAGTT	5580
GTTTTGGTCT TTGGTACAAC GACAGACTAC ACTCGTAAGT ACGACTTGGA CTTGGTTCGT	5640
GAAGTTGCTG GTGACCAGAT TGCTCGTCGT GTTGTGCTTT TGACTGATCA AGCTTTTGGT	5700
CTTGAAAATG TCAAAGAAGT GGCCCTTGGT TGTGGCGGTG TCTTGAATGA TATTTACCGT	5760
GTCTTCCCTT ACATCGTTTA TGCCCAACTC TTTGCTTTAT TGACTTCACT CAAGGTAGAA	5820
AATAAACCAAG ATACACCGTC TCCTACAGGT ACAGTAAACC GTGTAGTACA AGGTGTCATA	5880
ATTCACGAAT ATCAAAAGTA AGACAGTGTT TATGAATTCT TGACAAGAGG ATTTGTAAAT	5940
TATCAGATAA ACCATAGATT GTCAGTACGC TTTCTATGGT TTGTTTGCTT GAGAGAAATA	6000
GTAAAAGGAG AACAGAATGA AAGCATACAC AGAGCGTGTA TTTGGAAATG TTGAGGGTGA	6060
GGATGTCTTG GCCTATCGAT TTGAGACAGA CGGTGGCTAC CAACTTGAGG TTATGACTTA	6120
TGGTGCGACT ATCTTGCGCT ATGTGCGACC TGACAAGGCT GGAAATTTTG CCAATGTTAT	6180
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AGGTCCTGTA GCGGGTCGTA TTGCAGGTGC GACCTTTGAG CTCAATGGTA AGACCTATGA	6300
CCTTGAGGTT AATAATGCTA GCAACTGTAA TCACAGTGGT TCAACTGGTT GGGATTCCAG	6360
CTTGTTTGAA GTTGAAGAAG TAAGCGATCA TGGCTTGACT CTCTACACAG AGCGTACAGA	6420
TGGGACAGGA GGGTTCCCTG GAAATCTCAA GATTTGGATC AGTTATCACT TGGAAGAAAC	6480
TGGTGCCTAT GAAATCAGCT ACAAGGTAAC GACCGATCAG GATACGCTGG TCAATCCAAC	6540
CAACCACAGC TATTTCAACT TGTCTGGTGA TTTACGCGAG ACGATTGACC GTCATGTCTT	6600
CCAACTAAAC ACAGAGGGCA TTTACTCAAT CGCTCCTGAC GGTGTTCCCTG CCAAACTCC	6660
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TGCAGAAGAA GATGAGCAAA TCCAGCTGGC ATCAGGTTTG GATCATCCAT TTGCCCTTCC	6780
TGCAGGCCAT GACAATGCTG GATTCCTTTA TGACCAAAAT TCAGGTCGCT TCCTGCTTTT	6840
CAAGACAGAA GCTCCTTGCT TTGTGGTCTA CACAGCAAAC TTTGTGGATG AAAGTGTCAT	6900
CATAGGAGGT CAGCCAATGC TACAGCACAA TGGGATTGCT CTTGAAGCGC AAGCTTTACC	6960
AGATGCCATT CACAGTGACC TTAAAGGCCA AGTCATTCTT AAAGCTGGTC AAACCTTCAC	7020
CAGTAAGACA CGTTATGAAC TTGTTGTGAA GTAAAAGAGT CATTCGCCCT ACTTTTGGGA	7080
GCTAGGAATA GGTACGCAGA GACAAATAGT AGGAAAATAT GATATAACTA AGCGTTGAAA	7140
GCTATCTGTT AATATAATAT TCAAAC TACA ATAAGGAGTA AGAAAGAAAC GAAGAAAATT	7200
GTATTTGCTA GTGCCCTGGC TTTGACCTTG GCTGGAGCAG TTTTGACAAA TGATGTTTTT	7260

1090

GCGAACGACA GACTTGTGGC AACACAACT ACTGATGGTA AAAATGAAA TGTATTGACC	7320
TCAGAGGTGC TAAAACCTTC TAGTGGCAAT GTTTTGGTTG GAATCAAAGG AGAATTTGTG	7380
GCTCCTCATC AACAATCTAT TTGGATGCC ATCAATGCTA TCTGTAAAGA AGCGGCTGAC	7440
GAAGGTTTGG TAGATAAGTA TGTCCCTATC AAATGATCAA CTGACCTAGA AAAGGCAGCT	7500
TTTGCCAGAG CTACAGAAGC ATCTATAACC ATGGATCATA CCCGTCTTTC TAGCAAAGAT	7560
CTTTGGAGTG CCTTTCCAAC TTCTAATAGT ATAATGGGAG AAAATTTGGC ATGGAATCAT	7620
GACGGTTTTTC TAAAAGCTAT TGAACAATGG CGTGCTGAAA AAGCAGATTA TGTGGAGAAA	7680
AAAATAGTGG TTCAGACAAC GGGAAATCTG GTCACATGA GTCGCTAATT AACCTAAAT	7740
TTACACACAT GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA	7800
TTGCTCAAAC TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG	7860
CTGTTCACTG TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAACT AAAGCTACGG	7920
TTGTAGAAAA ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG	7980
AATCTAATGG TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA	8040
CAGATGGTAA ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAT	8100
TTTCTGGTAG CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTACAGGC TGGGGAACAG	8160
ATGGTAGCAG ATGGTTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG	8220
AAAATGGCAC TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG	8280
TCGGACCACA CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC	8340
CAGATGGTTA CCGTGTAAT GGTAAATGGT AATGGGTAAA CTAGGCTCAG GCCATAGGTA	8400
AAGCATTCAT CTTACTTAGC AAAAGAATG AACGATAAGA AAGAGGTGA TGGCGAACAT	8460
TGGCCTCTTT TGATTTATAA AGATTGGATT CTTGTGCCT CAATTTTCTATT	8520
GTAAGCTAAT ATTTTATAGC CCATTAAAAG CATAAGCGGT AATCTAATTT AAAAAATGCT	8580
GTAATTAGTC TGAAGTCCAC ACTTACTTGT TGAGATGTTA TCTCTGTTTT TTATCGTTA?	8640
AATTTACTGT ATTTTTTATA GTATGCAGAA TATTTTTAAG TATATTTCAA TAGAAATTC	8700
TATCGATTTA TTGTATAATG ATAAGTAATT GTTGAAAAGT ACTCAGAAAA TTCCATACTA	8760
TATTATTTTT ATGTTTATAC TTTTATGCTA TAAAATATAG ATTGATATAA AGAATATAGA	8820
AAAAGCGAGG TTAATATGAG CCGAAAAAGC ATTGGTGAGA AACGCCATAG TTTCTCGATG	8880
AGAAAGTTGT CAGTGGGATT GGTATCAGTT ACTGTATCTA GTTTCTTTTT GATGAGTCAA	8940
GGGATTCAAT CCGTATCGGC CGATAATATG GAAAGTCCAA TTCATTATAA GTATATGACC	9000
GAGGGTAAAT TGACAGACGA GGAAAAATCC TTGCTGGTAG AGGCCCTTCC ACAACTGGCT	9060

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GAAGAATCAG ATGATACTTA TTACTTGGTT TATAGATCTC AACAGTTTTT ACCGAATACA	9120
GGTTTTAACC CAACTGTTGG TACTTTCCTT TTTACTGCAG GATTGAGCTT GTTAGTTTTA	9180
TTGGTTTCTA AAAGGGAAAA TGGAAAGAAA CGACTTGTTC ATTTTCTGCT GTTGACTAGC	9240
ATGGGAGTTC AATTGTTGCC GGCCAGTGCT TTTGGGTTGA CCAGCCAGAT TTTATCTGCC	9300
TATAATAGTC AGCTTCTAT CGGAGTCGGG GAACATTTAC CAGAGCCTCT GAAAATCGAA	9360
GGTTATCAAT ATATTGGTTA TATCAAACT AAGAAACAGG ATAATACAGA GCTTCAAGG	9420
ACAGTTGATG GGAAATACTC TGCTCAAAGA GATAGTCAAC CAAACTCTAC AAAAACATCA	9480
GATGTAGTTC ATTCAGCTGA TTTAGAATGG AACCAAGGAC AGGGGAAGGT TAGTTTACAA	9540
GGTGAAGCAT CAGGGGATGA TGGACTTTCA GAAAAATCTT CTATAGCAGC AGACAATCTA	9600
TCTTCTAATG ATTCATTTCG AAGTCAAGTT GAGCAGAATC CGGATCACAA AGGAGAATCT	9660
GTAGTTCGAC CAACAGTGCC AGAACAAGGA AATCCTGTGT CTGCTACAAC GGTGCAGAGT	9720
GCGGAAGAGG AAGTATTGGC GACGACAAAT GATCGACCAG AGTATAAACT TCCATTGGAA	9780
ACCAAAGGCA CGCAAGAACC CGGTCATGAG GGTGAAGCCG CAGTCCGTGA AGACTTACCA	9840
GTCTACACTA AGCCACTAGA AACCAAAGGT ACACAAGGAC CCGGACATGA AGGTGAAGCT	9900
GCAGTTCGCG AGGAAGAACC AGCTTACACA GAACCGTTAG CAACGAAAGG CACGCAAGAG	9960
CCAGGTCATG AGGGCAAAGC TACAGTCCGC GAAGAGACTC TAGAGTACAC GGAACCGGTA	10020
GCGACAAAAG GCACACAAGA ACCCGAACAT GAGGGCGAAG CCGCAGTAGA AGAAGAACTT	10080
CCGGCTTTAG AGGTCACTAC ACGAAATAGA ACGGAAATCC AGAATATTCC TTATACAACA	10140
GAAGAAATTC AGGATCCAAC ACTTCTGAAA AATCGTCGTA AGATTGAACG ACAAGGGCAA	10200
GCAGGGACAC GTACAATTCA ATATGAAGAC TACATCGTAA ATGGTAATGT CGTAGAACT	10260
AAAGAAGTGT CACGAACTGA AGTAGCTCCG GTCAACGAAG TCGTTAAAGT AGGAACACTT	10320
GTGAAAGTTA AACCTACAGT AGAAATTACA AACTTAACAA AAGTTGAGAA CAAAAATCT	10380
ATAACTGTAA GTTATAACTT AATAGACACT ACCTCAGCAT ATGTTTCTGC AAAAACGCAA	10440
GTTTTCCATG GAGACAAGCT AGTTAAAGAG GTGGATATAG AAAATCCTGC CAAAGAGCAA	10500
GTAATATCAG GTTTAGATTA CTACACACCG TATACAGTTA AAACACACCT AACTTATAAT	10560
TTGGGTGAAA ATAATGAGGA AAATACTGAA ACATCAACTC AAGATTTCCA ATTAGAGTAT	10620
AAGAAAATAG AGATTAAAGA TATTGATTCA GTAGAATTAT ACGGTAAAGA AAATGATCGT	10680
TATCGTAGAT ATTTAAGTCT AAGTGAAGCG CCGACTGATA CGGCTAAATA CTTTGTAATA	10740
GTGAAATCAG ATCGCTTCAA AGAAATGTAC CTACCTGTAA AATCTATTAC AGAAAATACG	10800

1092

GATGGAACGT	ATAAAGTGAC	GGTAGCCGTT	GATCAACTTG	TCGAAGAAGG	TACAGACGGT	10860
TACAAAGATG	ATTACACATT	TACTGTAGCT	AAATCTAAAG	CAGAGCAACC	AGGAGTTTAC	10920
ACATCCTTTA	AACAGCTGGT	AACAGCCATG	CAAAGCAATC	TGTCTGGTGT	CTATACATTG	10980
GCTTCAGATA	TGACCGCAGA	TGAGGTGAGC	TTAGGCGATA	AGCAGACAAG	TTATCTCACA	11040
GGTGCATTTA	CAGGGAGCTT	GATCGGTTCT	GATGGAACAA	AATCGTATGC	CATTTATGAT	11100
TTGAAGAAAC	CATTATTTGA	TACATTAAAT	GGTGCTACAG	TTAGAGATTT	GGATATTAAA	11160
ACTGTTTCTG	CTGATAGTAA	AGAAAATGTC	GCAGCGCTGG	CGAAGGCAGC	GAATAGCGCG	11220
AATATTAATA	ATGTTGCAGT	AGAAGGAAAA	ATCTCAGGTG	CGAAATCTGT	TGCGGGATTA	11280
GTAGCGAGCG	CAACAAATAC	AGTGATAGAA	AACAGCTCGT	TTACAGGGAA	ACTTATCGCA	11340
AATCACCAGG	ACAGTAATAA	AAATGATACT	GGAGGAATAG	TAGGTAATAT	AACAGGAAAT	11400
AGTTCGAGAG	TTAATAAAGT	TAGGGTAGAT	GCCTTAATCT	CTACTAATGC	ACGCAATAAT	11460
AACCAACAG	CTGGAGGGAT	AGTAGGTAGA	TTAGAAAATG	GTGCATTGAT	ATCTAATTCC	11520
GTTGCTACTG	GAGAAATACG	AAATGGTCAA	GGATATTCTA	GAGTCGGAGG	AATAGTAGGA	11580
TCTACGTGGC	AAAACGGTCG	AGTAAATAAT	GTTGTGAGTA	ACGTAGATGT	TGGAGATGGT	11640
TATGTTATCA	CCGGTGATCA	ATACGCAGCA	GCAGATGTGA	AAAATGCAAG	TACATCAGTT	11700
GATAATAGAA	AAGCAGACAG	ATTTCGCTACA	AAATTATCAA	AAGACCAAAT	AGACCGGAAA	11760
GTTGCTGATT	ATGGAATCAC	AGTAACTCTT	GATGATACTG	GGCAAGATTT	AAAACGTAAT	11820
CTAAGAGAAG	TTGATTATAC	AAGACTAAAT	AAAGCAGAAG	CTGAAAGAAA	AGTAGCTTAT	11880
AGCAACATAG	AAAACTGAT	GCCATTCTAC	AATAAAGACC	TAGTAGTTCA	CTATGGTAAC	11940
AAAGTAGCGA	CAACAGATAA	ACTTTACACT	ACAGAATTGT	TAGATGTTGT	CCCGATGAAA	12000
GATGATGAAG	TAGTAACCGA	TATTAATAAT	AAGAAAAATT	CAATAAATAA	AGTTATGTTA	12060
CATTTCAAAG	ATAATACAGT	AGAATACCTA	GATGTAACAT	TCAAAGAAAA	CTTCATAAAC	12120
AGTCAAGTAA	TCGAATACAA	TGTTACAGGA	AAAGAATATA	TATTCACACC	AGAAGCATTT	12180
GTTTCAGACT	ATACAGCGAT	AACGAATAAC	GTAATAAGCG	ACTTGCAAAA	TGTAACACTT	12240
AACTCAGAAG	CTACTAAAAA	AGTACTAGGA	GCAGCGAATG	ATGCAGCCTT	AGATAACCTA	12300
TACTTAGATA	GACAATTTGA	AGAAGTTAAA	GCTAATATAG	CAGAACACCT	AAGAAAAGTA	12360
TTAGCGATGG	ATAAATCAAT	CAATACTACA	GGAGACGGTG	TAGTTGAATA	CGTAAGTGAG	12420
AAAATCAAAA	ATAACAAAGA	AGCATTTATG	CTAGGTCTTA	CTTATATGAA	CCGTTGGTAC	12480
GATATTAATT	ATGGTAAAAT	GAATACAAAA	GATTTATCTA	CGTACAAGTT	TGACTTTAAC	12540
GGAAATAATG	AGACTTCAAC	GTTGGATACT	ATTGTCCGAT	TAGGAAATAG	TGGACTAGAT	12600



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AACCTGAGAG	CTTCAAATAC	TGTAGGTTTA	TATGCGAATA	AACTTGCATC	GGTAAAAGGA	12660
GAAGATTCAG	TCTTTGACTT	CGTAGAAGCG	TATAGAAAAC	TGTTCTTACC	AAACAAAACA	12720
AATAACGAGT	GGTTTAAAGA	AAATACAAAG	GCATATATAG	TCGAAATGAA	GTCTGATATT	12780
GCAGAAGTAC	GAGAAAAACA	AGAATCACCA	ACAGCCGATA	GAAAATATTC	ATTAGGAGTT	12840
TACGATAGAA	TATCAGCACC	AAGTTGGGGG	CATAAGAGTA	TGTTATTACC	ACTACTAACT	12900
TTACCTGAAG	AATCTGTGTA	TATTTTCATCG	AATATGTCTA	CACTTGCATT	CGGTTTCGTAT	12960
GAAAGATATC	GTGATAGTGT	GGATGGAGTT	ATTCTTTTCAG	GAGATGCTTT	ACGAACTTAT	13020
GTAAGAAATA	GAGTTGATAT	AGCAGCGAAA	AGGCATAGAG	ACCATTATGA	TATTTGGTAC	13080
AATCTTCTTG	ACAGTGCTTC	AAAAGAAAAA	CTTTTCCGTT	CTGTGATAGT	TTATGATGGA	13140
TTCAATGTAA	AAGATGAGAC	AGGAAGAACT	TATTGGGCAA	GGTTAACGGA	TAAAAACATC	13200
GGCTCTATTA	AAGAATTCTT	CGGACCTGTT	GGGAAATGGT	ATGAGTATAA	TAGTAGTGCA	13260
GGAGCGTATG	CGATGGGAAG	TTTAACGCAC	TTTGTGTTAG	ATAGATTATT	AGATGCTTAT	13320
GGAACGTCGG	TTTATACTCA	TGAAATGGTT	CATAATTCTG	ATTCTGCAAT	CTACTTTGAA	13380
GGAAATGGTA	GACGTGAAGG	ATTGGGAGCG	GAGTTATACG	CACTTGGTTT	ACTGCAATCT	13440
GTAGATAGTG	TAAATTCTCA	TATTTTAGCT	TTAAATACGT	TATATAAAGC	AGAAAAAGAT	13500
GATTTGAATA	GATTGCATAC	ATATAATCCG	GTGGAACGTT	TCGATTCGGA	TGAGGCGCTT	13560
CAAAGTTATA	TGCTGGATC	ATATGATGTA	ATGTATACAC	TTGATGCGAT	GGAAGCAAAA	13620
GCGATATTAG	CTCAAAATAA	TGATGTTAAG	AAAAAATGGT	TTAGAAAAAT	AGAAAAATTAT	13680
TACGTTCTGT	ATACTAGACA	TAATAAAGAT	ACACATGCAG	GAAATAAAGT	CCGTCCATTA	13740
ACAGATGAAG	AAGTAGCTAA	CTTAACATCG	TTAAACTCAT	TAATCGACAA	CGACATCATA	13800
AATAGACGTA	GCTATGATGA	TAGTAGAGAA	TATAAACGAA	ATGGCTACTA	TACTATAAGT	13860
ATGTTCTCTC	CTGTATACGC	AGCGCTAAGC	AATTCGAAAG	GTGCTCCTGG	AGATATTATG	13920
TTTAGAAAAA	TAGCTTATGA	ATTACTTGCG	GAAAAAGGTT	ATCACAAAGG	ATTCCTACCT	13980
TATGTTTCTA	ATCAGTACGG	AGCAGAAGCA	TTTGCCAGCG	GAAGCAAAAC	ATTCTCATCA	14040
TGGCATGGAA	GAGATGTTGC	TTTAGTGACA	GATGATTTAG	TATTTAAGAA	AGTATTCAAT	14100
GGTGAGTACT	CATCATGGGC	TGATTTCAAA	AAAGCAATGT	TTAAACAACG	TATAGATAAA	14160
CAAGATAATC	TGAAACCAAT	AACAATTCAA	TACGAATTAG	GTAATCCTAA	TAGTACAAAA	14220
GAAGTAACTA	TAACAACGGC	TGCACAAATG	CAACAATTAA	TTAATGAAGC	GGCTGCGAAA	14280
GATATTACTA	ATATAGATCG	TGCAACGAGT	CATACCCAG	CAAGTTGGGT	GCATTTATTA	14340

1094

AAACAAAAAA TCTATAATGC ATATCTTCGC ACTACAGATG ACTTTAGAAA TTCTATATAT	14400
AAATAAGATT GTAGAGTTTC ATTGTTGAGT AGTGTTCCTT GTAAGGATGA GGAGTCAGAT	14460
GACAAATCGA CTCCTTTTTC TTATGGATCG ATGTAGAGAT TTGATTGAAT GCAGATTGCA	14520
GGAATCATCT TCAACTCATC AACGACCAAT GGTGACAAGG TGGATTTCAA TCCCACAGAA	14580
AATGTTGATT TGAGAAATAA CTTTGCTAGT CTAGTAAAT AAATACAAAA CAATCCTAGA	14640
AGATTTTTTC TGGGATTGTT TTTTGCTGAG TGGGATGCTT CAAGTTGTCT GGCTTGACTT	14700
TCTTGAGGGA AGTTATATAA TAGTTGTAAT AATTAG	14736

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11770 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

ACAGGAAAGC ACGATAGCAA TCTCTTTGGA AGATTTAAAA AATATTCCTC AAAGTTTCGC	60
TGTTGCTTAC GGTGATACGA AAGTATCTTC GATTCTCTCT GTCTTGCGTG CTAATTTAGT	120
AAATCATTTG ATTACAGACA AAAATACAAT TTTAAAAGTT TTGGAAGAAG ATGGGGATTT	180
GACTTTTAGA GAGATTCTAG GTGAGTGAAA ATGATAGACT GATTCAGTTT ATCGTTTTTC	240
TTTTTAGTTG ATTGCACATT TGTGCTTATA TAAACAAAA TAGTTTATCT GTTGTTTTTG	300
GATTGACAAC TTTATTATGT AGTTGTATTC TATAGTTACA AAAGAAAATT TTAATAATTC	360
AAATGAAAAA AGCTTTTTTAC ATAGTGAAAT GAGGAGGAAT TTATGGAAAT GATTGTTCCA	420
GATCAAATTA TCATGGGTTT AATTTTATAT GCTGGTGATG CGAAACAACA TATTTATAAA	480
GCGTTAGATT ACATAAAAAA TGGTACATGT GAACGGTG TG AAGAAGAAAT ACAGTTAGCT	540
GATGCAGCCT TATTAGAAGC TCATAATCTA CAAACAAAAT TTTTGGCACA GGAAGCGTCT	600
GGTACAAAGA CAGAAATTAC AGCTCTCTTT GTTCATTCAC AAGATCATCT CATGACCAGT	660
ATGACGGAGA TTAATTTAAT CAAAGAAAT ATTAGTTTGA GAAAAGAACT TCATAAAAAA	720
TAATACTAGA GTATTATCAT TGTTATTAAC ATAGAGGAGG AAAACATAAT GGTGAAGATT	780
GGTTTGTTTT GTGCAGCAGG TTTTCTACT GGTATGCTTG TAAATAATAT GAAAATTGCA	840
GCGCAATCTA GTGGAGTTGA GGCAGAAATA GAGGCGTTTT CTCAGTCTAA ATTAGCGGAT	900
TATGCGCCAA ATATAGATGT TGCACATTG GGTCCACAAG TTGCTTATAC ATTAGATAAA	960
TCAAAAGAAA TTTGTGATAA GTGTGATGTT CCGATAGCTG TTATCCGAT GATGGACTAT	1020

1095

GGTATGTTAG ATGGGAAAAA AGTATTAGAT TTGGCCCTAT CTTTGATTAG TGGGTAAGAA	1080
AAGGAGATTT ATTATGTCAA AGATGGATGT TCAGAAAATC ATTGCACCGA TGATGAAGTT	1140
TGTGAATATG CGTGGCATT A TAGCTCTAAA AGATGGGATG TTAGCAATTT TGCCATTGAC	1200
AGTAGTTGGT AGTTTGTCT TGATTATGGG ACAATTGCCG TTCGAAGGAT TAAATAAGAG	1260
CATTGCTAGT GTTTTTGGAG CTAATTGGAC AGAGCCGTTT ATGCAAGTAT ATTCAGGAAC	1320
TTTTGCTATT ATGGGTCTAA TTTCTTGTTT TTCAATTGCC TATTCTTATG CTAAGAATAG	1380
CGGAGTAGAG GCTTTACCAG CTGGAGTTCT ATCTGTATCT GCATTCTTTA TTTTGCTAAG	1440
ATCATCTTAT ATCCCTAAAC AAGGTGAGGC GATTGGGGAC GCTATTAGTA AAGTTTGGTT	1500
TGGAGGCCAA GGAATTATCG GTGCTATCAT TATAGGTTTG GTAGTAGGAA GTATTTATAC	1560
CTTCTTTATA AAGAGAAAAA TTGTTATTAA GATGCCAGAA CAAGTTCCAC AAGCTATTGC	1620
CAAACAGTTT GAAGCAATGA TTCCAGCATT TGTAATTTTC TTATCTTCTA TGATTGTATA	1680
TATTTTAGCG AAGTCATTGA CTAATGGCGG AACATTGATA GAAATGATTT ATTCTGCTAT	1740
TCAAGTTCCG TTGCAAGGTT TAACTGGATC TTTGTATGGT GCTATTGGAA TTGCATTCTT	1800
TATATCATTT TTGTGGTGGT TTGGTGTTC TGGGCAATCG GTAGTAAATG GAGTAGTGAC	1860
AGCTCTGCTT TTATCTAATC TTGATGCTAA TAAAGCTATG TTAGCCTCTG CTAATCTATC	1920
ATTAGAAAAT GGTGCACATA TTGTTACTCA ACAATTTTTC GATTCATTTT TAATCTATC	1980
AGGTCAGGG ATTACGTTTG GTCTTGATG TGCCATGCTT TTTGCAGCAA AATCAAAACA	2040
ATACCAAGCC TTAGGAAAAG TTGCAGCTTT TCCAGCAATA TTAAACGTAA ATGAGCCAGT	2100
TGTATTTGGA TTTCCGATTG TCATGAATCC AGTTATGTTT GTACCTTTCA TTCTTGTTCC	2160
TGTACTTGCA GCTGTGATAG TATATGGAGC TATTGCAACA GGTTCATGC AGCCATTCTC	2220
AGGGGTAACA TTGCCTTGGA GTACACCAGC TATTTTATCA GGATTTTGG TGGGTGGATG	2280
GCAAGGAGTT ATTACTCAGC TGGTGATATT AGCGATGTCT ACATTGGTTT ATTTTCCATT	2340
CTTTAAAGTA CAGGATCGTT TAGCTTACCA AAATGAAATC AAACAATCTT AGAGGTATTT	2400
GTGTGTTACT GTTAAACTCA CACATTTGTG CTAATAATTA GAGAGTTAAA ATTTTCTAG	2460
TTAAAGCTT GAAAATTTCT ATAAAAATCG GTATTATATT TTCGAAAGAA ATAAAAATAT	2520
TTTCGAAAGA AAGGTGCTTA CGATGGTAAA TACAGAAGTA GCAAGAACAA CAATCAAGAC	2580
AGAATATTTT GGCAGCCTTA CTGAAAGGAT GAACAAATAT CGAGAAGATG TTTTAAATAA	2640
AAAACCTTAT ATTGATGCTG AGAGAGCAGT TCTAGCAACA CGCGCCTATG AACGATACAA	2700
GGAACAACCT AATGTCCTAA AACGTGCATA TATGCTGAAA GAAATTTTGG AAAATATGAC	2760

1096

TATCTATATT	GAAGAAGAAT	CTATGATTGC	GGGAAATCAA	GCTTCTTCCA	ATAAAGATGC	2820
TCCTATTTT	CCGGAATATA	CGCTAGAATT	TGTTCTCAAT	GAGTTGGATC	TTTTTGAAAA	2880
GCGTGATGGA	GATGTTTTCT	ATATTACAGA	AGAAACAAAA	GAACAACTTA	GAAGTATTGC	2940
TCCGTTTTGG	GAAAATAATA	ATTTACGTGC	TAGAGCTGGT	GCCTTATTAC	CTGAAGAAGT	3000
GTCTGTTTAT	ATGGAAACAG	GATTCTTCGG	TATGGAAGGT	AAGATGAATT	CTGGAGATGC	3060
TCACCTAGCA	GTTAACTATC	AGAACTTTT	GCAATTTGGT	TTAAGAGGTT	TTGAAGAGCG	3120
GGCTCGTAAA	GCAAAAGTAG	CTCTAGATTT	AACAGATCCA	GCAAGTATTG	ATAAATATCA	3180
TTTTTACGAC	TCTATATTTA	TCGTAATCGA	TGCTATTAAA	GTATATGCAA	AGCGCTTTGT	3240
TGCTCTTGCT	AAAAGTTTAG	CCGAAAATGC	AAATCCTAAA	CGTAAGAAAG	AATTACTTGA	3300
GATTGCAGAT	ATTTGCTCTA	GAGTCCCAT	TGAACCGGCA	ACTACTTTTG	CAGAAGCTAT	3360
TCAATCAGTT	TGGTTTATTC	AATGTATTTT	ACAAATTGAA	TCTAATGGCC	ACTCTCTTTC	3420
ATATGGCCGT	TTTGATCAAT	ATATGTATCC	ATATATGAAG	GCTGATTTAG	AAAGTGGTAA	3480
AGAAACAGAA	GATAGCATTG	TTGAACGTCT	GACAAATCTT	TGGATTAAGA	CAATTACAAT	3540
TAATAAGGTT	CGCAGTCAAT	CACATACATT	TTCTTCAGCA	GGAAGTCCTT	TATATCAAAA	3600
TGTTACAATT	GGTGGACAGA	CTCGAGATAA	GAAGGATGCT	GTTAACCCAT	TATCTTATTT	3660
GGTATTAAAA	TCAGTTGCAC	AAACCCATCT	ACCGCAACCT	AATCTAACTG	TACGTTACCA	3720
TGCAGGTTTA	GATGCTCGTT	TCATGAATGA	GTGTATTGAA	GTGATGAAAC	TTGGTTTTGG	3780
TATGCCTGCA	TTTAATAATG	ATGAGATTAT	TATTCCTTCT	TTTATTGCAA	AAGGAGTATT	3840
GCAAGATGAT	GCTTATGATT	ACAGTGCCAT	TGGATGTGTT	GAAACGGCAG	TTCCAGGGAA	3900
ATGGGGCTAT	CGTTGCACAG	GTATGAGTTA	TATGAACCTC	CCTAAGGTTT	TACTTATCAC	3960
GATGAATGAT	GGAATTGATC	CGGCTTCGGG	TAAACGGTTT	GCACCAAGCT	TTGGTCGTTT	4020
TAAGGATATG	AAGAACTTTT	CTGAATTAGA	AAATGCTTGG	GATAAAACAC	TAAGATATTT	4080
GACACGAATG	AGTGTTATTG	TTGAAAATTC	TATTGATTTA	TCATTGGAAC	GAGAAGTTCC	4140
TGATATTCTA	TGTTCAGCAT	TGACTGATGA	TTGTATTGGT	CGTGGAAC	ACCTTAAAGA	4200
AGGTGGAGCA	GTATATGATT	ATATATCAGG	ATGCAAGTT	GGAATTGCAA	ATTTGTCGGA	4260
TTCATTAGCT	GCAATTAAAA	AATTGGTGT	TGAGGAAGAA	CGTATAAGCC	CAAGTCAGCT	4320
TTGGCATGCA	CTGGAAACAG	ATTATGCCGG	AGAAGAAGGT	AAGGTCATTC	AAGAAATGTT	4380
GATTCATGAT	GCACCTAAGT	ATGGTAATGA	TGATGATTAT	GCTGACAAAT	TGGTTACTGC	4440
TGCTTATGAC	ATTTATGTTG	ATGAAATTGC	TAAATATCCT	AATACACGTT	ATGGAAGAGG	4500
GCCTATTGGA	GGAATTCGTT	ATTCAGGAAC	ATCTTCTATC	TCAGCCAACG	TAGGGCAGGG	4560

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ACGTGGAACA	TTAGCAACTC	CAGATGGACG	CAACGCGGGT	ACACCGTTAG	CAGAGGGTTG	4620
TTCACCATCA	CATAATATGG	ATCAACACGG	CCCTACATCT	GTTTTAAAAT	CTGTTTCAAA	4680
ATTACCAACA	GATGAAATCG	TAGGTGGGGT	TCTCTTAAAT	CAGAAAGTAA	ATCCTCAAAC	4740
GTTAGCCAAA	GAAGAAGATA	AATTAAAAC	AATTGCTTTG	TTACGAACAT	TCTTTAATCG	4800
TTTACATGGG	TACCATATTC	AATACAATGT	TGTTTCCAGA	GAGACGCTGA	TTGACGCTCA	4860
GAAACATCCT	GAAAAACACA	GAGACTTAAT	TGTTCTGTGT	GCAGGATACT	CTGCATTCTT	4920
CAATGTTCTT	TCTAAGGCAA	CCCAAGATGA	CATTATAGGA	CGTACTGAGC	ATACTTTGTA	4980
AAATAAAGAG	GTTCTTTTTA	TGGAATTTAT	GCTTGACACA	TTAAATTTAG	ATGAGATTAA	5040
AAAGTGGTCT	GAAATTTTGC	CGCTAGCTGG	GGTAACTTCA	AATCCCACTA	TTGCAAAAAG	5100
AGAGGGTTCT	ATTAATTTTT	TTGAACGAAT	CAAAGATGTA	AGAGAATTGA	TTGGCTCTAC	5160
ACCTCTATT	CATGTTTCTG	TGATTTCTCA	AGATTTTGAA	GGCATCTTAA	AGGATGCTCA	5220
TAAAATTCGA	AGACAAGCAG	GAGATGATAT	ATTTATCAAA	GTACCTGTTA	CTCCAGCTGG	5280
ATTACGTGCA	ATAAAGGCGC	TAAAAAAGA	GGGCTACCAT	ATCACTGCAA	CAGCTATTTA	5340
TACAGTTATT	CAGGGATTAT	TAGCTATCGA	AGCAGGAGCG	GATTACCTAG	CTCCATATTA	5400
TAATAGAATG	GAAAATCTGA	ACATTGATTC	AAATTCTGTC	ATTCGTCAAT	TAGCTCTTGC	5460
TATTGATAGA	CAGAACTCTC	CTAGTAAGAT	TTTAGCTGCA	TCCTTTAAAA	ATGTAGCACA	5520
AGTAAATAAT	GCTTTAGCTG	CAGGTGCGCA	TGCTGTTACA	GCAGGAGCGG	ATGTTTTTGA	5580
ATCAGCTTTC	GCCATGCCAT	CTATCCAAAA	GGCGGTTGAT	GATTTTCTG	ACGATTGGTT	5640
TGTTATTCAA	AATAGTCGTT	CCATTTAGAT	AGAGAGGAAA	TACATATGAG	AATTTTGTCT	5700
AGTCCTTCTA	GATATATTCA	GGGGGAAAAT	GCCTTGTTTG	AAAATGCCAA	ATCAATTTTG	5760
GATTTGGGAA	ATTGCCCTAT	TCTATTATGC	GATCAGTTGG	TTTATGATAT	TGTTGGAAAA	5820
CGATTTGAAG	ATTACCTACA	TAGGTATGGT	TTCCATATTG	TTCTGGCGCT	ATTTAATGGT	5880
GAAGCTTCTG	ACAATGAAAT	CAATCGAGTT	GTTGCCCTTG	CTGAGAAAGA	AAATTGTGAT	5940
AGTATTATCG	GTCTTGGTGG	GGGAAAGACG	ATTGATAGCG	CAAAAGCTAT	TGCAGATTTG	6000
ATTGAAAAGC	CTGTTATTAT	TGCTCCAACA	ATTGCATCGA	CCGACGCACC	TGTATCTGCT	6060
TTATCTGTTA	TTTATACAGA	TGAAGGTGCA	TTTGATCATT	ATCTATTTTA	TTCTAAAAAT	6120
CCAGATTTAG	TTTGGTTTGA	TACAAAAGTT	ATTTACAAG	CCCCTAAGCG	TTTATTAGCG	6180
TCTGGTATTG	CAGATGGTTT	AGCAACTTGG	GTTGAGGCGC	GTGCGGTTAT	GCAGGCAAAT	6240
GGAAAACTA	TGTTGGGACA	ACAGCAAACA	TTGGCTGGAG	TTGCAATTGC	GAAGAAATGT	6300

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GAAGAAACGC TGTTCGAGA TGGTTTACAG GCTATGGCAG CTTGTGAAGC TAAAGTGGTG	6360
ACACCAGCAT TAGAAAATAT TGTGAAGCT AATACTTTAT TGAGTGGTCT AGGTTTTGAA	6420
AGTGGAGGAT TAGCTGCGGC GCATGCAATT CATAATGGTT TTAGTGATT GACAGGTGAC	6480
ATTCATCATT TAACACATGG TGAAAAAGTA GCTTATGGAA CTTTAGTACA ACTATTATTG	6540
GAAAATAGAC CTAAAGAAGA ACTTGATAAG TATATTGAGT TTTACAAAAA AATTGGTATG	6600
CCAACAACCTC TAAAAGAAAT GCATTTGGAT CAAGTTGGAT ATGATGATTT AATAAAAGTT	6660
GGTAAACAAG CAACTATGGA GGGTGAGACA ATTCATCAGA TGCCGTTTAA GATTCGCCT	6720
TCAGATGTTG CTCAAGCTAT TATCGCTGTA GATGCCTATG TAAATTCAAA ATAAACAATA	6780
AGGACTACTG TTTTCCAAAT GGTAGTCTTT TATTGATCCC TGTATTGAAT TCTATAGAAG	6840
ATTGAAATAG GATGAGAACA AATCGATTGG GAAAGTAAAA TTAATTTCTA TAAATGTTTT	6900
AGCAATTGTT TCGTACTATT TCAGATTCAG TCTACTATAT GTTCTTCATA AATCAAAAAG	6960
CGACATAGGT TGTGCGCTAT TTATTGTGAA TACATTAATT AGCATTCCAG TTTTATCTTC	7020
GGTCTAAAAT AAGTATTTTG TGCTATACGA GATAAGCTTC TTGACTTACT CCTTGATTTA	7080
CTGCATAACA ATGGGATAAA AAGTGGGAGA TAGAGCAATT CATAGTCATC AAAATTAATG	7140
AGATACAGTA TACAGTTTTT CCTTTAAACA CATTTCAAAT TCCCTCAAAA ATGGTATAAT	7200
AGTAACATCA CAAAATTGGA GAGAGACCAT GAGTTTTTAC AATCATAAAG AAATTGAGCC	7260
TAAGTGGCAG GGCTACTGGG CAGAACATCA TACATTTAAG ACAGGAACAG ATACATCAAA	7320
ACCTAAGTTT TATGCGCTTG ATATGTTCCC TTATCCGTCT GGAGCTGGTC TGCACGTAGG	7380
ACACCCAGAA GGTATACTG CAACCGATAT CCTCAGTCGT TACAAACGTG CGCAAGGCTA	7440
CAATGTCCTT CACCCAATGG GTTGGGATGC TTTTGGTTTG CCTGCAGAGC AATACGCTAT	7500
GGATACTGGT AATGACCCAG CAGAATTTAC AGCGGAAAAC ATTGCCAACT TCAAACGTCA	7560
AATTAATGCG CTTGGATTTT CTTATGACTG GGATCGTGAA GTCAACACAA CAGATCCAAA	7620
CTACTACAAG TGGACTCAAT GGATTTTCAC CAAGCTTTAC GAAAAAGGCT TGGCCTATCA	7680
AGCTGAAGTG CCAGTAACT GGGTTGAGGA ATTGGGAACT GCCATTGCCA ATGAAGAAGT	7740
GCTTCCTGAC GGAACCTCTG AGCGTGGAGG CTATCCAGTT GTCCGCAAAC CAATGCGCCA	7800
ATGGATGCTC AAAATCACGG CTTACGCAGA GCGCTTGCTC AATGACTTAG ATGAACTAGA	7860
TTGGTCAGAG TCTATCAAGG ATATGCAACG CAACTGGATT GGTAATCAA CTGGTGCCAA	7920
TGTAACTTTC AAAGTAAAAG GAACAGACAA GGAATTTACA GTCTTTACTA CTCGTCCGGA	7980
CACACTTTTC GGTGCGACTT TCACTGTCTT GGCTCCTGAA CATGAATTAG TAGACGCTAT	8040
CACAAGTTCA GAGCAAGCAG AAGCTGTAGC AGACTATAAA CACCAAGCCA GCCTTAAGTC	8100

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TGACTTGGCT	CGTACAGACC	TTGCTAAAGA	AAAAACAGGG	GTTTGGACTG	GTGCTTATGC	8160
CATCAACCCT	GTCAATGGTA	AGGAAATGCC	AATCTGGATT	GCAGACTATG	TCCTTGCTAG	8220
TTATGGAACA	GGTGCGGTTA	TGGCTGTGCC	TGCCCACGAC	CAACGTGACT	GGGAATTTGC	8280
CAAACAATTT	GACCTTCCAA	TCGTGGAAGT	ACTTGAAGGT	GGAAATGTCT	AAGAAGCTGC	8340
CTACACAGAG	GATGGCCTGC	ATGTCAATTC	AGACTTCCTA	GATGGATTGA	ACAAAGAAGA	8400
CGCTATTGCC	AAGATTGTGG	CTTGGTTGGA	AGAAAAAGGC	TGTGGTCAGG	AGAAGGTTAC	8460
CTACCGTCTC	CGCGACTGGC	TCTTTAGCCG	TCAACGTTAC	TGGGGTGAGC	CAATTCCAAT	8520
CATTCAATTG	GAAGATGGAA	CTTCAACAGC	TGTTCTTGAA	ACTGAATTGC	CGCTTGTCTT	8580
GCCTGTAACC	AAGGATATCC	GTCTTCAGG	TACTGGTGAA	AGTCCACTAG	CTAACTTGAC	8640
AGATTGGCTT	GAAGTGACTC	GTGAAGATGG	TGTCAAAGGT	CGTCGTGAAA	CCAACACTAT	8700
GCCACAATGG	GCTGGTTCAA	GCTGGTACTA	CCTCCGCTAT	ATTGACCCGC	ACAATACTGA	8760
GAAATTGGCT	GATGAGGACC	TCCTCAAACA	ATGGTTGCCA	GATGATATCT	ACGTGGGTGG	8820
TGCGGAACAT	GCTGTACTTC	ACTTGCTTTA	TGCTCGTTTC	TGGCATAAAT	TCCTCTATGA	8880
CCTCGGTGTT	GTTCCGACTA	AGGAACCAT	CCAAAACTC	TTTAACCAAG	GGATGATTTT	8940
GGGAACAAGC	TACCGTGACC	ACCGTGGTGC	TCTTGTGGCA	ACCGACAAGG	TTGAAAAACG	9000
TGATGGTTCC	TTCTTCCATG	TAGAAACAGG	GGAAGAGTTG	GAGCAAGCGC	CAGCCAAGAT	9060
GTCTAAATCG	CTCAAGAACG	TTGTTAACCC	AGACGATGTG	GTGGAACAAT	ACGGTGCCGA	9120
TACCTTTCGT	GTTTATGAAA	TGTTTATGGG	ACCACTCGAT	GCTTCGATTG	CTTGGTCAGA	9180
AGAAGGTTTG	GAAGGAAGCC	GTAAGTTCCT	TGACCGAGTT	TACCGTTTGA	TTACAAGTAA	9240
AGAAATCCTT	GCGGAAAACA	ATGGTGCTCT	TGACAAGGTT	TACAACGAAA	CAGTCAAAGC	9300
TGTTACTGAG	CAAATTGAGT	CTCTCAAATT	CAACACAGCT	ATTGCCCAAC	TTATGGTCTT	9360
TGTCAATGCT	GCTAACAAGG	AAGATAAGCT	TTATGTTGAC	TATGCCAAAG	GCTTTATTCA	9420
ATTGATTGCA	CCATTTGCAC	CTCACTTGGC	AGAAGAACTC	TGGCAAACAG	TCGCAGAAAC	9480
AGGTGAGTCA	ATCTCTTATG	TAGCTTGGCC	AACTTGGGAC	GAAAGCAAAT	TGGTTGAAGA	9540
TGAAATTGAA	ATTGTCGTCC	AAATCAAAGG	AAAAGTTCGT	GCCAAACTCA	TGGTTGCTAA	9600
AGATCTATCA	CGTGAAGAAT	TACAAGAAAT	CGCTTTAGCT	GATGAAAAAG	TCAAAGCAGA	9660
AATTGACGGT	AAGGAAATCG	TGAAAGTAAT	TGCGGTACCG	AATAAACTCG	TTAATATCGT	9720
CGTTAAATAA	CGAGTTTATT	AGCTCTATCT	GCCACCTTCA	ATAGTCCACT	GGACTATTGA	9780
AsCCAACATA	ATTAGTTAAC	ATTGTTGTGA	AATAAGATAG	GAGTCCTTCA	GAGTAGAATC	9840

1100  
TGGAGGATTT TTTGAATCTT CTTATGAAAG TATGATATAC TATGGGCAAC TATAAAGTTT 9900  
GAAAAGTGAA ATAAGGAGAA TAAGATGCCA GTAAATGAAT ATGGTCAAAT GATTGGGGAG 9960  
TCAATGGAAG CTTATACTCC AGGTGAATTG CCTTCTTTTG ATTTCTTAGA AGGGCGTTAT 10020  
GCTAGGATAG AGGCTCTTTC AGTGGAAAAG CATGCCGAGG ATTTATTAGC TGTTTATGGC 10080  
CCTGATACGC CTCGGGAGAT GTGGACCTAC CTCTTTCAGG AGTCAGTAGC AGACATGGAG 10140  
GAACTGGTCA GCCTTTTAAA TCAGATGTTG GCTCGTAAGG ACCGTTTTTA TTATGCAATC 10200  
ATAGACAAGG CAACTGGTAA GGCTTTGGGA ACTTTTCCC TCATGCCAAT TGATCAGAAT 10260  
AACCAGTAA TAGAAGTGGG AGCTGTCACT TTTTCTCCAG AGCTCAGGGG GACACGGATA 10320  
GGAACAGAAG CCCAGTATCT CTTGGCTTGC TATGTCTTTG AGGAGCTTAA CTATCGTCGC 10380  
TATGAGTGGG AATGCCATGC TCTTAACCTG CCATCCAGAC GAGCAGCGGA ACGTTTGGGA 10440  
TTTATTTATG AAGGAACCTT CCGTCAGGCA GTGGTTTATA AGGGGCGTAC AAGAGATACG 10500  
GATTGGTTGT CTATGATTGA TAAGGACTGG CCTCAAGTCA AAGCTCGATT GGAAATATGG 10560  
TTGCGTCCTG AAAACTTTGA TAAAAATGGA CGACAGCACA AGAGCTTGAG AGAACTTTAA 10620  
GAGGTGTTGA GATGATTACT ATTAAAAAGC AAGAAATTGT CAAGCTAGAG GATGTTTTGC 10680  
ATCTCTATCA GGCTGTCCGT TGGACAACT ATACCCATCA AACAGAGATG CTGGAGCAGG 10740  
CCTTATCTCA TTCATTAGTA ATTTATCTGG CACTTGATGG TGATGCTGTG GTGGGCTTGA 10800  
TTCGTTTGGT TGGAGATGGT TTTTCATCAG TTTTGTACA GGATTTGATT GTTTTGCCTA 10860  
GCTATCAGCG TCAAGGGATT GGTAGCTCCT TGATGAAAGA GGCTTTAGGA AATTTTAAAG 10920  
AGGCCTATCA AGTCCAGCTG GCGACAGAAG AGACAGAAAA AAACGTGGGA TTTTATCGTT 10980  
CTATGGGCTT TGAAATCTTA TCCACCTATG ACTGTACAGG AATGATTTGG ATAAACAGAG 11040  
AAAAATAAAA AAACTTGTTT GTTCTTAAGC AAAGTTTAAG GATGGTCTAG TATCATATAG 11100  
TCATTAAATA AAGACCTCCT AACTTTATTT AATAAAATCC TAAACTTTTT TCATCACAAT 11160  
CTCCTAATGA AGCCACCCAA TCAGGTGGCT TTTTGTGCGT ACGACGGGCA TGTCGTATAT 11220  
CTGAGGTGTA AGTCCTCAGC CTGACTATCG TGAGGTAGCA GGGAGAGGAA GGGATAGCGA 11280  
AATCGTGGCT CTACGAACAG GAACGTGATA GTAAGGCGTA TATAGCGGAT AAGGAGGCTT 11340  
CAAACCTAA AGTCCAAAAA GGTAGTCGTA ACCTATATGT GTAAATCACG AGAGTAATTG 11400  
AATTCGGACT AAGGTTTGTG TGAAAAAGAT AAATCTTTCT AGAGTCTAAA GACTCTGCGT 11460  
CAGATTTCTT ATTTTCACTG TAACCTTTTA ACGTCTCAT ATCTTGATA AACGAGGAAA 11520  
GATGTACGAC TTATCCCGTG AGGTTTCATG AGCGCTGAAA GCGTAGTAAC AACGAATCAT 11580  
GAGAAGTCAG CCGAGCCCAT AGTAGTGAGG AAACCTCCGT AATGGAAGTG GAGCGAAGGG 11640



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GTGAATACTC AAACAGTCTG GGGAGAGACT GTTTGAGGTC TGTCGCTAGA AAGAGAAAAC 11700  
GACAGATCGA AGTAATCCTA CTTCACTTGT GTCTGTAAAA TGAGTGGTCT GATAGAACTG 11760  
GACTTTGAGG 11770

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAAACTA CTTTCTTAGT ATAACACTTT CAGAATCATT GTCAATAGAA ATGACTTGAT 60  
TTTTTCAATT TTTTCAAGCT ATTTCCAAGG GTTGTAAAAT CGTCCCTGAT TCTGCAAGAT 120  
AAGTAGTAAA CTAACACTA AAAACAAGGT TGCCAAGAGC AAGGTAATAT AGTCTCCTTT 180  
TTTCAAGGCC TGATAACTAT ACCATGTGCG TTTTTTCTCT TTCCCAAAGC GGCGAACTCC 240  
ATGGCAGTCG CAATGGTATC AATGCGTTCT AGCGAGCTAA AAATCAAGGG CGTAATAATG 300  
AGCAGATTGC CTTTGATTCT TTGCATAAGA GAAGCTTTCT TGGATAATTC CATCCCACGC 360  
GCCTCCTGAG ACATCTTGAT AGTAAAGAAT TCTTCCTGCA AATCTGGAAT ATAGCGCAAG 420  
GTCAGGCTGA CAGAATAAGC AATCTTATAG GGCACACCAA TTTGATTTAA ACTGGAAGCA 480  
AACTGACTAG GATGGGTTGT CATCAAAAAG ATAATAGCCA GAGGAATGGT GCAAAGATAC 540  
TTAATGGCCA AATTTAGCAG ATAAAAGAGC TCCTGGCTGG TTAGAGTGTA GACACCGATT 600  
CCCTGCCAAA TCACACTTCT CTCTCCATAA AGTCCAACCC CATACTCGGG AGAAAAGAGA 660  
TAGACCATCA AACCGTTTAA AACGGCAAAT ATCGTCGCAA AAACGGCTAC AAAGGAAACA 720  
TCTTTAAAGC GAATTTCTGA TAAATAGAGG AGAAAGACTG AAAAGATGGC AATCAGCAAG 780  
AGCATCTGG TATCATAGCT AATCATGGCC GCCAATGATA CCAGAATGAA AAAGAGAAGT 840  
TTCCCAGCTC CTGACAAGCG ATGAATCACA GTATCTCTAT GCTGGTAACC GATTAATTTA 900  
GCTTGCAATC CTCTCTCCTT TCTTTGTAAA ATGCCGTTAA ATCCAGTGGG TCCACATCTA 960  
GTTTCTTAGC CAAGTTAAAG ATGGAGGTTT CTTTLAGATT GGCTTTTACT AACAGCTCAG 1020  
GATCGCTCAA CAGACTGGCT GGAACAGTAT CGGCAATCAA TTCTCCATCC ACCATGACAA 1080  
GGACCCGGTC TGAATAATCC AGCATCAATT GCATATCATG GGTAATCATG ACAATGGTAT 1140  
GCCCTTTTGT ATGTAACCTT TCGAGAAATT CCATAATCTC AGTATAGTTC TTCTGATCTT 1200

1102

GACCTGCAGT	CGGTTTCATCT	AGGAGAATAA	TTTCAGCTCC	TAAGACCAAA	ATTGAAGCAA	1260
TGGTGACACG	TTTTTCTGA	CCAAATGACA	GGGCAGAAAT	AGGCCAATTA	CGGAATTCAT	1320
AAAGTCCACA	GATTTTCAAG	GTTTCATATA	CTCTCGTTTC	AATTTCTTTC	TCATCCACAC	1380
CTCGCAAACG	GAGCCCTAGA	GCCACCTCAT	CAAAAATCAT	ATTGGTTGAA	ATCATTGAT	1440
TAGGATTTTG	TAGCACATAT	CCTACTCGTT	CGCCCCGCTC	TGCAACAGAA	TCGCCTTTTA	1500
TATCCTGTTT	TTCCCAAAGA	TAGCGTCCCT	CCGTCTGAAT	AAAGCTACTT	ATAGCCTTGG	1560
CTAGAGTTGA	TTTCCCTGCT	CCATTTTTTC	CGACAATAGC	AATCTTTTCA	CCCTTTTTAA	1620
TATCTAAATG	TAGGGATTTT	AAAATCGGTC	TATCATCATA	AGAAAAAGAT	ACTTCCTCTA	1680
GTCTAAAGAG	TGACTGCAAT	GCTGGGGTTT	CTTTTGCCAG	TTCATTCTGC	AACTGAACCT	1740
GACCTTTTGA	GATAGACAAG	TTATCCAGAT	TCGCTAATTG	TTCTTCCTTG	ACTAAGTCCA	1800
CACCTAATTG	ACGGAGAGTC	GTTAGATAAA	GGGGTTCTCG	AATTCATTTT	TGAGTCAATA	1860
AATCAGTCGC	AAGCAACTGG	TCAGGGCTCC	CATTAAAAAG	GATACGACCA	TCGTTTATCA	1920
AGACAATCCG	ATCCACAGGG	CGATGCAGAA	CGTCTCCAA	ACGGTGCTCG	ATAATAAGAG	1980
TCGTCTCCC	CTCTTCCTTA	TGAATCTGGT	CAATCAATTC	GATAATATCC	TGACCTGACT	2040
TGGGATCTAG	ATTGGCGAGT	GGCTCATCAA	ACAAGAGAAT	CGGACTTTCA	TCAATCAAGA	2100
CACCAGCCAG	ACTGACTCGC	TGCTTTTGTC	CACCTGACAA	ATCCTGAGGA	CGCTGATCCA	2160
GTAAAGGAAG	AAGGTCCAGC	TTTTCAGCCC	ATTTATAAAC	ACGACCTTTC	ATCTCATCTA	2220
GGGCTGTCAC	ATCATTTTCC	AGAGCAAACG	CCAAATCTTC	TGCCACAGAC	AAGCCAATAA	2280
ACTGCCCATC	TGTATCCTGC	AAAACGTGTC	TAACCAGATG	AGACTTATCA	TAGATGCTCA	2340
TATCAAAGGC	TACTTGACCC	TTTATCAAAA	ATTCTCCATA	TGTCTGACCC	TTGTAAATAT	2400
TGGGAATAAT	CCCATTCAAA	CACTGACCCA	AGGTAGATTT	ACCTGACCCA	GATGGTCCAA	2460
CAATTAAGAC	TTTCTCTCCC	TTGTAAATGG	TCAAGTCTAT	CCCTTGCAAG	GTGGGTCTTT	2520
GTTGTGTTTC	ATACCGGAAA	GAGAAATCCT	TCCACTCAAT	TaTAGCTTCT	TTCATCTTAC	2580
TCTCTTCATT	CGCTTCTTAG	ACTTCTATTT	TATCATAAAT	CAAGCCCTTC	TTGCAGTCTC	2640
TCCTCTTAAA	ATCTTAGCGC	CAAAAAGATT	CCTATCCTAG	CTTACTTGCC	TAACTAATCT	2700
ATAAACATCG	AAAAAGACTA	GTTGCCCAGC	CTTCCCCATC	ATTTTATACT	CTTCGAAAAT	2760
CTCTTCAAAC	CACGTCAGCT	TCGCCTTGCC	GTAGGTATGG	TACTGACTT	CGTCAGTTTC	2820
ATCTACAACC	TCAAACCAT	GTTTGTAGCC	TGCTTCGTCA	GTTCTATCCA	CAATCTCAA	2880
ACACTGTTTT	GAGCAACTGC	GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	2940
TAGTCCTTTT	TCAAACCTTC	TGCACGAGTT	TGGGTTCTTG	CATAGGCAAG	TAAGAGAAGA	3000

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G TTCCTGCAA TAGCTACAGA TACACCATTG GCAATTCCCC CAACAATCCC TTGTGCAAAT 3060  
A CTTTTTCTG CCGCTTCTTG ATAAATCACA ACATCTCCAA GTGGTGCCAA GACACCCCAA 3120  
A CAAGGGCAT TTGCAAGTAG TTGAATGAGA TTA AAAAATAA GAATATCTTT CCAGTCAAAA 3180  
A CACCATTGA TCACGCGAAC GTACTTTCTA AAAAGTCCCA CAACTAAACC AAAGAGTCCG 3240  
C TAGCGATAA TCCAAGTCCA CCATAGACCA TAACCAACAA GAGAGTCCTT GATTGCATGA 3300  
C CAATCAACC CGACAAGCAA ACCGATAATC GGTCCAAAAA TAATAGAAAG TAGCGCTTGT 3360  
A CCGCATACT GAAGCTGGAT GCTTGTATTT GGAACAGGGG TTGGAATGTT GATCATCCCC 3420  
A TGACGACAA AGAGGGCAGC GCCAATCCG ACAGCAACAA CTTGTTTAAT TGTAATTTG 3480  
A TTTCCATAC TATTCTCCTA TTTTATCCTT CTATTTCTT TATTTCAATG GTCCAAGATG 3540  
A ACCGACACC TACATTATAG GCCTTGGCAA AGGAACCTTG GTTGATAGCC AAACCTAAAC 3600  
G ATAGAGAGA GTTGATGTAA AGGATGGGT GCCCAATTCT CACATCTGCA AATGATTTGC 3660  
C ATAGACAAC CTGATTTTGA TAGACCAGCA TATCAGCATG ATAGATGGTC ACTTCAAAAC 3720  
G ATCACCAAA TTCTGGTTCC AGCTTGTAAG ATTCTTCCCC TGTGATAGAG GTCCAAAGCG 3780  
A ACCGAAACG CACATCCAGA ATATCAATGG CTCCCTTCAC CAGATGATCT TCTATGATGG 3840  
T CGCTACGAC TGAAGCTCT ACAATCTGTT CCACACTGAG CTCTGGCCCT ACTTCCTCAA 3900  
A AGTAATGTG ACCACTGGCC AGTTTAGCAC CAGTATAGGC ATAGACATCA CGACCGTGGA 3960  
A AGTATAAGA ATGCTCTGTG TTTTGACGCC TATTGGCCAC CTCAGAAATC TCACGAATGG 4020  
C TACAATGCC AACGTGTTT TGTATAAAGG AAAGCGTCCC ATTATCTGGC GTGACAATGT 4080  
A TTGATTTTT TGCAGTCTTG GCAACTACAC TCTTACGTTT CGAACCGACA CCTGGATCGA 4140  
C AACCGATAC AAACGTCGTT CCCTCAGGCC AGTAATCCAC CGTCT 4185

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGATAGAGTT AAAGCCGCTG AGTCATTCAA TCCATCTCCA ACCATCAAAA TAGTGTGACC 60  
TGCTTTCTGC AGTTTCTCTA CTAAC TCAAA TTTCCCATCA GGTTC AAGT CTGTATAGAC 120  
CTGATCAAAG GGCAAATCTT TGACTAATTC CTCTGTCTTA ATCAAGGTGT CTCCTGTTGC 180

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CAGAATCAAT TTTTCCCCCT GTGCCTTAAG TTTATCCAAG GCTGTTTTTG CTTCTTTTCT	240
CAAAGGAGTA TGAATGCAGA ACATTCCAAT CAATTCATTT TGATAAGCCA AGAATAAGAG	300
ATTGTAGTGA CTCTTGTA CTTCATTAA AGCATTTTGT TCTGAACTGA TATGAATCTG	360
CTCATCCTGC ATCAAGACAT AATCCCAAT AAGAACTGGT TGGCCATCTA TATGAGATTT	420
GATCCCCTTG CTTGCGATAT ATTGGAGTTT CCCATGCATT TCCTCATGTT CAATTCCTC	480
TATCTCAGCT TGCTTGACGA TGGCATTAGC AATAGGATGA TAAATGTGTT CCTCAAGACA	540
GGCACTGATT CTGAGAATAT CTTCTCACT ATAGTCTCCA AAAGGTAACA CCTTTTCAAC	600
TATAGGATAA CTAGTTGTGA TTGTTCTGT CTTATCAAAC AAGAAAGTAT CAACTTCCAG	660
ATATTTCTCC AGAACATCTC CATCCTTAAT CACCATTTCA CGGTTCAACC CTTCTTGAT	720
AACTGTCAAA TAAGCTACAG GAGTAGAGAT TTTCAAAGCG CAGGAGAAAT CGACCAATAG	780
GAAAGAAATA GCCTTAGAAA AAGAACCTGT CAATAGGTAA GTCAGCCCAG CCCCCAAGAA	840
ATTATATTTG ACGACTTTAT CCGCCATCTT GATGAAATAG CGTTGTTTCG TTTCTTGTT	900
TTCTTCAGAT TTCTTCATCA ACTCAATCAG CTGTAAAATA CGGCTGTTCA TCTGATTATC	960
TGTTACACGA ATGCGTAACT CTCCAGTTTC TAATACTGTA TTTGCACAAA CCAAATCAGA	1020
CTCTCTTTT TCAACTGGAA AACTCTCTCC TGTCAAGGAA CTTTCGTTGA CCATACCTAA	1080
ACCTGAACT ACTTGTCAT CAAACAGAAT TTCATTTCTT TGAGATAAGA TCAAGACATC	1140
TCCTATTTGA ACATCGGAAC TCTTGATACT AACAACCGTA TCGCCCTGTA CTAGGAATAC	1200
ATCGCTCTCT TTTGCAAGAA GACTCTGTTT TAAATCTGTT GCAGTTTTTT TCAAGGACCA	1260
CTGATCTAAA TGATTCCCCA AATCAAGCAT AAACATGATA TTGCTAGCTG TCTTGGATTG	1320
GTTTCATAAAC AAAGACAATA AAATAGCCGA ACAGTCCAAG ACTTCCATCG TTAGTTCCTT	1380
ACGCGCTAGT GTTTGATAGG CTTCTCTAAT ATAACCCAAA GCCTGATAAC AAGTCCATAT	1440
ATAGCGAATA GGATACGGCA CAAACTACG AAAAAGTACA CGCTTAACCG CTGCACCTGA	1500
AACAATAGAA TAAGCACTCT CTTCTCTACG AATGGGAAGA GTCATCAACT CAGAACTTT	1560
CCCTTTATCA ATTCTTTTAA AAAAGGCTTC TGCATTATCT AATACAGAAA AGCCTTCTTT	1620
TATGCGTAGA GTAAAGTGCT GTTGATCCAT GTAAACTGG ATAGACTCAA TCCCCTTTTC	1680
ATCTCTCGCC AAGGAACGAA GATAGTCTTG AATATCCAAG GTAAGTGAAA AAGAAGATGA	1740
TAGTCGGATA TGTTGGTATC CTCTATGTAG CACTTTAAAA GACATATTAT TCACCTATAA	1800
GGCTATCTAA TTGCTCTTCT TTTTCTCTT GCTCGTACAA ATATTTGGCA TCTTGCAAGA	1860
CATCGTCTCC ATGTTGCTTC ACAACAGAAA CAGATGCATC TAGCTCGTCT TTCAACTTGT	1920
AAGCCTTAGC CAAAGCTTTA GAATAACCTT TTTTAGCTTC CTTACTTGCT AAGATTTTCA	1980

1105

AACCAAGGGT ACCAAATGCG ACACCACCCA AAAATAATGA AGATTTTTTC GCAACTTTTG 2040  
CAACGGTTAA TACTTCTTTT AACATAGGG 2069

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AAATCTTGCG CAATAAGCT CATCTCCATC TCCCGATTGA AACAGTCACT CCCC GGACTG 60  
TTTCAACGTC CCAAGACATA ATCTTAGGCA GATTTCTAAA ATTACACTCA AAGTGGAAGT 120  
CATTGAGCTT TCGAATGACA GTTGAAGTTG AAATGGCCAG CTGATGGGCA ATATCGGTCA 180  
TAGAAATCTT TTCAATTAACT TTTTGGCGAA TCTTTTGGTT GATAATACGA GGAATTTGGT 240  
GATTTTTCTT GACGATAGAA GTTTCAGCGA CCATCATTTT CAAGCAATGA TAGCACTTAA 300  
AACGACGTTT TCTAAGGAGA ATTCTAGTAG GCATACCAGT CGTTTCAAGG TAAGGAATTT 360  
TATAGGGTCT TTAATGTCTA GTAATTTTGT GATAAAATGT AATTGTTCCA TATGATTCTT 420  
TCTAATGAGT TGTTTTGTCT CTTTTCATTA TAGATCTTAT GGGACTTTTT TTCTACCCAA 480  
AATAGGCTCC ATAATATCCA TAGGGAATTT ACCCACTACA AATATTATAG AGCCCAAAGT 540  
TTTAGGTCGC TTGATAATAT GCGTTTTTTG AATTTTATAG ACTGCTCGTT TAAACTCTAT 600  
TTACTTCGTA CCTTCTGGAG CGAGACGGAA TATTAGTCAC ATACAAAATG AGTACTATTA 660  
GGATTTTATT TTCATGTACA ATTTTCAGCCA GTCTTGTTAT AATCAGCCTA TAGGAATCAA 720  
GGAGGTGACT CTTATGGCTG TTTTGTGTCT TTTGGATGGA ATTGTGGTAG AAGTCCTTGA 780  
TGTCTTTTCT TCTTTTAATG GGGATAGTGA GTTTTCTTTG TGTATAGCAT TTTGAATCTG 840  
GAATAGGACG CCATGACTGC TAAAAGATTT CTATAAATTA ATTTGATTTT CCTAATCAAT 900  
TTGTTTCATAT CTTATTTTCT TCCACTATAA ACGTCTTAAA GACAAGAGTC AGTTTGTAT 960  
GGAACGCTCT CAGTTCGAGG AGATGTTCCA ACTTCAAAGT AGTCGCTTGA CGACGCAAGA 1020  
AAAATTACAA TTGTTTACCT CTGTGTTTGC TGGCCGTTAT GATGTTTATG CTAAGAATTT 1080  
TATCAATGAA CAAGGGAAAA TTCAGTATTT TCCTTCCTAT GATTATGGTT GGAAGCAGTT 1140  
GCCACCTGAA AAACGGAGTT TCCAGACATT GACGAACTCC GTTTTGAAAT CTCATTTTCG 1200  
TGGGGAGGCA GCTATCGGTA TCTTTCCTAT GCACTTAGAT GATAGCTGTT ATTTTTTGGT 1260

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ACTGGATTTG GATGAAGGAG ATTGGAAAGA AGCTGGTTTA ACCATTCGAA GAATAGCCAG	1320
GGAACGCCAG ATGGAAGCCC ATTTAGAGAT TTCTCGTTCG GGTACGGAC TCCATATTTG	1380
GTTCTTCTTT GAGGAAGCGA TTCCGAGTCG AGAGGCTCGC TTGTTTGAA AGAAACTGAT	1440
AGAACTGGCA ATGCAGGAAA GTATGCAACT GTCCTTTGAT TCTTTTGATC GCATGTTTCC	1500
AAATCAGGAT GTCCTTCCTA AGGGGGGATT TGGAAATTTG ATTGCCTTGC CTTTTCAAGG	1560
AGAAGCTTAC CATCAAGGGC GAACGGTCTT TGTGGATGAA CAGTTTCAGC CTTATGAAGA	1620
CCAATGGAGG TATCTACAAG AAATTCAGAG GATTTCAACT GCTAAAGTGG CACTGTTAAT	1680
CCAAGAGGAG TTAGGCAAGC AAGAATTGGA TAAGGAGTTG AAGGTCGTTT TATCCAATAT	1740
GATCCAACCTT GAAAAATCGT CTGTGACATC CAAGGCACTT TTTTCTTGAA AAATATGGCT	1800
TCCTTTTCTA ATCCCGAATT TTATAGTAGA TTGAACTAG AATAGTACAC CTCTGCTTCT	1860
AAAACATTGT TAGAAATCGA TTTGACTTTC CTGATCGATT TGTCTGTTA TTATTTCAAT	1920
TTACTATATT TAAAGCAGGC TATGCGACAG CCAACCTATC AAATTCCTGA GAGAATGTAT	1980
TTATTTGGAG AATCCGATCA TTATTTATGG TTGCCAAGAG GTTTGCTGTA TCCATTGCAA	2040
GATAAATTTA AGCAGGTATC TGTGGAAGAT AGGAGAAAGG TACAAAGGTC TATTAGCGTG	2100
GAATTTAAGG GAGAACTCAC TTTGAGCAA GAGTTAGCCC TGTGAGATAT GACTTCTAAA	2160
GAAATGGTT TACTTCATGC GGAGACTGGT TTTGGGAAGA CCGTTTTAGG TGCTGCTCTT	2220
ATCTCTGAAC GGAAAACAAA AACAATTATT CTAGTCCATA ATAAGCAACT CTTAGACCAA	2280
TGGCTAGATC GCTTAACTG CTTTTGACT TTCCAAGAGG AGGAGGCTAT CCGTTATACG	2340
GCATCAGGTC GTGAAAAGGT AATCGGCTAT GTTGGGCAGT ACGGTGGGAC TAAGAAATGG	2400
CTGAGTAAAC TGGTTGATGT CGTTATGATT CAATCTCTAT TTAAGTTGGA AAATAGTCAA	2460
AGTCTTTTGG ATGAGTATGA GATGATGATT GTGGATGAGT GTCATCATGT CTCTGCCTTG	2520
ATGTTTGAAA AAGTTGTTGC TCAGTTTAGA GGGAAGTATC TTTACGGTTT GACGGCTACG	2580
CCTGAGCGTA AGAATGGTCA TGAGCCTATT GTTTTTCAGA GAATTGGTGA GATACTCCAT	2640
ACTGCTGATA AGAGGGAAAC GGATTTTAAA CGGCAATTGC AATTAAGATT CACTTCTTTT	2700
GGTCATTTGG AAATTGAAAA GACCAAAGCA AGTAATTTTA TACAGCTTAG TGATTGGATT	2760
GCTACTGACT CAGTGAGGAA TCAGATGATT CTCAAGGATA TTCTAGCCCA AGTGGCAGAA	2820
GGACGGAATA TCTTGGTTTT AGTTAATCGA ATTCAACAGA TAGATGTCTT TGAAAAATTA	2880
TTGAAAGAGA AAGAGGTTGA TGACTGTTAC ATTATTAGCG GAAAAACCAA AGTCCGAGAG	2940
AGAACGAGTT TACTGGAGAC GTTAGAACAG TTAGATAAAG GGTGTGTTTT GTTGTCTACT	3000
GGAAAATACA TTGGCGAAGG TTTTGACTTA CCTCAGTTGG ACACGCTTAT CTTGGCAGCA	3060

1107

CCCTTTTCTT	GGAAAAATAA	TTTGATTGAG	TATGCAGGTC	GGATTCATAG	AAACTACAAG	3120
GATAAGTCCT	TGGTGCGTAT	TTTCGATTAT	GTGGATATTC	ATGTTCTTA	TTTAGAAAAG	3180
ATGTTTCAGA	AACGACAAGT	AGCTTATCGA	AAGATGGATT	ATCGTGTCAT	CGAGGGTGAG	3240
GAGAAACAAT	TCGTTTATGT	TGATAGTAGA	TATGAGAAGG	TGTTGAGAGA	GGACTTAGCA	3300
GGGGAAAGAC	AGGAATGTCT	GCTTATTTTA	CCTTATGTGC	ACCAGACAAA	ACTGATGAAT	3360
TTTCTAAAAG	AATTTAGGAT	TAGTCAAATT	GAGATATGTA	TACCAGAGAC	GGTTGCAAAT	3420
AAAGCATGGC	TAGACCAGTT	GAAGAGCCAG	AAAATPAAAG	TGTCTTTTAC	TCAATCAAAA	3480
ATAGTAACGC	CTATTCCTTT	GGTGAATAAG	ACTATTGTTT	GGTATGGTGC	AATGCCATTA	3540
TTAGGGAAGG	TAGATGAGAT	GACCATATTA	CGTTTGGAAT	CAGCTAGTAT	AGTTTCTGAA	3600
CTAGTGGCAG	GTTTACGATA	GAGAAAATTT	TTAAAATTT	CTATGTATGA	TTTTCATTTT	3660
TTTAGTGAGA	CTGTTGCCAT	TATCACATTC	GAATCACACA	AAATAAAAAA	ATTTTATAA	3720
GTACTTGACA	AATAGATTGA	AATATCATAA	AATAAAAACG	GTTACAGAGT	TATTAATTAT	3780
TTAAGCTTCA	TGTCACCATT	AAAAATTGAA	ATAAAGGAT	GTTATCACTA	ATACAAGTGA	3840
GCAGGAACCT	ATTTAATCAC	ATCAGAAGAA	GTTTCTTGAT	GTTTTTAAGT	AGGTTCTTTT	3900
TATTTTAAAA	GGGAAATTTT	ATGATCATAA	AACGAATACT	AAACCACAAT	GCCGTAATTG	3960
CGCAAAGTAA	AAAAGATATC	GATATTCTTC	TTTTTGGAAG	GGGAATAGCT	TTTGGAAGAA	4020
AAACTGGAGA	TAAAGTAAAT	CCAATTGATA	TTGAGAAAAG	TTTTTTTCTC	AAAAATAGAG	4080
ATAATATGAC	CCGTTTTACA	GAGATGTTTA	TTAACGTTCC	TTGGAGTTG	GTGTACATCA	4140
CCGAAAAAAT	AATTAACCTA	GGTAAAATAA	CATTGGGTAA	TAATTTTGAT	GAAATTATCT	4200
ATATTAAATTT	AACGGATCAT	ATTTCTTCGA	GCATAGAACG	TTATAAAGAA	GGGATTATTA	4260
TTTCGAATCC	CCTACGCTGG	GAAATATCGA	AATATTATAA	AGAAGAATTT	GAACTTGGGA	4320
AAAGGGCTTT	ACAAATAATA	AAAAAAGAGT	TAGGTATTGA	ACTTCCAATT	GACGAAGCTG	4380
CATTCATAGC	GCTACATTTT	GTTAATGCTA	ATTTAGAAAA	TAATTTTCAA	GAGTCGTATA	4440
AAATCACTGA	AATAATTATG	GGAATTGAGA	AAATCATTCA	AGATTTCTAT	TGTACTGAGT	4500
TTAACCAAGA	TTCTATTGAT	TATTATAGAT	TCATAACTCA	TATGAAATTA	TTTGCCCATC	4560
GCTTGGTTGA	GAATACAACT	TATTGTGACG	ATGATGA			4597

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3984 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

1108

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CGGCTTATTT ACTACTTGTT CCATCATATA TGGAATATGC ATGAAACCTG CTCTCATATT	60
AGGGAATTTT TTATCCACTA AATAAAGAGC TTGGTACATC AATGATTGC AAACAAAGGT	120
TCCTGCACTA TTGGATACAA CTGCCGGAAG TCCCTGTTTT TTGATAGCTT GTACCATCGC	180
TTTGATAGGT AAACACTAA AATAGGCCGA TGCTCCATCA ATACGAATCG GTGTATCAAT	240
TGGTTGATTG CCTTCGTTAT CAGGTATGCG AGCATCATCT TGATTAATAG CCACTCGTTC	300
AGGTGTTAAG CCGGTCCTGC CGCCTGCTTG TCCAATACAA AGTACAGCAT CTGGTTGATA	360
TCGTAATATT TCTGCCTCTA AAACCTTCTGA CGACTTATAA AAAACCGTTG GAATTTCTAC	420
CCAGCGAACT TCAGCCCCAT TAATCTCAGA TGGTAATAAT TTTACAGCCT CCAAAGCTGG	480
ATTAATCTTT TCACCTCCAA AAGGATTAAA ACCTGTAACC AATATTTTCA TTTTATTTTC	540
CTTTACTAAA ATGCGAGAAA GTACATTAAG AATATGTGAA TAACAATCAT TACTAGAGCA	600
ACACCTGCTT GAGCCTTTAT AACGCCATTC TGATCTTTCA TATCCATCAA TGCTGCTGGT	660
AGAGCGTTAA AATTAGCAGC CATTGGGGTC AATAAGGTCC CACAATAACC TGCTGTCATG	720
GCAAGAGCAC CAGCCACAAT TGGATTAGCT CCCAGAGCAA ATACAAAGGG AACTCCAACA	780
CCTGCTGTAA TAACGGTGAA TGCTGCAAAA GCATTTCCCA TAATCATTGT GAATAGAACC	840
ATTCCAAGAA CATAGGCCAA AACTCCTATA AAGCGACTAT CTGAAGGAAC AATACCGCTA	900
ATCAGATGAG AGATAACATC ACCAACACCT GCTACAGTAA AAATAGCCCC CAAAGCCCCT	960
AATAATTGAG GAACAATCCC ACTTGTTGAA ACTTGCTGAG TCATTGATT ATTTTCTGAT	1020
AACAGACTCT TAGGGTGACT ATTGGTAATC ACAAGAACAG AAATTGTAGC AAACAAGGCG	1080
GCAAGGCTAA TCGAAATCTT GCTAAATTCT GGAATCATTT GCGCTAAGAC CAACGCAAGT	1140
ATTGCCATCA GCATAACTGG AATAAAATT TTATTTTCA ACCTGTTAGA TTCAATATTG	1200
GCTTTCATTT CATCTAAGGA TGGCAAGGTT CCGATACGGA CTTGCTTAAA CAATGTTAAC	1260
AGCGATAATA GGATTACAAT AATACCAATA CTCATATTTG GCATATAGGA ACCACCTATA	1320
AACGTAATAG ACAATAGAGT CCAAAATGCA GATGTCCCAA GTCGAACTGG GTTTGTTTTA	1380
TCTTTATAAC TACAATAGGC TGTATGGAGA AATTGACAAC CAATCACAAT ATAGGTCAAC	1440
TCTAATAGTT GCTTTGCCAA CTCTGTCATT TTTGTTCTCC TCCCCTAGTC TTTTTTGATA	1500
TCAATTTTTT ATCAAATAAA TAATTATAAA TCCCCACTAC AATAAGTGTT ATAACAGCAA	1560
CAATAATAGA TGTAGAAGCA ATCCCTGCAT AATTGCTTTC ATAGCCTAAC TGATCTAATG	1620



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TTCCCCCTAT CAAGAGGACT CCCCCAGCAC CTACAAACGT ATTTTGAGCA AAGAAATTTT	1680
CAAAATTTTC ATTGCGAGCC GCACGCGCTT TTATTGTCTC ATCTTCAACC TCTGTAACT	1740
TTCTACCTAA TTGAGACTCT GCAGCTGCTT CTCCCATAGG TTGAACCAAA GGTCTGACAA	1800
ACTGAGGGTG TCCTCCTAGA CGAATTGAAA AGAAACCAGC TAACTCTCGA ATAAAGAAAT	1860
AAACTGTATA GAAGTTTCCA ACTGTCAGAC CTTTAATCTT TCGAATCAAA TCGATTGATC	1920
GTTGCTTGAG TCCAAAGGTT TCTGACAGCC CCACAAGAGG CAAGGTAACC ATAAAAATCG	1980
TGAGCACTCG CTGATTGCTA AATTCTTTTC CCAAAATCTC CAAAAATTCA ACGAGAGAAA	2040
CACCTGAAAC TAAAGCTGTA ACCAAACCAG CTAAGACTAC TGTTGCAATT GTATCAAATT	2100
TTAAATAAA ACCCACAACA ATGATTGCTA TTCCTATTAA TCTAATCCAC TCCATATCAA	2160
ACTCCTTTAT ATTCAAAATG ACAGTATTTT TAAAATTTTA TCAAGATCAA TACCATTCTT	2220
TATTTAATGT GTTTTCTAG TTCTTTTGG TATTTGCTAT TGGATTCCAA TTTTCTTTT	2280
TGCCATTTTT TAAAAACCTC GTTATATTCT TTTGTTGTAA CAATATCTTT TTGCAATTTT	2340
ATTCCTTTAA AGATATATGG ATCCCCCTTA ATACCAACTT GTGAGTATGG TTTGAGAAT	2400
GGTACTACGT TACTTACAAC TGGAGAACCA CCAGATGAAG CTGTTGGCAT CAATAATGAA	2460
CTATCTGTCG ACCAAGCTTG AGCTTTGGCA TATTTTTCAT ATCTTTTCTC TAGGTCAGTG	2520
GTCTCAGAAA CAGCATCTTC TAACAATTTT TTATATTTAT CCAAACCAGG TTTAGCTACA	2580
ACATCCTTAT CTTTTCCTTT CGTAATACCA AGGTGTTTCA TGGCAGAACC AGATTTTGA	2640
TCTATAATAT TCAAGTGAGA CGCTGGATCT TGATAGCTTG GAGCCCATCC TGTACTGTTT	2700
AAATCATAGT CTTTTTGAGA AGGAGCAACA TTGCCGTATT TATCATTTTC CATCAAACCA	2760
TCAATAACAT TTCCAATAAC GTCTGTCTC GATGTTGAG TCGCTATACT GTAGCCCAAT	2820
GATGCTGGAT CTACTGCATA GACATAAGAA AATGTTGTCG GTGCATCTGC TTCTTTATCA	2880
GTTTTTCCAC AAGCCACTAA AATAGCTGAC GTGCTCAGGA CCACTCCTGC TGTTAAGAGC	2940
CACTTTTTCT ATTTTATAAA GAATCTCCTT TGGTTTATTT TAATCTACTT TTACAATCCA	3000
ACCTTCTGGC GCTTCAATAT CGCCAACTG AATACCCGTC AATTCATTAT ATAATTTACG	3060
CGTCACAGGA CCTACTTCTG TTTCACTATA GAATACATGG AAATCATCAC CATGTTGAAT	3120
ACCTCCAATT GGAGAAATAA CCGCTGCTGT ACCACAGGCA CCTGCCTCTA CAAAACGGTC	3180
AAGATTATCA ATTGGAACAT CACCCTCAAT AGGAGTTAAT CCCAAGCGAT GTTCTGCCAA	3240
ATAAAGCAAG GAATACTTGG TAATAGATGG CAAGATAGAT GGACTCAATG GTGTTACAAA	3300
TTCAATTATCA GCTGTAATTC CAAAGAAGTT AGCTGATCCG ACTTCTTCAA TCTTTGTATG	3360

1110

AGTTGATGGG TCCAGATAGA TAACATCTGA GAAATGACGT GACTTGGCCA TTTTTCCTGG	3420
TAAGAGACTT GCAGCATAGT TTCCACCAAC CTTAGCCGCA CCTGTACCAT TTGGTGTCTGC	3480
ACGGTCGTAC TCATCCTGAA TCAAGAAGTT GGTGGGACC AAACCACCTT TAAAGTAATT	3540
TCCAACGGC ATAGCAAAGA TGGTGAAAT GTACTCTTCT GCCGGTTTTC CCCCATAAT	3600
ATCTCCGACA CCAATCAAAA GAGGGCGAAG ATATAAGGTT CCACCTGTTC CGTATGGTGG	3660
TACGTATTCT TCATTGCGAC GGACAACGTC TTTACAAGCT TCTACAAACA TGTCTGTCCG	3720
AACTTGTGGC ATCAAGAGAC GGTCACATGT ACGTTGCAGA CGTTTAGCAT TTTCATCAGG	3780
ACGGAACAGT TGAACACTGC CATCCTTAGT ACGATAAGCT TTCAAACCTT CAAATGCTTG	3840
TTGTCCATAG TGAAGACTTG GAGAAGACTC TGAAATATGC AAAGTTGCAT CCTCTGTAAG	3900
CTCTCCTTGA TCCCATGTGC CATTTTTGAA ATGAGCAAGA TAGCGATAAG GTAATPTCAT	3960
ATAGGAAAAA CCGAGGTTTT CCGG	3984

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TATCTAATTA TTGGTTTTTA TCGCTGACCT TGGCTATTGT TGGGGTTGTT TTACCCTTGT	60
TGCCTACAAC ACCTTTCCTT TTGTTGTCTA TTGCTTGTTC CTCCAGAAGT TCCAAGCGAT	120
TCGAAGATTG GCTTTATCAT ACCAAGCTCT ATCAAGCATA TGTAGCTGAT TTTCGTGAGA	180
CCAAGTCTAT TGCGCGTGAA CGAAAGAAAA AAATCATCGT CTCTATCTAC GTCTTGATGG	240
GAATTTCTAT TTATTTTGCA CCTCTTTTAC CAGTCAAAAT CCGTCTGGGT GCTTTGACCA	300
TCTTTATTAC TTATTATCTC TTCAAGGTCA TTCCAGACAA AGAATAGTTA AAACAGTAGT	360
TATTTGCCTT GATAAAATTG AAAGCATATT CATAACAATA TGATATAATA AAATTGAAGT	420
AATATTCAAG GAGAATCAAA TGATTTACGA ATTTTGTGCT GAAATGTGA CTTTACTTGA	480
AAAAGCGATG CAGGCTGGAG CTCGTCGGAT TGAACCTCTGT GATAATCTAG CAGTTGGTGG	540
GACAACACCC AGCTATGGAG TGACTAAGGC AGCGGTTGAA CTGGCAGCTA ACTACGATAC	600
AACCATCATG ACCATGATTC GGCCACGTGG TGGTGACTTT GTCTATAATG ACCTAGAAAT	660
TGCTATCATG CTAGAAGACA TTCGTTTGAC TGCTCAGGCT GGAAGTCAAG GGGTTGTATT	720
TGGAGCTTTA ACTGCTGATA AAAAGTTGGA TAAGCCTAAT CTGGAAAAGT TAATTGCTGC	780

1111

ATCAAAAGGA ATGGAAATTG TCTTTCACAT GGCCTTTGAT GAACTAAGTG ATGAAGATCA	840
AGCGGAAGCT ATTGACTGGC TCAGTCAAGC CGGTGTCAC TCGTATCCTAA CTCGTGCTGG	900
TGTGTCTGGC GACTCCTTAG AAAAACGTTT TGTTCACAT CACAGAATTT TGGAGTACGC	960
TAAAGGTAAA ATTGAAATTC TACCAGGTGG GGGGATTGAC CTTGAAAACC GTCAAACCTT	1020
TATCGACCAG GTGGGGGTAA CACAATTGCA TGGTACTAAG GTTGTTTTTT AAAAATAGA	1080
AAGGAACTGC TAGCTTTGGG TAGCAGTTTT CACTTATGTT TGAAATTTTT AAATCCTATC	1140
AATTTAATCA AGAAAAGGCT CATGATTATG GTTTTATAGA AAATAGCGAA GTCTGGACAT	1200
ATAGTTGCCA GATTTTGCAA GGTGACTTTG TCATGACTGT GTCCATCACT GCTGATAATG	1260
TGAACTTTCA AGTCTTTGAC CAAGAGACTG GTGACCTCTA TCCTCACGTT TATATGGAAA	1320
GCATGAGGGG AAGTTTGTG GGAATGTCC GTGAGGCTTG TCTGGAGATT CTTTACCAGA	1380
TTCCGAAGGC TTGTTTGTG GTGCAAGATT TTATCTGTCA TCAGACTAAG CGTATCATGA	1440
CTCAAGTTCA GGAAAAGTAT GGAAACCAGT TGGAGTATCT GTGGGAAAAA TCGCCTGATA	1500
CAGCTGTATT GCGCCATGAA GGCAATCAAA AGTGGTATGC CGTCTTGATG AAAATCTCTT	1560
GGAATAAGCT GGAAAAGGCC AGAGAAGGAC AAGTGAAGC AGTCAACCTC AAGCATGACC	1620
AAGTAGCTAA TTTGCTTTCA CAAAAGGGGA TTTATCCAGC CTTCCATATG AGCAAGCGCT	1680
ACTGGATTAG TGTGTCCCTT GATGATACTT TATCAGATGA AGAAGTACTG GAATTGATAG	1740
AAAAAAGTTG GAACTTAACC TCTAAAAAAT GAAATATTTT AATAATTTTC ATGAACTTTC	1800
AATTAGCTAA ATATTCTTTA CTGAAGAGAT TTTTAGAAAA TATAGGATTT ACCACACTAG	1860
AGGAATATGG TGCCATCTTC AAATACCTGA TTGAGAATGT CAAGACGGAT CGTCAGATCA	1920
TCTATTGCCC TCACTGTCA TATGACCTCG GAATGGCAGT GGCAAATAGC CTTGCTGCTG	1980
TCAAGAATGG TGCAGGACGT GTTGAAGGGA CTATCAATGG TATTAGGGAG CGAGCTGAAA	2040
ATGCTGCTTT GGAAGAAATT GCAGTGGCTC TCAATATTCG CCAAGATTAC TACCAAGTAG	2100
AAACCAGTAT TGTCCTAAAT GAGACCATCA ATACGTCAGA AATGGTTTCT CGCTTCTCTG	2160
GTATTCCAGT TCCTAAAAAC AAAGCCGTCG TTGGTGGCAA TACCTTCTCC CACGAATCTG	2220
GTATTCACCA AGATGGAGTC CTTAAAAATC CTCTCACTTA TGAGATCATC ACACCTGAAT	2280
TGGTTGGTGT TAAGATTCTG CTTGGAAAAT TATCTGGTCG CCATGCTTTT GTTGAGAAAC	2340
TGAGAGAATT GGCCCTAGAT TTTACAGAAG AGGATATCAA ACCACTCTTT GCTAAGTTCA	2400
AGGCACTGGT CGATAAGAAG CAAGAAATCA CAGATGCAGA TATTCGAGCT TTGGTAGCTG	2460
GAACCATGGT TGAAAATCCA GAAGGCTTCC ACTTTGATGA TTTACAACCT CAACTCATG	2520

1112

CAGATAATGA CATTGAAGCG CTCGTTAGCC TAGCCAATAT GGATGGTGAG AAAGTCGAAT	2580
TTAATGCGAC AGGGCAAGGT TCCGTTGAAG CAATCTTTAA TGCTATCGAT AAGTTCTTTA	2640
ACCAATCTGT TCGTTTGGTG TCCTACACTA TCGATGCGGT AACAGATGGA ATCGATACCC	2700
AGGATCGGGT TTTGGTCACT GTTGAAAACA GAGATACAGA AACCATCTTT AATGCAGCAG	2760
GGCTTGATTT TGATGTGTTG AAGGCTTCTG CTATTGTCTA TATAAACGCT AATACCTTTG	2820
TTCAAAAAGA GAATGCAGGT GAGATGGGAC GCAGTGTTC TTACCACGAT ATGCCTAGTG	2880
TGTAAAGGAG AAGGCTATGG CAAAGAAAT AGTAGCTCTA GCAGGAGACG GAATTGGCCC	2940
AGAAATCATG GAGGTTGGTT TAGAAGTTCT GGAGGCTCTA GCTGAAAAA CAGGTTTGA	3000
CTATGAGATT GACAGACGAC CGTTCGGAGG TGCAGATATT GATGCAGCAT GACCTCCCTT	3060
ACCTGATGAA ACCCTTAAGG CAAGTAGGGA AGCAGATGCT ATCCTACTAG TAGCTATCGG	3120
TAGTCCTCAG TATGATGGAG CAGTGGTTCG CCCTGAACAA GGCCTGATGG CTCTCCGTAA	3180
GGAACCAAT CTTTACGCTA ATATTCGTCC TGTAAAAATC TTTGACAGTC TCAAGCATTT	3240
GTCACCACTC AAAGTGAAC GAATTGCTGG TGTAGACTTT GTCGTGGTGC GTGAATTGAC	3300
AGGCGGGATT TACTTTGGAT ATCATATTCT TGAAGAGCGC AATGCGCGTG ATATCAACGA	3360
CTATAGCTAT GAGGAAGTGG AGCGGATTAT TCGCAAAGCC TTTGAAATTG CAAGAAATCG	3420
CAGAAAAATC GTTACTAGTA TCGATAAGCA AAATGTTCTA GCGACCTCAA AACTCTGGCG	3480
GAAAGTAGCT GAGGAAGTCG CACAGGATTT CCCAGATGTA ACCTTGGAAC ATCAGCTGGT	3540
AGACTCAGCT GCTATGCTTA TGATTACCAA TCCTGCTAAG TTTGATGTTA TTGTAACGGA	3600
GAATCTTTTT GGAGATATTT TATCTGATGA ATCAAGCGTC TTATCTGGTA CACTTGGGGT	3660
TATGCCATCA GCCAGTCATT CTGAAAATGG ACCAAGTCTC TATGAACCTA TTCACGGTTC	3720
AGCACCTGAT ATTGCAGGTC AAGGAATTGC CAATCCTATT TCCATGATTT TATCAGTTTC	3780
CATGATGTTG AGAGATAGTT TCGGACGTTA TGAGGATGCA GAGCGTATCA AACGTGCTGT	3840
TGAGACAAGT CTGGCGGCAG GAATTTTAAC GAGAGATATA GGAGGTCAGG CTTCAACAAA	3900
GGAAATGACG GAAGCTATTA TTGCAAGGTT ATGAAGTTAG ACGAAAAAT TACTCTAGTC	3960
CTTTTGATTT GGAATGTCAT CATTTTCTTG ATTTATGGTA TTGACAAATC TAAGGCAAGG	4020
AGAAGAGTTT GGCGCATCCC TGAGAAAATC TTACTTATTT TAGCCTTTAC TTTTGGTGGT	4080
TTTGGTGCCT GGCTAGCAGG AATCATCTTT CACCACAAGA CTCGAAAATG GTACTTTAAA	4140
ATAGTTTGGT TTCTTGGGAT GGTGACCACA CTAGTAGCCT TATATTTTAT TTGGAGGTAA	4200
TGGATGGCAG GGTCTTCGAG GGAATACGCT GCTTGGGCTC TAGCGGACTA TGGTTTTAAG	4260
GTCGTGATTG CAGGATCTTT CGGTGACATT CATTACAATA ATGAACTCAA TAATGGCATG	4320

1113

TTGCCAATCG TTCAGCCTAG AGAGGTTAGA GAGAACTAG CCCAGCTAAA ACCAACCGAC	4380
CAGGTAAC TGACTTGGA ACAACAAAA ATCATCTCAC CAGTTGAAGA ATTCACCTTC	4440
GAGATAGATA GCGAGTGGA ACATAAACTC CTAAATAGTT TGGATGATAT CCGTATTACC	4500
TTGCAGTATG AAGAGTTGAT TGCTGCTTAT GAAAAACAAC GACCAGCCTA CTGCCAGGAT	4560
TAGAAAAAAT AGAAAAGGAG ATATAGTAAA CTGAAATAAG ATGTAAACAA ATGAATTGGA	4620
GCTTAACATC CATTTCCAGC AATTTTTTAG AAACCTACAGT GGACTATTCT GGATTCAACA	4680
CATTATAAAA TTATGACAAA ACACATTCAC AAGAAGGCTA CGACATTTTA AAAGGTGAGG	4740
GCGGATGTAT CGTTTGCCCT ACTAAAGTTG GTTACATTAT CATGACCAGT GACAAGGCAG	4800
GACTTGAGCG TAAGTTCGCA GCCAAAGAAC GTAAGCGTAA CAAACCAGGT GTTGTCTCT	4860
GCGGTAGCAT GGATGAACTT TGCGCTTTAG CGCAACTCAA CCCAGAAATT GAAGCATTCT	4920
ACTAAAAACA TTGGGATGAA GATATTCTTC TTGGTTGTAT CCTTCCTTGG AAACCAGAAG	4980
CCTTTGAAAA ACTCAAAGCA TACGGGGATG GCCGTGAAGA ACTTATTACT GATGTACGTG	5040
GTACTAGCTG TTTTGTATC AAGTTTGGA AAGCAGGTGA ACAATTGGCT GCCAAGCTTT	5100
GGGAAGAAGG TAAATGGTC TACGCCTCAT CTGCTTCAAT GACAAAACGA TTGAAACTCG	5160
CTATGAGCAA GGTGTAATGG TGTCTATGGT CGATAAGGAC GGCAAACTCA TCCCAGAACA	5220
AGGAGGAGCA CGTTCAACTT CACCAGCTCC AGTTGTGATC CGTAAAGGGC TTGACATTGA	5280
TAAATCATG ATGCACCTGT CAGATACTTT TAACTCATGG GACTACCGTC AGGTTGAGTA	5340
TTATTAGGAT AGAGAAGAAG TCTAGTGTTA TGAGATATTA AAGCTCCTAA CACTGGGCTT	5400
TTGTTTAGAA TTTCTTTCT TTTTCTATAG GATATGGTAT TCTATGTAGA AAATATATGT	5460
TAATAAGTAA TGCCAATATT TAAACATCAT TAGTAAAGG AGTTAGATTG ATGAATAAAA	5520
GAAAAGTTAG TTPAGAAGAT TTTTATAAAT GGTATAGTCT AAATAAAGAA GAGTTATTAA	5580
ATAAGGCAAC TGTTGGTGAA AAGTTTAATG ATAAATTAAA AGAAGAGTTT CTCCAGGAAT	5640
GGCCTTTGGA TAGGATTTTA ACAATGTCAA TCGATGAATA TGTAATAGGA AAGGGACAGC	5700
AAAATAAGTC TTTATGCTAC GCTCTTGAGA AGGGAAAATA CAAAAATCTA TTTCTTGGA	5760
TTTCTGGTGG CTCAGCTTCA AAATTTGGTA TTTATTGGAA TAAAAAACA AACAAATATA	5820
AAGATCAAGC TAATAATGAG ATTTACAGAGT TGGATCAGCG ATTTTCAAAA TTAAATCAG	5880
ATTTGTATGA AATTATCAA GAAGGTATTC GTTTTAACTT TGAAAATCCT ATTTTGTATA	5940
TGAAAAGATC AACAAATGAA TTTATTGGTC GTTCTGCTAT GGTGACAAAA TTACTTTGTA	6000
TCTATACTGA GGGAGATCCT TTCTTTGGTG TAAATATTAA TAGTCAGAAA GAATTTTGGA	6060

1114  
ACCACTTTGT TTCTCAGACA AATCAAGGTG GACCTTATCT GCAAAATCAT AAAATAATTG 6120  
AACTGGTGTC CAAAACCTTAT CCTGAGTTGG AGCCATCGAA ATTAGGAACT ATGCTTTTTG 6180  
AGTATTCTAA GCTTTTTATG GAAAATAAGG AAGACAATAG TACAATGGAT TCATCAAACA 6240  
ATTTTCGTCA TCAATTAACCT CAATCTCTAT TAAAGTCTCC AAACCTCATC CTCCGCGGTG 6300  
CTCCTGGCAC GGGAAAAACT TATCTTGCTA AAGAAATTGC TAAAGAATTA ACGGATGGCA 6360  
ACGAAGATCA AATCGGATTT GTACAATTTC ACCCATCATA TGATTATACG GATTTTGTAG 6420  
AAGGTTAAG ACCAGTATCA AATGGGGATG GAGCTATTGA GTTTAGGCTA CAGGACGGTA 6480  
TTTTTAAAGA TTTTGTGTCAG AAAGCAAAAG AAACCCAATT GATTGGAGGA CAAGATAATT 6540  
TTGATGAGGC TTGGGATTCT TACTTAGAAT ATATAAATGT TGCTGAAGAA AAAGAATATA 6600  
TAACAAAAAC ATCTTACTTA TCTGTTAATA GTAGACAAAA TTTGTCAGTA AATTATGATA 6660  
GTGGTGTTC AGGATGGTCA CTACCTAGCA AATATGTTTA CGAGTTGTAT AAAGATAAAA 6720  
ATTATAATAA GCAAGAATAC TACAAAAGTG GTGGAAAAAC TGTCTAGAA ACATTGAGAA 6780  
AGAGATTTGG TTTGAAAGAC TATGTTTCCC CAACAGAAAT TGATACTGAT AAGAATTTG 6840  
TCTTCATCAT CGATGAGATC AATCGTGGG AGATTCTAA GATTTTGGC GAACTCTTT 6900  
TCTCTATCGA CCCC GGCTAT CGTGGTGAAA AAGGAAGTGT TTCTACCAA TATGCAAATC 6960  
TACACGAAAC TGATGAAAAG TTCTATATCC CCGAAAATGT TTACATCATC GGAACATGA 7020  
ATGATATTGA TCGTTCAGTG GATACCTTTG ATTTTGCTAT GCGTCGTCGT TTTCGTTTTG 7080  
TTGAAGTTAC TGTCGAGGGT CAAGCTGGCA TGTGGATAA AGAGTTGAAT ATCCATGCAG 7140  
AAGAAGCAAA AATTCGTCTA AGAACTTGA ACGCTGCTAT CGAAAATATT CAGGAATTAA 7200  
ACAGTCATTA TCATATTGGA CCAAGTTATT TTCTTAAGTT GAAGGATGTA GATTTTGAAT 7260  
ATGAATTACT CTGGTCTGAT TATATTAAGC CTCTCCTAGA AGACTACTTG CGAGGTTCTT 7320  
ATGATGAGGT TGAACTTTG GAaACTTTGA AAAAAAGCATT TGATCTGACA AATAATGAGC 7380  
AAAAAGATCA GGCAGTAGCT GATGACAATG AAGGCGATGA AAACGATGAT GCGGATTACT 7440  
GATAATCAAC ACAAGATTAT TAAAGAAAAA TTTGTTGAAG AATATCCTAA ACTAAGCAAT 7500  
CCTCTTTTAG ACAGAACCTT GGAAAGTCTA TCCCAAGATG AACGTATTTT CATTTTCCA 7560  
AATGATTGA CTCATACTCC TGATTGGAT AAGGACCAA AGATTTTGA AACAGTCAAT 7620  
CAGAAAATCA AGACAGGGAA CGTGATTGGT TTTCTTGAT ATGGTCAGGA AAGATTAACG 7680  
ATTTCTCAC GATTTTCTGA TGAGAGTAAT GACCACTTTT TGCATTATCT CTTAAACAAG 7740  
GTTCTTCATA TCAATCTCAC TAGTTTAGAT GTTGCTTTGT CTCGTGAAGA GAGGCTTTAT 7800  
CAACTTTTGG TGTATCTCTT TCCCAAGTAT CTACAAGCTG CTATTCGAAA AGGTCTTTAT 7860

1115

AAGGAATATC ATCGATTTTC TCATAACGAC AGTCATGTTA AGGGAGTGAT TGATGTAAGA	7920
AACCATCTCA AGAAAAATCT TCCTTTCACG GGAAATATTG CCTACGCAAC GAGAGAGTTC	7980
ACCTATGATA ATCCCCTCAT GCAGTTGGTC CGTCACACTA TTGAATACAT TAAGAATCAG	8040
AAAAGCATTG GTCAACGGGT ACTAGATAAT CTCTCAACTA GTCGTGAAAA CGTATCTGAA	8100
ATCGTGCGTG TAACGCCCTC TTATAAACTA GCTGATCGTG CTAAGATTAT TCGGGGAAAT	8160
CAATCTAAAC CTATACGTCA TGCATACTTT CACGAGTACA GAAACTTACA AGAACTTTGT	8220
CTGATGATCC TAAACCAAGA AAAGCACGGT TTAGGGTATC AAGATCAAAA AATCTATGGT	8280
ATTCTCTTTG ATGTTGCCTG GCTTTGGGAA GAGTATGTTT ACACCTTGTT GCCAAAAGGT	8340
TTTGTACATC CCAGAAATAA GGATAAGACG GATGGAATTT CAGTATTTTC TGTGGGAAA	8400
CGAAAAGTAT ATCCAGATTT TTATGACAGA GAACGAAAGA TTGTTCTAGA TGCAAAATAT	8460
AAAAAACTGG AATTGACTGA AAAAGGAATC AACCGTGAGG ACTTATTCCA GCTGATTTCC	8520
TATTCTTATA TTTTAAAGC TGAGAAGGCT GGACTGATTT TTCCTAGTAT GGAGCAGTCA	8580
GTAAATAGTG AAATAGGAAA AGTAGCTGGC TATGGAGCTC AATTGAAGAA GTGGTCTATT	8640
CGAATCCCTC AGAATGCCTC ATTCTATAGT ACATTTTGTA AAATGATGGA AAATTCAGAA	8700
GAG	8703

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CATCACCAGT TTTAGATGGC TTTAACAGTG AAATTATTGC TTTAATCTT TCTTGTTCCG	60
CTAATTTAGA ACAAGTACAA ACAATGTTGG AACAGGCATT CAAAGAGAAG CACTACGAGA	120
ATACGATTCT CCATAGTGAC CAAGGCTGGC AATATCAACA CGATTCTTAT CATCGGTTC	180
TAGAGAGTAA GGGAATTCAA GCATCCATGT CACGTAAGGG CAACAGCCAA GACAACGGTA	240
GGATGGAATC TTTCTTTGGC ATTTTAAAT CCGAAATGTT TTATGGCTAT GAGAAAACAT	300
TTAAATCACT TAACCAATTG GAACAAGCCA TTATAGACTA TATTGATTAT TACAACAATA	360
AGAAAATTAA GATAAACTA AAAGGACTTA GTCCTGTGCA GTACAGAACT AAATCCTTTG	420
GATAAATTAT TTGTCTAACT GTTTGGGGGC AGTACACAAG AAAGCGCTTT AAAACCAGTA	480

1116

GACCTTTTCA TAAGGTTTCGC TTGATGTACC AAGATGAGGC TGGTTTCGGT AGAATCAGTA	540
AACTGGGATC TTGTTGGTCT CCAATAGGAG TAGGTCCACA TGTCCATAGT CACTATATAC	600
GAGAATTTTCG CTATTGTTAT GGAGCTGTTG ATGCCCATAC AGGCGAATCA TTTTCTTAA	660
TAGCTGGTGG ATGTAATACT GAGTGGATGA ACGCCTTTTT AGAAGAGCTT TCACAAGCTT	720
ATCCAGATGA TTATCTTTTA CTCGTTATGG ACAATGCTAT ATGGCATAAA TCAAGTACCT	780
TAAAGATTCC GACTAATATT GGTTTTACCT TTATTCCTCC ATACACACCA GAGATGAACC	840
CATTGAACAA GTGTGGAAG AGATTTCGTAA ACGTGGATT T AAGAATAAAG CCTTTCGAAC	900
TTTGGAAGAT GTCATGAATC AACTCCAAGA TGTCATACAA GGATTGGAGA AGGAGGTGAT	960
AAAGTCCATC GTTAATCGGA GATGGACTAG AATGCTTTTT GAAAACAGAT GAGTATAAAA	1020
TTGAATTGCT TATAAAAAAG CTCCATACAC TGGATGTGTA TAGAGCAATG GGGCTTTATT	1080
TGATATAGAG TTCTTGTTTT TTTAGGACAA TTTCTCGGAT ACTTGCAAAC TTTTAAAGTT	1140
TTTTGATTTTCT TTTCTGGATGA GTGACGAGAG TGATAACATA ACCTTCCTTG CCCATACGAC	1200
CAGTACGGCC AGCACGGTGT GTGTAGGTTT CGCTATCTCT AGGAATATCA AAGTTTACGA	1260
CACATTCTAG GCTATCGATA TCAATTCCAC GAGCCAAAAG GTCAGTTGCA AGAAGCAGGG	1320
TTAGTTGGTT ATCTTTAAAC TTTTCTAAGA TGATTTTTCT AAATTTAACA TTAACATCAC	1380
TAGCGAGGGA AACAGCCAAT ATATCAGGAT ACTGTAGTTT TTCCTCGGCA TTCCCAAGGT	1440
CTGACAGGCT ATTGAAGAAG ACTAGACCAC GGAAATCCTC TACATGAGCC AGTTTTCGTA	1500
GCATATCCAC TCGATGACGT TGGTCTACCT GCATGTAGAA ATGCTGGATA TTGTCCAATT	1560
TTTGATCAGA GAGATCAATA GTGCGTGTAT TCGGCACAAT CTTTTCTTGG TCAAACTTGG	1620
TCGTGGCACT CATGTAGACC AGTTGGTGGT CACGAGGTGC GTAGTGAGTG ATTTTTCTA	1680
CAAAGTGAAT CTGAGAATCA TCTAGTAATT GGTCAAATTC ATCCAGGATG ATGGTTTCCA	1740
CATTCATCAT CTTGATTTTT TTAAGTTTAA TGAGTTCAA GATACGGCCA GGAGTTCCAA	1800
TCAGAATTTT TGGCCCCCTT TTAAGACGTT CAATTTGTCT TTTCTGACTT GAACCTGAAA	1860
GGAAGAGTTG AGCAGTCAAT CCGATAGCTT CTGCCCACGT TTTACATACA TCAAAAATCT	1920
GTCCAGCAAG TTCCGTATTT GGTGCTAGAA TCAAGAGTTG TTGGGCTTTT TTCTTTTGTA	1980
GTCTGAGAAG ACTTGGTAGG AGATACGCTA GGGTCTTACC AGTTCCGGTT TGGCTCACTC	2040
CTAGGAGGTT TTCTCCAGCA AGAAGGGGCT CAAATAGTTG AGTTTGAATG GGGGTGAATT	2100
CTTGGAACC GAGTTGGTCA CTCAGTTCTT GCCATTCACT CGGTAGTTTG GTTTTCATTT	2160
TTCTGCCTCA AATCTAATGC CAGCAGTCTG GCGCATGGTA TATAGTAGCT CATGAACAGA	2220
GCCTGCATCA TACAGCCAAG TTTGGTAGAG ATTCAATCTT GGTGCTGGA TCATGTGTGC	2280



1117

AAATGCAGCG ACTTCCTCAG TCATCGTATG AGGAGCCTGT TGGATAGGAA GCTGGACTTG	2340
ATTTCCCTTGG TGGTCGGTAA AAATAGCTGA GCGAATATGC TCAATCGTGT TGAGAGTCAA	2400
GGTTCCATCT GTTGATATAA TCTCGCAAGG AAGATTGGAA GTGATGTTTT TTCCAGCCTT	2460
GATGTGAACT TGATAGTCTG GGTAGAAGAG GATACCATCT CCATTTAGGT CAATGCTATT	2520
GTCAAGCTGT TGAGCATGGT AAGTCGCGTC ATTGGCTTTT CCAAAAAGAC GAACAGCAGC	2580
ATAGAGGGGA TAAATCCCCA AATCCATGAG GGCTCCACCA GCAAAACGGT CTGAAAAGAC	2640
ATTTGGTGTT TGTCCAGCCA ACAAGTCAGG CATCTTGGAA GAGTATTTGG CATAGTTGAA	2700
ATCTGCTCCT AACACTTGCT TATCTGCTAA AAAGTTTTTG ATAGTAGTAA AGGCTTTCTC	2760
GTGGTAATTA CGAGCTGCTT CAAAGATAAA ACAGTTATTT TTTTCAGCTG TTTGAATCAA	2820
ATCAAACCAT TCTTGTGGTT GAGAGACAGC TGGCTTTTTCG AGAATAACAT GTTTACCAGC	2880
AGACAAGGCA GCTTTTGCCT GAGCAAAATG TAAGGAGTTT GGAAGTGGCA TATAGACTAA	2940
ATCAAAAGAA GATTTGAAGA AGACTTCTAA TTGATCGAAT AGTTGGATAT TCTGATAGCG	3000
AGAAGCAAAG GTTGCTGCAG TTTCTAGTTT TCTAGAATAG ATTGCGACCA GTTGGTATTC	3060
TCCACTGGTA TGGGCTGCTT CTATGAAATG ATGGCTGATA GCGCCAGTTC CGATGACACC	3120
TAATTTTAGC ATAAATACTC CTTTTCGGAT TTAAATCCT TCTTTCATTA TAACATAGAT	3180
AGACGGGACT ATCCAACAGA GAGGAGAAAA TTTCAAATAA GCTATTAGCT TTCTTTTCCG	3240
AATAAATAGA TAGAAGCATA GAATCTAGCA AACCTAGATT TAAAAATGTG CTATAATAGA	3300
AGGAGGAAAA GGAGGATTCT CAGACATCTA GGTATCAGCC CAACTAATGA TTTGTCAATT	3360
TATCCGCGAT ATGCTGGACT TGCCAGCAAA AAATGTGACG ATTTTGGAGG GAAGTAACAT	3420
TCACGTCTTG CCTTCCATGC CCTACTCAGC GTAAGATTTC TATACTAGTA TAGACGTCTT	3480
GGCGGAGTTA GATAATGGAA TCCAAGTTAT CATCGAAATT CAGGTTTCATC ATCAGAATTT	3540
TTTCATCAAT CGCCTATGGC CTTATCTGTG CAGTCAGGTT AATCAAAACC TAGAAAAAAT	3600
TCGCCAACGT GAAGGTGATA CCCACCAGAG CTACAAACAA ATCGCACTAG TATACGCTAT	3660
CGCAATTGTC GATAGTAATT ACTTCTCAGA TGACCTAGCT TTTCATAGTT TTATAGTAAA	3720
ATGAAATGAG AACAGGACAA ATCGATCAGG ACAGTCAAAT CGATTTCTAA CAATGTTTTA	3780
GAAGTATAGG TCTACTATTC TAGCTTCAAT CTACTAGAAA TTCCATAGAT AGAAAACCTAC	3840
ATAATCTCTA CAGATACGGA TGTGGGAGTT GATGTAAGAT GCTTTGGCTT GCTAGAGGAA	3900
TTGTGGATTG CCAAAATGTA TCATTGAAAT TATTGCTCAA ATTTGTTATG ATATAAATAT	3960
GAATAAAAGT AGACTAGGAC GTGGCAGACA CGGGAAAACG AGACATGTAT TATTGGCTTT	4020

1118

GATTGGTATT TTAGCAATTT CTATTTGCCT ATTAGGCCGA TTTATTGCTT TTAAGATCTA	4080
CCAGCAAAAA AGTTTTGAGC AAAAGATTGA ATCGCTCAAA AAAGAGAAAG ATGATCAATT	4140
GAGTGAGGGA AATCAGAAGG AGCATTTTCG TCAGGGGCAA GCCGAAGTGA TTGCCTATTA	4200
TCCTCTCCAA GGGGAGAAAG TGATTTCTC TCCTAGGGAG CTGATAAATC AAGATGTTAA	4260
GGACAAGCTA GAAAGTAAGG ACAATCTTGT TTTCTACTAT ACAGAGCAAG AAGAGTCAGG	4320
TTTAAAGGGA GTCGTTAATC GTAATGTGAC CAAACAAATC TATGATTTAG TTGCTTTTAA	4380
GATTGAAGAG ACTGAAAAGA CCAGTCTAGG AAAGGTTTAC TTAACAGAAG ATGGGCAACC	4440
TTTTACACTT GACCAACTGT TTTGAGATGC TAGTAAGGCT AAGGAACAGC TGATAAAGA	4500
GTTGACCTCC TTCATAGAGG ATAAAAAAT AGAGCAAGAC CAGAGTGAGC AGATTGTAAA	4560
AACTTCTCT GACCAAGACT TGTCTGCATG GAATTTTGAT TACAAGGATA GTCAGATTAT	4620
CCTTTATCCA AGTCCTGTGG TTGAAAATTT AGAAGAGATA GCCTTGCCAG TATCTGCTTT	4680
CTTGATGTT ATCCAATCTT CGTACTTACT CGAAAAAGAT GCGGCCTTGT ACCAATCTTA	4740
CTTGATAAG AAACATCAAA AAGTTGTCGC TCTAACCTTT GATGATGGTC CAAATCCAGC	4800
AACGACCCCG CAGGTATTAG AGACCCTAGC TAAATATGAT ATTACAAGCG GGGT	4854

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2186 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TAAACAGGTG TTAGGTGCTC TAAACTATTA AAATTCTAAG GAAATAAGGC TACTTTTTCT	60
GGGTCTTGT CATAGTAGGT GTGGTTCTTT TTTTCGAGTG TAGCCCATAG CTTTGAGCGC	120
ATAGTGGATG GTAGTTGGAT GACAGCCAAA TTCAGAAGCT ATTTCAAGTCA AATAAGCAAC	180
TGGATTGTCA GTAAGATAGT TTTAAGTCT ATCTCTATCA ACTTTTCTTG GTTTTGTTC	240
TTTTACTTGG TGGTTTAGCT CTCCTGTTTT CTCTTTTAGC TTTAACCAGC CATAAATGGT	300
ATTACGTGAG ATTTGGAATA CGTGTGATGC TTCTGTTATA CTACCTGTTT GCTCACAATA	360
AGAGAGAACT TTTTACGAA AATCTATTGA ATATGCCATA AGAAGATTAT ACCACATTGT	420
GTACTATTTT TGGTTCATTT TACTATATTT CTAAACACTT AGAAATAATA AAACAAATTA	480
AATATTATTT CTAAATATTT GAAATAACA TCTATTTGTA TTATACTATC TTTGAGGTAA	540
CTATTATGAA CTATATCAAA AGACCACATT ATTTAGATTT TTTAAGAAAA CATCGTGACC	600

1119

GACCAATCAT CAAAGTTGTG AGTGGAGTTA GACGAGCTGG TAAATCTGTG CTTTTTCAAC	660
TCTATAAAGA GGAGTTACTA GCAACTGGGG TAGACGAGGA TCAGATTATA TTCATCAATT	720
TCGAAGATTT GAGTTACTAT GATCTGCGAC ATTTTCAAAC ATTATTGCT TATATAAAG	780
ATCAATTAGT TAGCAAGAAA ACATACTATA TCTTTTGA TAGAAATTCAA TATGTTGAAA	840
AATTTGAACT GGTAGCAGAT AGTCTATTCA TCTTAGCAAA TGTAGACCTC TATTGACTG	900
GATCTAACGC CTACTTTATG AGTAGCCAAT TAGCAACAAA CTTGACTGGT CGGTATGTTG	960
AGATAGAGGT TCTTCCTTTG TCATTTGAAG AATATCTATC AGGTCAATCT CTCACAGAGA	1020
ATCTGAATAC AACAGAAATT TTTAACAATT ATCTCTTTAG TGCTTTCCCT TACTTATTGC	1080
AAACATCATC TTACGATGAA AAAATTGACT ATCTCAGAGG AATATATAAC TCCATACTGT	1140
TAAATGATAT TGTCCTAGA TTGGGAAAAC CAAATCCTAC TATTATTGAG CGCATTGTCC	1200
GAACCTTCT CAGTAGTACA GGTAGCTTAA TATCAACAAA TAAGATTGCG AATACCTAG	1260
TCAGCCAAA TGTTCATA TCCATAATA CTTTGGAAAA TTATTTGACA ACTTTGACAG	1320
ATAGTTTACT TTTTATTCC GTTCCACGTT TTGATGTAAA AGGTAGAGCA TTATTGCAAC	1380
GTTTAGAAAA ATATTATCCC GTTGATTTAG GTTTACGACA TCTCTTATTA CCAGACCAGA	1440
AAGAAGACAT TAGGCATATC TTGGAAAATA TGGTATATTT GGAATTGAGA CGTAGATATT	1500
CACAAGTATA TGTTGGTAAT TTAGATAAGT ATGAGGTTGA TTTTGTGTT GTAAGTGATC	1560
TTGGCCACTA CGCTTATTAT CAGGTCAGTG AAACAACACT TGCTCCAGAA AACTAGAAA	1620
GAGAACTTAG ACCACTAGAA GCCATTAAAG ATCAATTCCC TAAATATCTA TTAACAATGG	1680
ATACGATTCA GCCAACAGCC AATTACAATG GAATCGAGAA GAAAACCATT ATAGATTGGT	1740
TACTAGAAAA ATAGATAAAT ATAAATCATA CAGCTAATTA GATTGCAAC AGTCTGTTAT	1800
CAATGATTCT ACCCAAATCC TAACAAGATA TAGTGAATTT CGAATACGCT ATATAATACG	1860
GACACTTGAA AATAGAAATT GGGGATGAAA GGGGATCTAT AATTCTGGA AGTACTATCA	1920
AAAATTAATA TCATAGTCTT ATTAGAGAAT AGCATCACCC ACTTCTCAA ATAAGATTAA	1980
ATTGTAAGT AATTATAATG AAAAAGAGAC TGAGCAATCA GTCTTAAAA TCAGAAAAGC	2040
GCATAGTATC AGGTATTGAA CAACCTTGAT AATATGCGTT TTATTATGGA AATATTGCT	2100
TCATTTTCTC CTGAAATAGA GCTTTTGCTA TCCTATTTTT CTCTATTTCT AATGATTAC	2160
TTCAACTTCT TACCTCTTGG GAAAAA	2186

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3236 base pairs

1120

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GTCACACGTT TGA	60
CTTCACG TAT	
TCATAA GT	
AATACTT	
TATTTT	
TATC GGT	
TAGATAA	
ATCTTCATGC	120
CATTTT	
TAGC ATT	
TATCTAAA	
GGAGAAA	
ATA AC	
ATTATT	
TATT AG	
CATTATCA	
ACACCAAAGA	180
TATGGTGACT	
AGCTAGACTA	
TAATTT	
CTCTT	
CTCCATTAC	
TTGCTCGCGT	
TTCATTGTAC	240
CAGCTCCGTA	
GAAGAGATTA	
ACATTATCAA	
GTCTTT	
TAAA AAT	
CGGCAAA	
TTCATTTCCA	300
ATTCAGGAAT	
TGCAATTCCC	
CCAATAACTG	
GTAATTTT	
TG AGCAT	
CCCCAT	
TGAGAAGTTA	360
GAACAGCTTC	
CGAAGAGATA	
GCTTTGACAG	
AATCAAAGTC	
AAAATTGCCT	
TCTGTATCCT	420
GATTTTCTTC	
TAATTTTCT	
TTTGATACCT	
GGCTAACTG	
ATACTTATTG	
GTATTCCAGA	480
CTATGAAAAT	
ATTTCGAATT	
TGAGTATTAA	
AAATCAAAGC	
CAGTGACAGT	
AATATCAGAA	540
ATCCTGCTAG	
GATATTTGTC	
AGCAGATTTT	
TTGCTTGT	
TTTCTTTT	
TTA	
TTATTTTTTT	600
GAGACATTAT	
GCTTCACCTT	
CTGTTTCGTT	
TTCTGTCCCA	
ACTTCTTCTT	
TTTCTGCCAC	660
CGCAACCGTT	
GTGAAAGTCA	
CTATCTGAGC	
ATCTTGATCC	
AGGCGCATTA	
CTTTAACTCC	720
CATAGTTGCA	
CGTCTGTTT	
GTGAAATATT	
GGCAAGATTG	
GTTCGAATCA	
TGACACCTGT	780
ATCAGTGATA	
ATCATCAAAT	
CCTCATCCCC	
TTGAACAGTC	
ATAAGACCGG	
CCAGCAAGCC	840
ATTTTTCG	
GTAATTTTAG	
CTGTCTGCAT	
TCCCTTACCA	
CCAGACCTT	
TTGTTGGGTA	900
TTCACTAGCG	
ACTGTACGCT	
TACCATATCC	
TTTTTCTGTG	
ATAATAAGAA	
CCTCATCTTG	960
ATCAGTAATC	
AAGCTGGCAC	
CAACAACTGT	
GTCTCCTTCA	
CGAAGGTAA	
CACCTTTCAC	1020
ACCAGTGGCG	
ATACGGCTCA	
TACCACGAAC	
GGCTGATTGA	
TTAAAGCGAA	
CTGCATAACC	1080
AAACTTGGTA	
CCAATGATAA	
TATCCATATC	
TCCTTCTGCC	
AACAAGACAT	
TGATTAACTC	1140
ATCTTCATCC	
TTTAAATTCA	
GCGCTTTGAG	
ACCATTTTGA	
CGAATATTGG	
CAAACCTCCTT	1200
AACACTGGTT	
CTCTTCACAA	
TACCGTGACG	
GGTTGTAAAG	
AAGAGATAAG	
CATCATCACT	1260
GCGATCAGAC	
TCAACATTGA	
TAACCGTCTG	
AATACTTTCG	
TCTTCATCCA	
ATTTCAAGAG	1320
ATTGACTACT	
GGTAGCCCTT	
TGGCAGTCCG	
ACCATACTCA	
GGAATTTTCA	
AACCTTTAAG	1380
ACGATAGACA	
CGTCCCTTGT	
TTGTGAAGAA	
GAGCAGATGA	
TCATGGGTGC	
TAGTTGACAC	1440
TAACTCACGA	
ACAAAGTCAT	
CATCTTTCAC	
TCCCGTTCCT	
TGGACACCAC	
GACCCCCACG	1500
TTTTTGAGCA	
GTGAACTCGT	
CCTGATCCAA	
ACGCTTAATG	
TAGCCTCTGT	
TAGAAAGGGT	1560
AATCAAGACA	
TCCGATTCTT	
CAATCAAGTC	
CTCATCCTCG	
AGACTCAAGA	

1121

CCTGTCCAAT CATCAACTCT GTACGGCGCT TATCAGAAAA TTTACGTTTA ACTTCATCCA	1620
ATTGCTCTTT GATAATTTGA GAAACACGTT CAGGCTTAGC AAGAATATCT GCTAAATCCG	1680
CAATCAGAGC CAAGAGGTCA TCATACTCAG ATTGAATCTT ATCGCGTTCC AAACCTGTCA	1740
AACGACGAAG ACGCATATCA AGGATAGCTT GACTTTGACG TTCAGAAAGC TTAAACTTGC	1800
TCATCAACTC AGCTTGAGCT TCCGCATCCG TTTCACTAGC ACGGATGATA CGAATCAyTC	1860
GTCGATATGG TCTAGCGCAA TCAAGAGACC TTCTAAGATA TGAGCGCGCG CTTCCGCTTT	1920
TTCTTTATCA AAACGTGTAC GACGAACAAC CACTTCTTTT TGGTGCTCGA TATAAGCATC	1980
CAAAATCTGA CGAAGAGACA AAATTTTCGG TATACCATT TGGATAGCGA GCATATTGAA	2040
ACCAAAATTG GTTTGCATTT GGGTCATTTT GAAGAGGTTA TTGAGAATAA CATTGGCTGA	2100
GGCGTCGCGC TTGACTTCAA TAACAAATCG AACACCTTCA CGGTTTGACT CATCACGTAC	2160
TGCTGTGATA CCTCAATGC GTTTTCTCTG AACCAAGCGA ACAATATGCT CATGCACCTT	2220
GGTTTATTG ACCATGTAAG GAAATCTGT TACAACGATA CGCTCACGAC CAGTCTTAGT	2280
CGTTTCAATC TCTGTACGAG AACGTAGGAC AATCGAACCT TTACCTGTTT CATAAGCCTT	2340
ATGGATACCT GATTTCCCCA TGACAAGAGC ACCAGTTGGA AAATCTGGTC CAGGCAAGAC	2400
TTCCATCAAG TCCTTGGTAG TCACTTCAGG ATTATCCATG ACCAACTTCA CTGCATCAAT	2460
GGTTTCACCC AGATTATGAG GTGGAATATT GGTTGCCATC CCAACCGCGA TACCAGTTGC	2520
TCCATTAACC AAAAGGTTTG GAAAACGCGC TGGCAAGACC AAGGGTTCCC GTTCATTGGC	2580
ATCATAGTTA TCAACGAAAT CAACTGTATT TTTGTTGATA TCACGAAGCA TTTCCAGAGC	2640
AATCTTGCTC ATACGTGCCT CGGTATAACG TTGAGCGGCA GCACTATCTC CATCCATGGA	2700
ACCAAAATTC CCATGACCAT CTACAAGCAT GTAACGGTAG CTCCACCATT GAGCCATACG	2760
GACCATGGCT TCATAAATAG AGGAATCCCC GTGTGGGTGA TATTTACCCA TGACATCCCC	2820
TGTAATACGA GCAGATTTTT TATGGGGTTT GTCTGGGGTC ACACCCAATT CATTCAATCC	2880
GTAGAGAATG CGACGGTGAA CAGGTTTTAA GCCATCTCGA ACATCAGGAA GAGCTCGCGC	2940
TACGATAACA CTCATGGCGT AGTCGATAAA ACTTGCCTTC ATCTCCTTTG TCAGATTGAC	3000
ATTCACTAAA TTTTATCCT GCATTAATAA ATGCCTCATT TCACAATTAG TAAGTAACAA	3060
CATTATACCA TAAATTCCCA TCTATTTAG CCTCTAAACC ACTAAAACGT TTACATCGAG	3120
AACTATAAGG CATATTCGTG ACAAAGTTTT TAAAAAGTGA TAGAATGAAG TTGTCTAGGG	3180
AAAACCCCTA ATAGAATAAG GAGATGGTTA TACAATGACT CTGACTAACA CACAAA	3236

(2) INFORMATION FOR SEQ ID NO: 181:

1122

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8651 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AGGTCCTGAA GTATTGGAAC AGGAAGGTCA AGAGTTTTTG GAACATTTCA AAAAAGCTCTT	60
GGAGTCAGTT GAAGTAGTAG CCATCTCAGG TAGTCTGCCA GCTGGCCTTC CAGTTGATTA	120
CTATGCGAGC TTGGTAGAAC TTGCTAATCA AGCTGGCAAG CATGTAGTCT TGGACTGCTC	180
AGGTGCAGCA CTTCAGGCTG TTCTTGAATC ACCCCATAAA CCAACAGTCA TCAAACCAAA	240
TAATGAAGAA TTGTCTCAGC TTCTTGAAG AGAAGTTTCT GAGGATTTGG ATGAATTAAA	300
AGAAGTACTT CAAGAACCTT TGTTCGAGG GATTGAATGG ATTATCGTTT CACTTGGTGC	360
CAACGGTACT TTTGCCAAAC ATGGTGACAC TTTCTACAAG GTAGATATTC CTAGAATTCA	420
GGTGGTAAAT CCTGTTGGAT CTGGAGACTC TACTGTGGCA GGAATTTCTT CAGGACTTCT	480
TCACAAAGAA TCGGATGCAG AATTACTCAT CAAGGCAAAT GTCCTTGTA TGCTCAATGC	540
TCAAGAAAAA ATGACTGGTC ATGTCAACAT GGCCAACTAT CAAGCTCTAT ATGATCAATT	600
AATAGTAAAA GAGGTATAAA ATGGCTTTAA CAGAACAAAA ACGTGTACGC TTAGAAAAAC	660
TTTCTGATGA AAATGGTATC ATCTCAGCTC TTGCATTTGA CCAACGTGGT GCTTTGAAAC	720
GCCTCATGGT TAAACACCAA ACAGAAGAAC CAACTGTGGC CCAAATGGAA GAACTTAAAG	780
TCTTGGTAGC AGATGAATTG ACTAAATATG CTTTCTCTAT GCTTCTTGAC CCTGAGTATG	840
GACTTCCAGC AACTAAAGCT CTTGATGAAA AAGCTGGTCT TCTCCTTGCT TATGAAAAAA	900
CAGGTTATGA CACAACAAGC ACAAACGCT TGCCAGACTG CTTGGATGTT TGGTCTGCAA	960
AACGTATTAA AGAAGAAGGT GCAGATGCAG TTAAATTCCTT GCTTTACTAT GATGTAGATA	1020
GCTCAGACGA ACTCAATCAA GAAAAACAAG CCTACATCGA ACGCATCGGT TCTGAGTG/G	1080
TGGCTGAAGA TATCCCATTC TTCCTTGAAA TCCTTGCTTA CGATGAAAAA ATTGCGGATG	1140
CAGGTTCTGT AGAATACGCT AAAGTAAAC CACACAAAGT TATCGGCGCT ATGAAAGTCT	1200
TTTCAGACCC ACGCTTTAAC ATTGATGTTT TGAAAGTTGA AGTTCCTGTT AACATTAAAT	1260
ATGTTGAAGc KTCGCTGAAG GTGAAGTAGT TTATACACGT GAAGAAGCAG CAGCCTTCTT	1320
CAAAGCGCAA GATGAAGCAA CGAACTTGCC ATACATCTAC TTGAGTGCTG GTGTATCAGC	1380
TAAACTCTTC CAAGATACTC TTGTATTTGC TCATGAATCA GGTGCGAACT TTAACGGAGT	1440
TCTTTGTGGC CGTGCTACAT GGGCAGGATC AGTTGAAGCT TACATCAAAG ATGGTGAAGC	1500

1123

AGCAGCTCGC GAATGGtCGC ACAACTGGAT TTGAAAACAT TGACGAACTC AACAAAGTTC	1560
TTCAAAGAAC AGCAACTTCA TGGAAAGAAC GCGTGTAAGA AAGTCCTCCT AGTTTAGGAA	1620
CATGAATCTA AAAAAATTA AAAAAAGTTG TATGTAAAGG CTTACAAAAT AACTTACTTG	1680
TGCTATACTT AAATCACAAG TTAATATGAA TTAGAAAGTA ACTATATGAA GTATAATAAA	1740
AATAGGATAT AGTTTATTTT ACGAGCTAGG AAGGAAAAAT ACGGAAACAA TATTGCCAGA	1800
ATAAACTATA TTTAGATGCA CATTTTATTC ATTGTTTAT AAAAGGAGAA GATAAACGGC	1860
TACTAAAAAG AGTTTAAAG CGTTAGTTGT AGGACTAGGT ATTGTTTCAA TATTCTTATC	1920
AGCCTTACCT ATGGTTAGTG GTTCTGTATT TGCAGATAGT GCCCTAACTA CAGTAGATAA	1980
AGCAATGAT ATTGTTTGA ATGTTGATGG GAATAAATTT TATAATGTTT CGGTTTCAGA	2040
AGATATTGTA AATGCTGGTC AAATTTTGA AGATTATTTT TATGTAGATA AATTTGGAAA	2100
TATAAATTTA AAAGGCACTC CTGAAGAGTT AGCAAAAAAT ATTGGTATTT CTGTACAAGA	2160
AGCAAGTTTG ATGTATGGAG CTGTAAAAGA GTTACCCAAC GTTTACGAAA GAGGTCCTGT	2220
AGGTTTTCGT TTCAATCTTG GTCCTCAAGT GAGGGGGATG GGTGGCTGGG CTGCTGGAGC	2280
TTTCGCTACT GGATATGCTG GATGGCATT GAAACAATTT GCGGTTAATC CTGTTACATC	2340
TGGATTTGTT GCTGTAATAA GTGGTGGAT TGGCTGGGCT GTAAAACTG CTGTAGAAAA	2400
TTATTGGACA GTTGCTGTAG CTACAGTAGA AGTGCCGTTT GTGAACCTTG TTTACCCAT	2460
AGATTTACCT TAGAGGTTAT TTCTTTATGA ATCATTCTTT TAAAAAATA ACTGTATTTT	2520
GTTTTATAGT TTCTTGTTT CTTTGTATAT TAGACTTAAT GAATTTTAAA AATGTAGCTA	2580
CTTTTATAT TTTCTGTCTT CCTGTTTTTG TTTTGATTTA CAAAAATAA TAAAAACAGA	2640
GCCTCTGTTT GATGAATTTT AGAACATAGT TAAGTTTAA AAAAAAGTTGT ATGTAAAGGT	2700
TTACAAAATA ACTTACTTGT GCTATACTTA AATCACAAGT TAATACAAGG TGAGTGTTAC	2760
TAAGTAATAT TAGGCATGAT CACAGGTGAA TTAGAAATCA GCTGATTTTC TAGTTCATTT	2820
GTGGTCATTT TTTGTACTTA TATACCTTTA AGATATAAAA GGAGGTTGAC ATGTATCGAA	2880
TTCTAAATCC AATGAATCAC AATGTCTCGC TTGTCAGAAA TGATAAGGGA GAAGAGGTGA	2940
TTGTAATTGG TAAGGGAATT GCATTCGGAA AGAAGAAGGG GGATTTGATT GCTGAAAATC	3000
AGGTTGAGAA AATCTTTCGG ATGAAGACCG AAGAGTCCAG AGAAAACTTT ATGGCTCTTC	3060
TCAAAGATGT TCCGCTTGAT TTTATCACAG TGACCTATGA AATCATTGAT AAGCTATCAA	3120
AGAAATATCA TTATCCGATT CAAGAGTATC TCTATGTAAC CTTGACAGAT CATATTTACT	3180
GTTCTTATCA AGCTCTAACT CAAGGAAGGT ACAAGGATAG TAATCTGCCA GATATTTCCG	3240

1124

CTAAGTATCC TGTCCGCTTTT CAAATCGCAA ATGAAGCTTT TGAAATTTAC CGTCAGAAGC	3300
TAGCAGATCA TTTTCCTGAG GACGAAATTA TTCGGATTGC TTATCATTTT ATTAATGCTG	3360
AAGGTGAAAA TGAAGTGGAA CTTGTGGAGT CGATTGATAA GAGGAAAGAA ATTCTCAGGA	3420
ATGTTGAAGA AGTTTTAACG GACTATGCAA TTCAACGAAC TAAAAAGAAT AACCATTTCT	3480
ATGATCGCTT TATGATCCAT TTGAATTATT TCTTGGATTA TTTAGACAGA TCTAGAGATG	3540
ATAACCAATC ACTTCTGGAT ATGGAAGATC ATATTAAACA ATCCTATCCA AAAGCCTTCG	3600
AGATTGGTTC CAAGATCTAT GATGTGATTA CGCAACATAC GGGTCTTGAT TTGTATAAAA	3660
GTGAACGAGT TTATCTAGTT CTACATATCC AACGTTTATT GTCATAAAAA TTTATTTAAA	3720
ACTATATAAG GAGAATTCTA TCATGAATAG AGAAGAAGTA ACATTGTTAG GTTTTGAAAT	3780
CGTAGCCTAT GCTGGCGATG CTCGTTCAAA ACTATTGGAA GCCTTGAAGG CTGCTGAAGC	3840
TGGTGATTTT GAAAAAGCGG ACGCTCTGGT AGAGGAAGCT GGTAGCTGTA TTGCAGAGGC	3900
TCACCACGCG CAAACAAGTC TATTGACTAA GGAAGCTTCA GGTGAGGACT TGGCTTATAG	3960
TGTAACCATG ATGCATGGCC AAGACCACTT AATGACAACT ATCTTGTTAA AAGATTTGAT	4020
GCATCATTTA ATTGAACTCT ACAAGAGAGG AGTTCAATAA TGAATAAACT AATTGCATTT	4080
ATCGAGAAAG GAAAGCCTTT CTTTGAAAA CTATCTCGTA ATATCTATCT TCGTGCTATT	4140
CGTGATGGTT TCATTGCAGG TATGCCTGTT ATTCTCTTCT CAAGTATCTT TATCTTGATT	4200
GCCTTTGTAC CAACTCATG GGGCTTTAAA TGGTCTGATG AAGTTGTAGC CTTTCTGATG	4260
AAACCTTATA GCTATTCTAT GGGTATTCTG GCTCTCTTGG TAGCTGGTAC AACAGCTAAG	4320
TCATTGACTG ACTCAGTAAA CCGGAGCATG GAAAAACCA ATCAAATCAA GTATATGTCA	4380
ACATTGTTGG CAGCAATTGT TGGTTTGTG ATGTTGGCAG CTGATCCTAT CGAAAGTGGT	4440
CTAGCTACTG GATTCCTGGG GACAAAAGGT TTGCTTTTCA CTTTCTTGC TGCCTTTGTT	4500
ACTGTAGCCA TCTATAAGGT TTGTGTTAAG AACAACGTCA CTATTCTGAT GCCTGACGAA	4560
GTTCCACCAA ATATCTCACA AGTCTTTAAA GATGTGATTC CATTCACCTCT ATCTGTTGTT	4620
TCTCTTTATG CTCTTGACTT ATTAGCACGT TATTTTGTG GTTCTAGTGT GGCAGAATCA	4680
ATCGGTAAAT TCTTCGCACC ACTCTTCTCA GCAGCAGACG GATACCTTGG TATTACCATT	4740
ATCTTTGGTG CCTTTGCCTT CTTCTGGTTT GTTGGGATTC ATGGTCCATC TATCGTTGAA	4800
CCAGCTATCG CAGCTATTAC CTATGCCAAT GCCGAAGTTA ACTTGAACCT TCTCCAACAA	4860
GGGATGCATG CAGACAAGAT TCTTACTTCT GGTACACAAA TGTTTATCGT TACCATGGGT	4920
GGTACAGGTG CGACATTGGT CGTTCCATTT ATGTTTATGT GGTGACAAA ATCGAAACGT	4980
AACCGTGCAA TCGGACGTGC TTCAGTAGTT CCTACCTTCT TCGGTGTAAA TGAACCAATC	5040



1125

TTGTTTGGTG CACCTCTTGT TTTGAATCCA ATCTTCTTCA TTCCATTTAT CTTTGCTCCA	5100
ATTGCAAACG TATGGATTTT CAAATTCTTT ATTGAAACTC TTGGAATGAA CTCATTCACT	5160
GCTAATCTAC CATGGACAAC TCCAGCTCCA CTAGGTCTAG TTCTTGGAAC TAACTTCCAA	5220
GTGCTATCAT TCATTCTTGC TGCCCTTCTA ATCGTGGTTG ACGTTGTCAT TTAATATCCA	5280
TTCCTTAAGG TCTATGATGA ACAAATCTT GAAGAAGAAC GTTCAGGTAA GTCTAATGAT	5340
GAATTGAAAG AAAAAGTTGC TGCAAACTTC AACACTGCAA AAGCGGATGC TATTCTTGAA	5400
AAAGCGGGTG TCGATGCAGC ACAAATACC ATCACTGAAG AAACAAATGT CCTCGTTCTC	5460
TGTGCAGGTG GAGGAACAAG TGGTCTCCTT GCAAATGCTT TGAATAAGGC AGCAGCAGAA	5520
TACAATGTCC CTGTGAAAGC AGCAGCAGGC GGCTATGGTG CTCACCGTGA AATGTTACCA	5580
GAGTTTGATC TTGTTATCCT TGCCCTCAA GTTGCTTCAA ACTTTGAAGA TATGAAAGCA	5640
GAAACAGATA AGCTCGGTAT TAACTAGCG AAAACAGAAG GCGCTCAATA CATCAAATTA	5700
ACTCGTGATG GAAAAGGTGC TCTTGCAATC GTACAAGCGC AATTCGATTA AGGCTAGAGA	5760
CTCTGAAATA GTCTCCCATC GTTACGGAAA TCGCTATGGC GAATTTCTTA TTATTAATTC	5820
GTCGGTAAAA AGATATCGTT TTTACCTCCT CATGTCACAA TTCGGTGAAT TGGTACAAGA	5880
AGTGAGATGG AGAAGGATGG CTCACTGACT CCTCTCCTCT CACTTTTACT TTATTTAAAT	5940
CAAGAAATAG GTGAAAAAA TGACAAAAAC ACTTCCAAAA GACTTTATTT TTGGTGGCGC	6000
AACAGCTGCT TATCAAGCAG AAGGTGCTAC ACATACTGAT GGAAAAGGAC CAGTTGCTTG	6060
GGATAAATAT CTTGAGGATA ACTACTGGTA CACTGCCGAA CCAGCTAGTG ATTTTACAA	6120
TCGATATCCA GTTGACCTCA AGCTAGCAGA AGAGTATGGT GTCAATGGTA TTCGAATTC	6180
TATTGCTTGG TCACGTATTT TCCCGACTGG TTACGGCCAA GTAAATGCTA AAGGTGTTGA	6240
GTTTTATCAT AATTTATTTG CAGAGTGTC CAAACGTCAT GTTGAGCCTT TTGTAATCT	6300
TCATCACTTT GACACGCCAG AAGCTCTCCA CTCAAATGGA GACTTCTTAA ACCGTGAAAA	6360
TATCGAACAT TTTGTAGACT ACGCTGCCTT CTGTTTTGAA GAATTTCCAG AAGTAAACTA	6420
TTGGACAACC TTTAATGAAA TTGGACCAAT CGGTGATGGT CAATATTTGG TTGGGAAATT	6480
CCCTCCAGGT ATCCAGTACG ACCTTGCCAA AGTCTTTCAA TCACACCACA ATATGATGGT	6540
GTCTCATGCA CGCGCGGTAA AATTGTACAA AGAGAAAGGC TATAAAGGGG AAATTGGTGT	6600
TGTTACAGCC CTGCCAACTA AATATCCTCT AGATCCTGAA AATCCAGCAG ATGTTCTGTC	6660
AGCTGAGTTG GAAGATATCA TCCACAATAA ATTCATCTTA GACGCAACTT ATCTAGGTCG	6720
CTATTCAGCT GAAACCATGG AAGGTGTCAA CCATATCTTA TTAGTCAATG GTGGTAGTTT	6780

1126

GGATCTTCGT GAAGAAGATT TTACAGCATT AGAAGCTGCA AAAGACTTGA ATGATTTCCCT	6840
AGGAATCAAC TACTATATGA GTGACTGGAT GGAAGCCTTT GATGGAGAAA CTGAAATTAT	6900
CCATAATGGT AAAGGTGAAA AAGGAAGCTC TAAGTATCAA ATCAAAGGTG TTGGTCGTCG	6960
TGTAGCTCCT GACTATGTAC CACGCACGGA TTGGGATTGG ATTATCTACC CTCAAGGTTT	7020
GTATGACCAA ATCATGCCGTG TGAAGAAAGA TTATCCTAAC TACAAGAAGA TTTACATCAC	7080
TGAAAATGGT CTCGGCTATA AAGATGAGTT CGTTGATAAC ACTGTTTACG ATGATGGTCG	7140
TATTGATTAC GTGAAGCAAC ACTTGGAGGT TTTATCTGAT GCGATTGCAG ATGGAGCTAA	7200
TGTAAAAGGT TACTTCATTT GGTCAATTAAT GGATGTCTTC TCATGGTCAA ACGGTTATGA	7260
GAAACGTTAT GGTCTCTTCT ACGTAGATTT TGAACTCAA GAACGTTATC CTAAGAAATC	7320
AGCTCACTGG TACAAGAAAG TAGCGGAAAC TCAGATTATA GACTAGTAGA ATTAGTCATT	7380
AGATATAGAA TTTTAGTGAG TCAAAAAGAT GTTCAAAGAT TTTATCCAAT CTATTTATGA	7440
AAAAAAGTTT ATATTATAAA TTTCGAAAA TGCTCTCAA TACCGTGTTT GACGAGTGAA	7500
GAATTGAAAA GTCTTGAAAA ATGGTATGTC TCGACTGGTA AAGAATGGAT TTGTCATTCA	7560
GATGATGAGC TGAAGAATT TAAAAATCTA TTTTAAATTT TTATCAATCC TGAAGAATGG	7620
GATACTATCT CCTTTGATTC AGATTTTATG CCGTTTCAAC AATCGTAACC AATTTCTCAA	7680
AAAAGTTAAA TCTTATATTT AGTACTCTGT AAAACTCTTA TCTAATCACG TTGCTTATAC	7740
TCAATGAAAA TCAAAGAGCA ACTTTAACT AGGAAGCGAG TCGCAGATTT CTCAATGCAT	7800
AGCTTTGAGG AATTGGGCAA AAAGTCTTTG ATATAGAAAA ACGCATAGTA TCAGGTGTTT	7860
CAACACCTGA TACTATGCGT TTTATTGTGG GAAGATTTAC TTTTTTCTT CTGAAATTGA	7920
GTGTTACCC AGGCTCTTTC AGTTTATTAA GGCTTGATGA CTTTAATGTG TTTAGATAGC	7980
TTAAAAAGGA TTGAATCACT TAGTTTAGAA TCTGAAACAA TAGTATCAAG ATTTGATACA	8040
TTATAAAAAG TATAAAAATC AACTTATTG AACTTGCTAT GATCTGCGAG TAAATATTTT	8100
TTATTAGAAT TATTTAAAGC GATGCGTTGA GCCTCTCCCT CTTCTCGCT AAAAGTAGCT	8160
AGAGCTCCGT TTTGAATACC ATTACAGCTA ACGAAAGCTT TAGAAAATTG GAGATTAGAG	8220
AGATTTTGTA GGGTCAATGT ACCAACAAAA GCACCTGTAA TATCGCGATA ATTTCCACCT	8280
ATTAAAATCA AATCTGTAA TTTCGTTTCG CTTAAAATCA GAAAAACAGG TAGACTGTTG	8340
GTTACGACGC GGATATTGTC AATAGGCAAC TCACGCGCAA AAAACTCTAA TGTGTTTCCT	8400
GGTCCAATGA AAATAGTTTC TCTTCTTCT ACTAGACTGC CTGCAAAATG GGCTATTTCT	8460
TGTTTTTCTG CCGTTTGGAG GGCTTGTTTT TCAATATTTG ATCGCTCATT AGTCAAAGG	8520
GAGTTGGTTC GAAGTTTTTC AGCTCCACCA TGCACACGAA TCAGCAAATC TTTATCAGCT	8580

1127

AATTCCTGTA AATAGCGCCT TGCAGTCATA TCTGAAACGG CTATTTTCGTC CATAATCTGT 8640  
TTAACTGTTA T 8651

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3786 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AATCTCCAAT CAGTGCCACT TCAGCTACAA AGAAGAGGAG GATAATAACT CCGTTCACAA 60  
GGACAGACAA GAATAATTGA TAGAAGGAGT CGGTTTCACT TGCTTGACTT GGTCTTGTA 120  
TGATWTGGAG ACTGGCAAGC AGAATGATTC CAATGCTAAT CACACACAAG AGGGCTGTAA 180  
ATCGTAGGCT ATCAAAGAAA GCAAAGAAAC TAGCAATAGC AGTGAGGAmG ATTGGAATTG 240  
CCAAGAGTTG ACTATATTGT TGGAGAACCT TGTCTAGCGT CCAGTCCTTT TCCTGGTGGA 300  
TAAATCGTCT CACAACGAAA CTACCCAAGA GGAATGAAAA GAAGAAGAGT GTTGTGCGTA 360  
CTAGGATAGA GATGATAGAA AAAAGAGTTA AAGGAGCTAG CTGCTCAGGG AAGCGACTGT 420  
TAATGCTTGC TATATGTCCA TAGTAAGCAT GTTTGATGTG ATAGATACTA AAGAAAAAGG 480  
AAGATGCAGA AAACAGAATG AGCAAGAGAA AGGCTGTGTA ACTGTGTGTG ATACTTGTTT 540  
CCAACCTACT TGTAGGAGAT TTGATCGCTT CCACTAGCCA AGACCAAAA TCAAGCACTT 600  
GCTCTTTCCA TTTATCCCTA GATTTTGGAG CTTGGTCGGG GATATAAGGA CTTTCTAAAG 660  
ATTTACTGAT AAGAAGTGGC TCTTTCTGGT TTGCTTTTTG CTGAGGAAGA GCTTCTTGGC 720  
TCTCTTCAGC TATAGTGACT TTTCTGTTT CTTTAGAAAG GTCTGGCTCT TCTTCAGTAG 780  
AATTAGATGC CTTCTTTTCT TCTATTTCTG TTCTCGCTTC ACTGTCTTCA GGAGCTTCAA 840  
TTTTCTCTTC TTGCTGGCTT TCCAATTCGA CTTCAGCTTG AGGGACTTCC TCCTCTAACT 900  
GAGTATTTTT TTCAATTGGT GTATCGAGAT CGGCTATCGT TTCTTCAGCC TTGCTGCAA 960  
CCTCTTGAGC TTGCTCTTCA GGCTTGTCTT TGCTTGTTGT TTTTACAAA TCATTACTTT 1020  
CAAACCATTC TTGTTTCATG GTAGAACCTC CTTTTTAGTT AGATAAATAT GTTCCATAG 1080  
TAGCAAATGT AAGCGTTTTT GTCAACGTCT GCTTGGTGTG GATATTAGAT CAATATTATC 1140  
ATCAGATCTC GCAATGAGTT GATCCTTGAC ATCGGTTTTT TCAGTTTTGT AAGGGTTGCT 1200  
TAATTCCGTA CCTCTTGATT CAGGCTTTTC TCTTGGAAT TGAAGATAG AACCATAGTT 1260

1128  
GCTTGAGATG TCCCAGTTAA TTCGTTGGCT TTCTTTCTGG TCTAGGATGA TTCTGAGATA 1320  
ATCTTTGGCA GTCAGTTCAA CCTTGCCATG GACTTGGATA TTTTCAGCGT GGAAGTGATT 1380  
CTCTGTTGAC TCTAGCTGAC TATCTGTAAG AACTGTATCA AAGATATTAA CGATATTGGG 1440  
CGTTGTGAGT TTACTGTTTT TGATACGACT TCCTTCAATT CCGAGGATAT AGCTGTTTGT 1500  
ATTGAGGGTC GCATTTTCAA GGCTAGCATT TATGATGGTG GTTTGTCCGC GATTGGCTGA 1560  
GATGTTGATC CCTTTTAGAG TTCTCCCTTT TGGTAGTCGG AGAATAACTT CTTCAAAACG 1620  
ACTAGAGTAG CTACTTGCGA TATGAAGAAT CCCACCAATT CCAGAAGAGA GAAACGGAGT 1680  
TTCAGACAGT TTCTTATCAG TGAGACTCAG AGTTCTATCG TTCTGATTGG TGATAAGATC 1740  
ATGGTGAGCA GAAAGAGATG GATGGTAAGA AATGTGGATT TGATCATCGA AAGAGTCTGT 1800  
GATGGTGAGC GTGTGTTGGT GGAGAGTAAT TTCTAGGTTT TCGACTTCCT TGCCAAAGGT 1860  
TAGCTTTTCC GTACGGCTAT CATAGACAGG TTCTTTGGAC ATGGAAAGTA GGCTCTTAAc 1920  
CCCGTCAGAT TGGATACCTA CAAAAAGCAG GATAAAGCCG ATAACGGTAG TCACCACACC 1980  
AAAGATGAGA AATCCTTTTG TCCATTTACG CATGCTGATT ACCTCTCTTT CCTTTTTTAA 2040  
GAACAAATTG TACCAGACGA ACAATGAGTA GACCGAAGAA GCGAGTTGCA TAGGAAATGC 2100  
CAAGTAAAC TAGCGAAGAA GCACCGATAG CCAGTAAACC AGAACCAAAA ATCAAGATAA 2160  
AGGCTGATTT GGCTTGGGCG AGGACAGTGA AACTTTCAAC TAAAAATAGG AATCCGCCGA 2220  
TGATACCCAG TATGGAACT GCAAAGAAAG CCAGAATGAC AGTCAAAGCG GCTACAAGAA 2280  
TTGCGAACAG GGTCACGAGG ATGGCGATTC CCAGAGGAAT GCCGATAGGT GCTGCAAGGA 2340  
GGGCTAACAA GCGGATATGT AAAATTTGTC GGTTATTTTT TTGAGCGGGT GCTTCATTGA 2400  
TTTTTTTATC GAGAAGATTG GATAGAACTT CGTGGGCCGC TTCTTTGGGA GTTCCCAAAC 2460  
TAGCGATGAG TTCTTCTTCT CCTTCGACTC CAGCATCGTC AAAGAGCTCT CTGAAATAGT 2520  
CCATGGCTTC GATACGGTCA GCTTCAGGTA GTTCTTTGAG ATAGAGTTCT AGCTGAGTCA 2580  
GGTATTCAGT TCTTGTCATG GCGGATACTC CTTCTATGA TGCCATTGAT GGTGTCTGTA 2640  
TAGAGTGCCC ATTCATCTTT TAGGGTCAAG AGCTGCTCTA TACCACCGTT TGCAAGGAG 2700  
TAGTATTTGC GCATGCGACC TTGGAACCTCT CTAGAATAGG TTGTCAGAAA GCTATTGCCT 2760  
TCCAATTTTT TGAGAATGGG ATAGAGTGTG GATTCTTTGA TATTAGCGAT CAGCTTAATG 2820  
GTTTGGCTAA TCTCATAACC ATAAGAATCA CCCTGCTCCA GTACAGCCAA GATGAGAAAT 2880  
TCAATCAAGG CAGAGGATGT TGGAAAGTAC ATGGGAAACC TCCTTTTCTA ATGTGTAAGA 2940  
TTTTTATATA TAATTTTTCT ACACATACAT TGTACATCTA AAAGAAAGCC CTGTCAAGAG 3000  
AAATGTGTAA AATTTTTATA TATAAAAAAC TTCTAGCTAA AACTAGAAGT TTAAAGGATC 3060

1129

TTATCCGCTC TGTCCACTGT AAAGAGGGCC ACAGTCATCA GGATATCGAT GAGCAAGAGG	3120
GCAGCTACAG ATGGTACCCA AGAGTGGAAC AGGTCAAAAC TGTAACCAAA GAGGGTTGGC	3180
CCAAAGGCTG CTAGGATATA GCCTCCTGTT TGAGATAGGC CGGACAATTG GGCTGTCTTT	3240
TCAGGGGCGC TTGTCTTGAG TGAAGAGTTG ACCATGAGAT AAGGGAAGAG GGCCTGGTT	3300
GCGGTTCCGA TGAGGAGATG GATGGCAAGC CAGTAAATGA AATTATTGAT TGGGAAAAAG	3360
AGCATGGAAA TGCCGACCAC ACCAGCTAGT GAAACCAGAG TGAGCATGAG CTGACGGTTG	3420
CGAGTAGATA AACTGGTTGT CAGGCTTGGG ATGGTCATTG AAAAAGGAAT GCTAATCAGA	3480
GATAAGATAG AAGTCAGCAA GCCAGCTTCG TGAAGTGATA GACCTGCATG GATAGACATG	3540
GTAGGTAACC AGGTCATGAC GGTGTAAAAG ATCAAGGATT GAAAACCTGA AAAGATAATA	3600
ATTGCCCCAA CCTGTTTATT ACGCATGACC TTTATTTGAC TTTTTTGTGTT GGTGTTGTGA	3660
GCTAGTCTAT GATTATAGCG GTGATTTGGG AGCCAGACCA AAAAAGTTGC TAGACAGAGT	3720
AACGTGAGGA GAAGGATAAG TCCTTTCCAA GAACTGGCTT GTGTAATGGG CACAGCTAGA	3780
TAGGAA	3786

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3054 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TCAGCTAAAA AACATTGCTA AATTGATTGA AGCTGGTGCT ACACATTCCG ATTCAACTTC	60
TCACACGGCG ACCACCAAGA ACAAGGTGAG CGTATGGCAA CTGTTAAACT TGCGGAAAAA	120
ATTGCAGGTA AAAAAGTTGG TTTCTTCTT GATACAAAAG GACCTGAAAT CCGTACAGAA	180
TTGTTGGAAG GTGAAGCTAA AGAATATTCA TACAAAAGTG GTGAAAAAAT TCGTGTGCA	240
ACTAAACAAG GAATCAAATC AACTCGTGAA GTGATTGCGT TGAACGTTGC TGGTGCTCTT	300
GATATCTATG ATGATGTTGA AGTTGGTCTG CAAGTTTTGG TTGACGATGG TAAACTTGGT	360
CTTCGTGTGG TTGCTAAAGA TGATGCAACT CGTGAATTTG AAGTTGAAGT TGAAAACGAT	420
GGTATCATCG CTAACAAAAA AGGTGTGAAC ATCCCTAACA CTAATAATCC TTTCCCAGCT	480
CTTGCTGAAC GCGATAACGA CGATATCCGT TTCGGTCTTG AACAAGGTAT CAACTTCATC	540
GCAATTTTCAT TCGTACGTAC TGCAAAAGAT GTGAACGAAG TTCGTGCAAT CTGTGAAGAA	600

1130

ACTGGAAACG GACATGTTCA ATTGTTTCGCT AAAATCGAAA ACCAACAAGG TATCGATAAC	660
TTAGATGAAA TCATCGAAGC AGCTGATGGT ATTATGATTG CTCGTGGTGA TATGGGTATC	720
GAAGTACCGT TCGAAATGGT TCCAGTTTAT CAAAAATGA TTATCAAGAA AGTCAATGCT	780
GCAGGTAAAG TTGTTATCAC TGCAACAAAC ATGCTTGAAA CAATGACTGA AAAACCACGT	840
GCAACTCGTT CAGAAGTATC AGATGTATTC AACGCTGTTA TCGACGGAAC TGACGCTACA	900
ATGTTGTCAG GCGAGTCTGC AAACGGTAAA TACCCACTCG AGTCAGTAAC TACAATGGCT	960
ACAATCGACA AGAACGCTCA AGCTCTTCTT AATGAATACG GACGCTTGA TTCAGATTCA	1020
TTTGAGCGTA ACTCTAAGAC AGAAGTAATG GCTTCTGCTG TTAAAGATGC TACTAGCTCA	1080
ATGGATATCA AATTGGTTGT AACTCTTACT AAGACAGGTC ATACTGCACG TTTGATTTCT	1140
AAATACCGTC CAAATGCTGA CATCTTAGCA TTGACATTTG ACGAATTGAC AGAACGTGGC	1200
TTGATGTTGA ACTGGGGTGT TATCCCAATG TTGACAGATG CTCCATCTTC AACTGACGAT	1260
ATGTTTCGAAA TCGCTGAACG TAAAGCGGTA GAAGCAGGTC TCGTTGAGTC AGGCGATGAT	1320
ATCGTTATCG TTGCTGGTGT GCCAGTAGGA GAAGCTGTTT GCACAAACAC AATGCGTATC	1380
CGCACAGTAC GTTAAGAAAA ATATAAAAAC CTATCATATC CAGCTTTAGA GCTTGTGTGA	1440
TAGGCTTTTT GTATAGAGGG TAAGAAATAG GCAAACTTT CATAATGGAT TGATACTCTT	1500
CGAAAATCTC TTCAAACCAC GTCAGCGTCG CCTTACCGTA TATATGTTAC TgACTTCGTC	1560
AGTTCTATCT ACAACCTCAA AGCAGTGCTT TGAGCAACtG CGGCTAGCTT CCTAGTTTGC	1620
TCTTTGATTT TCATTGAGTA TGAAATAGA TATGCACAAA TTGATTAGAA AGTCAAATGA	1680
ATTTCTACAA ATGTTTtagc AATCGTAATG TACTTGTCTA GATTGATCT GATATATTTT	1740
CGATTTAATG ATATGGTATT TAAAACCTCC AAAGTAGCTT ACTCCATTCT TTTACTTACG	1800
TGAGTGTAGA TGTTATTTAC TGTTTtagCG TTTTGTGTT CCACTCTAAC CATTATAGCA	1860
TTCTTCTCAG CTAGTGTACT AAGGAGTGTG TGCCTGAAAA TATGGGAAC T AAGGGGCTGG	1920
TTTATCGGTT TCTCTAGTTT AGTATTTGCC TTTTGCAAAG TGATCTTAAA TGCCTTTCTC	1980
TAAATTTACA TATCACTATT GTTTAACAAA ATCTAATCTA TTTTAGGTCA CTTATTCCTT	2040
TTTTGAAATG TAGAATGAAC TTTTTCAAAG TTTTTCGAAT CTTTAAAAT CTGTTTGCTT	2100
TATATCGCCA TTCTCCCCC TTTTTAATT CTCCCTATAT AGCCTGACAG CTTTCCCGAT	2160
GGTACGAATA TGGTTGCTTT CGTCTAGGTG GATGTCGGGG TATTCGGGAT TGAGTTTTTT	2220
TGAGGCAGCC TTGGCGGAGT TTCTTGACAT AGTTAGTGCC GTCTACTTGG AAGATGCCGA	2280
TGGTATTATA GTCAATCTGT GGGGTATTCT TGATAAATAG GTAGTCGCTG TTTCTTATCT	2340
TTGGCTCCAT GGACTTGCTG ACGACATAAG CGATTGGGTC GTAGTCGTCT GGGATAATGG	2400

1131

AAACTCCATA TCTAAATCGT TGTCCTGCAT CGAGCGGCTA CCTGCAGAGA TAAACTACCT	2460
AACACGAGAG TAAGTAGTCT GTCTGTAGTC GTCCAGTCTG ATGATTTTTA CGATACTTCG	2520
TTTTTCTGAT CATAAGTTG CCTCTCGGCA TAGGTCAGAA CTTTACCTTG TCTGGGTGGT	2580
TCCCGTTGGT CGTAGATAGA TTGGATATCG CTAGGAGAAT CCTTTTGAAC TGGAGGAAAG	2640
AGGGCATCGA TCAAGCTACT GAATACTTTA ACTAAGTCAA ATATAGTATT TTTCTTAGTA	2700
GACCTAACCC TTTTTCATA ATTTCTAATG GTGTTTTTAC TTATACCTAT CTTAGTACCC	2760
AATTCCTATT GAGTCCAACC ATTACTAGTC TATATTGTTT TATAGTTGAT TGAGTTTGGG	2820
ATAGTACGCT GTAGCTGCTA AAACATTTCT AGAAATTAAT TTGACTTTCC TAATAGAGTT	2880
GTTTCATATCT TATTTCAATC TATTATGTTT TTCACCTCTA ACAATCGCAA TCTCTTCTTT	2940
ATCCATGAAT GAAATCGCTT TCTATTTTGG TAAGTAAAGC ATAACACGAA ATCCACGAAA	3000
ATGAAAACCT TTGTTGTGTT TTCGTAAAAA ATTTGTTGAC AGAGCACGAA ACGC	3054

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1590 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TGTGATTTTC yGAAAATTG GTAAAATATA TCTTAATCAT TTTCAGGAGG AAAAAATTT	60
GACAAGATAT CAGAATTAG TAAATGGAAA ATGGAAATCA TCTGAACAAG AAATTACGAT	120
TTATTCACCA ATCAATCAAG AAGAATTGGG TACAGTTCCA GCCATGACTC AGACTGAAGC	180
TGATGAGGCT ATGCAAGCTG CGCGTGCAGC CCGCCAGCA TGGCGAGCTT TATCAGCAGT	240
TGAACGTGCG GCTTATTGTC ATAAAACAGC AGCTATTTTA GAACGCGATA AGGAAGAAAT	300
TGGTACTATC CTTGCCAAAG AAGTAGCAA AGGGATTAAA GCAGCAATTG GAGAAGTAGT	360
CGGTACAGCA GACTTGATTC GTTATGCTGC TGAGGAAGGT CTCCGTATCA CTGGACAAGC	420
AATGGAAGGT GGTGGTTTGG AGGCAACAAG TAAAAACAAA CTGGCTGTTG TCCGTCGTGA	480
ACCAGTTGGT ATCGTGCTAG CGATTGCTCC CTTTAATTAT CCAGTTAATT TATCTGCTTC	540
TAAAATTGCA CCTGCCTTGA TTGCAGGGAA TGTGGTCATG TTAAAGCCAC CAACACAAGG	600
TTCCATTTCT GGACTCTTGT TGGCTAAAGC ATTTGAAGAA GCAGGGATTG CGGCAGGTGT	660
TTTCAACACC ATTACAGGTC GTGGTTCAGA AATTGGGGAT TATATCATTG AGCACAAAGA	720

1132

AGTCAACTTC ATCAACTTTA CAGGTTCAAC TCCTATTGGA GAACGTATTG GTCGTTTAGC	780
TGGTATGCGT CCTATCATGT TGGAACTTGG TGGGAAAGAT GCAGCTCTTG TACTAGAAGA	840
TGCAGATTTG GAACATGCTG CCAAGCAAAT TGTTGCGGGA GCCTTTAGCT ACTCAGGACA	900
ACGTTGCACG GCCATTAAAC GTGTCATTGT TCTCGAAAGT GTAGCAGATA AATTAGCTAC	960
TTTGCTTCAG GAAGAAGTTT CTAAATTAAC AGTTGGTGAT CCATTTGACA ATGCTGATAT	1020
TACACCTGTT ATTGACAATG CTTCAGCCGA CTTCAATTTGG GGCTTGATTG AGGATGCACA	1080
AGAAAAAGAA GCTCAGGCTC TTACACCAAT CAAACGTGAG GGCAATCTTC TCTGGCCAGT	1140
GCTTTTGGAC CAAGTTACAA AAGATATGAA AGTGGCATGG GAAGAGCCAT TTGGTCCTGT	1200
TTTACCAATC ATTCGTGTGG CTAGTGTAGA GGAAGCTATT GCCTTTGCCA ACGAATCTGA	1260
ATTCGGCCTT CAATCATCAG TCTTTACAAA TGATTTCAAA AAAGCCTTTG AAATTGCTGA	1320
AAAACCTGAA GTAGGTACAG TCCACATTAA TAATAAAACC CAGCGTGGTC CAGATAATTT	1380
CCCATTCCCTT GGTGTCAAAG GTTCTGGAGC TGGAGTGCAA GGAATTAAAT ATAGCATTGA	1440
AGCGATGACA AATGTCAAAT CCATTGTTTT TGATGTGAAA TAACGTGTAA AACCAGGAAA	1500
TTGTTTCCTT GGTTTTATTT TTTTGCTATA AAATAATAAT AATTATAGAA AAAATACGAA	1560
CTTTTGGTA TTATAATAGA TTGAAACCGG	1590

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4848 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CCTGCAGTTG TCAGACCTGT AATTTTCTTT TTATCTGTAA TAAGAATCGT TCCAGCGCCT	60
AGAAAACCCA CACCTGATAT AACTTGAGCT CCTAATCGTG TAGGATCTCC TGTCCCAAAT	120
TTATAAGATA CGTATTCATT CGTCATCATA ATCAAACATG CAGCTAGACA AACAACTA	180
TAAGTTCGGA TGCCTGCAGG CTGGGATTTG CTCCCTCTCT CTAAACCAAT TATACTACCA	240
ATGACTACTG ATAAAACAAT CCTGACAACT ATTTCAATAT TTGATAACCC AAGACTAGTG	300
GCTGTCATGA TTATTTCCCT ACTTTACGCC CCGGTCTTTG TGTGAAGTAT AATACCGTTC	360
CAGAAATAAT CATCAGAACA ATTGTATAAA CAAATACCAG AGCTTGTGCA TTAGATGTTG	420
CTGTTTCATC ACCTGCAGAT CGAATCGTAA TACCTAATGG TTGAGCTAGG GGATGGTAAA	480
GGAATACAGA TAAGTCGAAG TCAGTTAATA AAGAGTTAAA GTTTAAAGCA ATAACAGAGA	540



1133

GAACAACCGG	TAAAATAAAT	GGAATGATAA	CCTTCATCAT	AGTATAAAAA	GGTGAAGCAC	600
CCATACTTCT	TGCTGCATCT	TCCATCTCAT	CATCAACACT	AAATAAAATA	GCACGTACCA	660
TTCTATAAGA	AAATGGGATT	TTTACAACTA	TATATGCAAT	AAGTAGAATT	ACCAAACACTAC	720
CTACCAAAAT	CTGATTCAAG	ACAAGAAATT	GTGGCTGATT	AAAAGTAAAT	AATAAACTTA	780
CTGCTAAAAG	TGTACTTGGT	AGTAACCAAG	GAAGTAGAGC	ACCATATTCA	AATAAGAAAT	840
CAAAACGAGA	TTTATGTTTT	CTGACAACAC	GAGCAAATAC	AACTGCGAGA	ATTGTTGCTG	900
TTGTCGCAGC	AATAATAGAA	TAAATAAAGC	TGACCAAGAA	TGGAGAGAAT	GCCGCACTAT	960
TACTAAAGAA	TAAGCGATAA	TTTTCTAAAG	TAAAGTTTGA	TAATGTTAAG	TTACCTGTTT	1020
GAATTGCAAC	TGGATCTGTA	AATGAGTATA	ATACTATAAA	AATTAGTGGA	AGCATGAAAA	1080
CTGTGAACAA	TCCATATGCT	ACAATGTGAG	CAATGATATT	CCAAGGCTTA	GACGCAATTT	1140
TTTGTTTTTT	AAGAGGCGCT	TTAGTCTTAG	AGATAGAAAT	ATAATTTCCA	CTTTTTCTA	1200
TCTTATTCAT	GATAGTAAGC	AAAATTGTAG	TTGCAATACC	TAAAATAATT	GCAAGTAGGG	1260
CAGCTAAATC	ACGAGAATTC	CCCATCCCTG	CAAATGTAAT	AATCATTGGA	TTTATAGTTT	1320
GAAATTCTTT	ACCACCAACA	ATCATGGGTG	CTGCTACTGC	AGATAAACCA	CTAAGAAAAA	1380
CCATAATAGT	AAGTGCAAAT	AGAGTTGGAA	TTAAGGTTGG	TAACACTACT	TTTCGGAAAA	1440
CAGTAAATGG	TTTTGCTCCC	ATATTTGAG	CAGCCTCAAT	AGTGTGATAG	TCAACGCTTC	1500
GAATTGTATT	TGTTAAAAAC	AATGTATGAT	TAGCAGTTCC	TGAAAATGTC	ATAATGAATA	1560
AGACTGCACC	ATACCCAATA	AACCAGTTAG	GGTCTAAAGA	AGGGATAACA	TTTTGTAAAA	1620
ATTTTGTAAT	CAATCCATAA	GGACCATAGA	CAAATTTATA	TCCAGTCGCT	AAAACCACTC	1680
CTCCATAAAT	TAAAGAGGTC	ATATAACCTA	ATTTTAAAT	TTTAGCACCT	TTAATATCAA	1740
AGTACTCTGT	AAATAGAACA	CAAAGAATAC	CTACGACATT	AACTGTAATA	ATGAGTGAAA	1800
ATGCTAACTT	AAAACGTGTC	ATAATACTCT	GAAGTGCCCT	CTGAGATTTT	AGAACACGAT	1860
GTACAGCATC	AAGGGAAAAT	TCTCCTCCTT	TTACAAATAC	ATTCACTACT	AGATCAAAGT	1920
TTGGATAAAT	AATAAATGTT	ACTAAGAACC	AGATTAACCC	TAAACGAATA	AGCCAATCTT	1980
TTAAATTTAA	TTTATGACGC	ATACTGCACC	TCCTTAAAT	TGCAGAACGT	CTGATGGTGT	2040
GATAAATAAT	TCCACACTTT	CTCCGACAGA	TCTAATAGCA	GCCTGACTAT	CAATACTTGT	2100
TACATTAAGA	ATCTGACTTT	CAGAACTTT	TATTGTATAG	TGAATTGTAA	CTCCAGAAAA	2160
CTCAACATCA	ATAATTGTCC	CTTTTAGAAT	AAAATCTTGT	TCAGTTTCAC	GATTGAATCG	2220
AACTTTCTCT	AATCGAATGT	ATCCTTTTTT	ATCCTCTAAG	AAAACGCTTG	TATTTTTCAA	2280

1134

TAATACTTCG TGGACTGTTT CATCGGTCAA AACATTAATA TCTCCAATAA AATCACATAC	2340
AAATTCAGTT TGAGAATTAT GATAAATCTC TACTGGTGTA CCGACCTGTT CGATGTATCC	2400
ATTGTTAAAG ACTGCAATTC TATCAGATAA AGTCAAGGCT TCCTCTTGAT CATGAGTAAC	2460
ATATAAAGTA GTAATACCTA ACTCTTTTTG AAGTCTTTTC AACTCTTTTC TCAAATCTAC	2520
ACGTAATTTT GCGTCAAGGT TTGACAATGG TTCATCTAGA CAAAGAATTT TAGCTTCAAG	2580
AACCAGAGCA CGAGCCAATG CTACCCTTTG TTGTTGACCC CCAGATAATT CTGATACATT	2640
ACGCTGTAAC TGTGATCAG AGATCTTAAT TTTTGCTGCC ACTGCTGATA CTTTAGCTTT	2700
AATAACATCT GGAGCTACCT TCTTAACTTT TAAACCAAAT GCAATATTAT CAAAAACAGT	2760
CATAGTTGGA AATAGCGCAT AAGATTGAAA TACAATACCA ATTCCACGCT TTTCAGGTTT	2820
CAAATGAGTG ACATCTGTTT CATTAACCTC AATACCTCCT GATGATGGAT CTAGAAAACC	2880
TACCAATGCT CTCAAAGTAG TTGATTTACC ACATCCTGAA GGCCCAAGAA ATGTAAAAAA	2940
TTCCCCTTCA TGTATATCTA AATTCAGATT ATCAATTGCA ACAAATCAC CATATTTAAT	3000
TTGAATATTA TCAAATTTAA TCATCTCACT AACTCCCTCT ATTACTAAAC CAAAAGCCTC	3060
TCTTTATTTT TTCCATAAAT TTAGAAATAA TAGAGAGACT TGGACATAAA AATTAACCTC	3120
TATTTCTTAT TGTACGTATT CTAATTCAGC TTTTCTACC CATTCATCCA AATGCTTTCC	3180
AACAGCTTCC CAGTCAATAT TTTGTGTTT CACTTGATCA ACAAATTTCT TCGTATCTTC	3240
AGGTAGATCT TTGAGGGCAT CTTTATTGTC AGGAATAGAT CCAAAGTTCT TACTATATTC	3300
TACTTGAATT TCTGATTGAC CAAACCAATC AATAAATCTT TTAGCTAACG CTTGTTTTTT	3360
ACTAGTGCTT AAAACCATAG TTTGTTCACT TACAAATGGT ACACCAATCT CAGGAGTCAT	3420
AACCTTGAAA ACAACATTTT GTTCTTTTTG TCCAACCTAAT GCACCAGAAC CCCACATCAT	3480
TCCATATTGT ATTGGATCTT CTTTGTCTAA CATCTTAACA ATTGAACTTT CTCCCTTTTG	3540
AAGAGTGTAT GCATTTTCA AATATTCTTT TGCTACTTCC CAACCTTTTT CGGAAACACC	3600
TAATTCACCT TTATCATCAA GGTATCGAAC TAAGATACTT GCTAGAATTG CCGTCCTGT	3660
ACCTCCTTGA AGACCAGAAA TTGAATATTT ACCTTTATAC TTACTACCTA ATTCAGTCCA	3720
ATCTTTAGGC ATTTCTTTTA CATCAGGCGC CCAATTAAA ACTAATGGTT GAACAATCAC	3780
AGGATTATAA TAATTATCTT TATCTGATAA AGATTGATCA ATTTTATCTA ACCATTTAGG	3840
CTTGACTGT ACTAGTAATT TTTGATCTCT AATTTTATTT GAATCAACAG CACCAATTCC	3900
AAATACCATA TCTGCAACTG CATTATTCTT CTCAGCAATA ACACGGTCTG CTAATTGAGC	3960
GCCAGCGATA TCAACCATTT TTATATTAAA ACCAGCTTCT TTTGCTTTAG CAGTTAACCA	4020
ATCACCACGA CCATTTGAGA CTGAGTTCGA ATAGATAACT AATCTTGAC TTTTATCAGC	4080

1135

TTTTCTTCA GATGAAGAAG CAGTCGTAGA ATTTGAACCT CCAGAGCAAG CAGCAAGTGT	4140
AGTAAGAGCA ACTCCCGTTG CAAGTACAGT AGACCAAACCT TTCATTTTTT TCATGATAAG	4200
TTCTCCTTTT TTATTATTTT ATTTAAATTT TTCGTGATAT GGAACAAATT GTCTCATATC	4260
TTCAAATACA GTATAGTCAA TACGGTTTAC AGTAATAGTT GGAATCTTCT CTAATAAAAT	4320
TTCAAGTAAAT TCTGCTCTGA CTTTAGTAAA CTCTTCTTCC TCCTCTTCGG TTAGAGGAAT	4380
CCGAAGATAC CCAATTGAAA TATGGAATTG ATATCTATCA TGATTAGGGA AACAAACACC	4440
TGCTTTTTCT GAGACATAAG TACGAATTTC TTCTAATCTC TTTGCAGAAG CTTTCATCTGC	4500
AGGTTCAACT AGTATGTTTT GTTTCCCAT TTCAGTTATA CGCATATGAA TTTCTTCATC	4560
CAACAATGGA AAAATTTCAA GTTGTTTAGC AAAGTAATCA TGTATTTCTT GTAAAGGTGT	4620
ATCTAGAGGA AGATTACTGC TCCAAAACCTC gttCAGGATT TTCATGGCAC AACAAATCAA	4680
TTACAGTCAT GTGAATAGAA TTCCTTGAG TTAAGTAAA CTTATCGATA AATGGTAATT	4740
CTCTATAACG TGATTGAATA ATATCAACAA CTTCCATCAA ATCTTGTTTA GTATAAAGAT	4800
TTGCTACAAC TGTATCCCA GGGAAATGAT TAAATCCCC ATTCTCGG	4848

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3763 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GTTATAAGCA ACACCTTCTT GCTTGCCATA AGTTGTGAAA TGGGTAGAAT CGATATCTAC	60
AATGAGTTGG TTTAGCTGGT GAAACTGTAA AAAGAATTCG ACCAATTCAA GGTGAGGCA	120
TCGCAAACTA TGGACTGTTT CCTCGTCAGT TCTGGAAAGA AACGGGATA AGGTTGGCTG	180
TGAAGCAAGC TGCCCTCCTT CCAATAATTT TGGAAAGTAG GCATCAGCTG ACAATTCTTT	240
ACAAGCATAG TCCGTTCCAT AACCTGTAA CAGTTGAAAG AGGAACTGGA CAAGGATATC	300
TGAATCCGAA TAACGACAGT AGCGGCGTTG GTCATTCTGT ACTAAATACT TAGAAATCCG	360
CTCTTTTAGT TTCAACTGGG AAAAAAGTTC CTGAAAAAG ATAAGACCAC CATACTGGGT	420
TAAATGACCT CCATCGAAAG ATAGTTGGTA AAAAGACTTG TTTTGGAAAGT GATGATTGG	480
TAAACTGTTT ATGTGAGTTT CCTTTCTTTT TGTGTTTTTT TCTACACTTA TACCATAAAG	540
GGGAAACTCT TTTTGTCTA GTAAAAACA CCCATTGGGT GAAAAAGAA ACCATCCAGG	600

1136  
ATCTAAGCTA AGGCAAGGAT TCTGGATGGT TTTTAGATTT GGGGTGAATA ATTGGGGATT 660  
TAGGAGAAAT GATGGTATCT TCCAAATCAA AATCAACTTC ACTCCATAGT CTCAACTGAT 720  
TGATTTTCCC ATCTTGATAG GTCACATCCT TGTCAAGGAT AAAGTGAGTC AACACCTCAT 780  
GTTGACCTTG ACACCTGATG TCATCTACCA AGAGCCAGAC ATCCTCTACC AACATGAGGA 840  
TTTTTCTCCT GTGAAGATAA GGCAAATCAG GTTCTGCTGA CCAATAAGCC CCCTCAATAT 900  
AATGCACTCC CTCCCTTTCT TTATGGTGAC AAAACAGGGA GTGAGGATAG TATTCATATT 960  
CCCAGGATCC CGTGATTCTT TCCGGAGCTT TCCCATCTAC AATGCAGGTC GAATGACTCC 1020  
AAGCACTCTT TAAGAGATAA CGTTCATATA TCTCCCGATA AGAATAACGC CCAGCATCTA 1080  
TGAAAATAGG TTGGCCTTGA TACTGTAAGC AAAAATATT CTCGTCACCTA TGACTATGGG 1140  
CACTTCCTAG CGGACCATTT TTGAAAAATA GATAACGATG TTCATCCTTA ATGCAGACAT 1200  
GTCCAGAGTC TTCAAAGATC ATGGACTTAG GCTGCCAAGC TCTCTTTTCA AATTCCTGCA 1260  
GTCGCTTGAC CTTTTCTCGC CCCAGGAACA AGAGGCTAAG CAAATCAACT TTAACATCCA 1320  
GACCGTTAAG AAGGTCTTCC TGGTTCAAAA CCACAGCAGA CAGGCTCAA AATTCTGTCTG 1380  
TTTCTGTAGA ATCGCTATCA CCAAAGCCA AAGTCCGTCC ATCTAAGCCT GTCATCATTT 1440  
GAATATAGGT CGCCATCTTT TCCAGCAACT CTTGGTAACT ATCTTGCAAG TCTGGAAGCA 1500  
AGAGACACAA ATCCAGCAAG GCTTTATAAA CCTCTACATG ATAGAGAATC GACTGTTCAA 1560  
ACTGGCTTCC ATCTCCTAAA ATCTGTGTCT CAATTTGCTG TTTCAACTCC TCTGAAGCAA 1620  
AATGGTAAGC TTCTTCTAGA TCCATCTTAT CTGAAAAGAA ATGATAGATA GCAAGCATCG 1680  
GAATTGTTTG TAAATCCCC CAGTTACTAA GGGTGTACTT GCGCGATAG TAGCTTTTCA 1740  
TAAAGTCAAT CTGCTTTTCT AGACTGACCA AAATTTTCTC TAGTTCTTTC TCCTCTAGCA 1800  
AGTCAAATTT CAAGAGGAGC AAGAGTAGTT TCAACCAAGT AAAGGAACGA ATACCCGTAT 1860  
CCAAGGTTCT AGTCATCAAG GATTGAGGAG AAAATTCTCT CACCTGCTCA ATCCAATCAA 1920  
ATAGAAAGAA CTTGCACTTT TGAATATAGT CCTTATCTCC TTCTACCAGA TACCCATCA 1980  
TAAACTGCAA GAGATATTCT TGTCGATTGA GCATATAAGA CCATTCTGGA TCATCTTCAA 2040  
ATACTTGATC CCATACCATC GGCTGGATTT GATGGATTTT TGAACAAGGC TCCATATCCC 2100  
AAGGACTATC AAACATAAAA CGATTGTCCA TCAAGCGTTC AAGGGAACCTC TTGACTTTCT 2160  
CATAGTCTTT TGAACAGTGC GACAAGATAT AATCAGGACA TTGATTTCCA TCGACTCTTT 2220  
CAAAAAATTG TCTTCTTTCT TCTTTCATTA TCTATTACCA GAAAAAGAAC TACTTAAAAA 2280  
GCAGTTCTTT TGTCTTTCCC ATTACACTTT CCTTTTCTAC ATGGATGACC ACACCTTTTG 2340  
CAATCTGCAA GGAGACCAAG TCATCTTGGA TAGAAATGAT TTTTCCATGA ATTCCAGACA 2400

1137

ATAACAACAC TTCATCACCA AATGTTAAAG AAGCTAAATA CTCTTGTCGT TGCTCCATCT	2460
GTTTGCGAAG CAACTTTTGC TGACGAATAG AATGAAAGCT TGACAGTAAA AGGGGACTCA	2520
CTGCCAAGAC AATCACTATT CCATAAAACA ATGTTGTATC CATTAAAGCTA TAATCTTAAG	2580
CCAGCTTCCG ATAATTCCGA TGATAACTGT TAAAATAACG AGTTTATATG TTGTCCATTT	2640
CTTTTCTTTG ATCAAGTAGT AAATAAAAG TGTAATAGG GCTGGTAGAA GAGCTGGAGC	2700
AACCTTATCA AGCATTCCTT GAATACTTAC GATACTTTGT TTAGCGTCTG CTTTAACTTC	2760
CCCTGCAGCA AAGGTAATCG GCACCATAAT CTTAACAGAT GTCGCTGCCA AACCAGCAAT	2820
TACGtTACAC CGATAATATT GGCAATACGA GAAATCGTTG CCATCTGTTC GCTTAGTTTA	2880
TCAATCACAG TTGTTCCCTAG TTTGTATCCA TACAGACCAG TTGACAATTT AATCGCTGTT	2940
AAAATCGTAT TCATCGCAAG GAAGAACAAG ATTGGACCGA CAACCAAGCC TTCTTGAGCA	3000
AACGAAGCTG CGATGGTTGA GAACAATGGA GCTAAACAGA ATTGAGAAAG AGAATCCCCA	3060
ATACCTGCCA ATGGTCCCAT CAAGGCCATC TTGATGCTAC GTGTTTCTTT TGCCGGACGG	3120
CCATTTTCCA ACATTACAAG ATGCAAGCTG GTAATAAAAG GCAGGAAGTG TGGGTTGGTA	3180
TTATAGAATT CACAGTTTTC TTCCAAGGCT TGGTAGAAAC CTTCTGATC CTCTCCATAG	3240
TGTTTTTTCA AAGCAGGATA CATCACATTG GCATATCCCA ACCCTTGATA GTTACTATAG	3300
TTAAATCCAT TTTGACAAA GAATGCCCGC AAAGACGTTT TAAGATAATC ACGTTTTGTT	3360
AATTTGTTAG ATCCAGTCAT CGTGTGCTTC CTCCTCTACC ACATGATCCG CTGTTTTTGG	3420
CTTGTTATAA AATTCAATCA AAGCAAAGAT AGTACCTACA ATTGCAATAC CAATTGTTGG	3480
GATGTTTAGA TAAGCTGCAC AAACATATCC CAACAAGACA AAGGGAATCA ACTCTTTCTT	3540
AGCCATCACT GACAAGATCA TCGCAAAACC GATAGCTGGG AGCATTTTAC CAGCAACTGT	3600
CAAACCTGTA AGTAATACCG GTGGAATGTA GTCTACGAGT TTCAACAAGG TATCCATTGA	3660
AAGGGCACCA AGCAACCCAA GGTAAATCCA ATAAAGGCAA ACAACCAAAT TGTTCATTT	3720
AGAGTGAAC TAAATTTCTT CAAATTATGG TTTTCAAGT GCT	3763

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5053 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

1138

CAATCTCTGA GTATGTGCGG TCAATACTAW CAAAGGGAAT yCCTGACGTC AAGTAATGTT	60
CAATTGGmCT ATAGGTAATG GCAACCACTC CATCAACTTT ATTATGACGC AACATCTCCA	120
GATAGTCTTG CTCTCTATTT GTACCATTGA TAGAACATAA GAGTAATTTG TTATTTCTCT	180
TATAGACTTC ATTTTCCACA TGCATAGCAA ATTCTGAAAA GAAGGGATGC CAGATACTTG	240
GTACAATGAT TGCAATCGTT TCTGTTGAT TTTTTTCAT TCCTCTAGCG TAGTAATCTG	300
GAATGTAATT CAAAGTTTAA ATCGCTTGTT CCACTTTTTT CAAAGTTACT TCTTTAATGC	360
CTTTTTCTTT ATTAATTACA CGTGAAACAG TTCCAACACT AACTCCTGCT TCTAAAGCAA	420
CATCTTTCAT GGTAATTGAT TTTCTTTGTT CTACCATATT ATCACCTCCT TTCAATATAT	480
AGTATCATGC AAATGCTTTT TAAGCAACTA TTTCTCAATC ATTTTGGCC AGATCATTTA	540
TCCCATCATG AATAAAATCA CTCCAATTAG CTTTGTAAAA TACTTCAATT TTCATGTGTA	600
AACATCTACA TAAACAGGA AAAGCCTTGG TTTCATGGCT TTTTTCGTAT CTTCTATAAA	660
AAAAGCAAGA GTTTTAGATG GCTATAAATC TAGATGTACA TTTTGCTTAA ATGATTGAAG	720
GTCTTTTCTT AACAAAAACA CCCCCAAAAT TAGACTTTTT CTGTCTAACT TTTGAGGTAC	780
AGTTCAAACG CGAAATAGCG TTTTTTTGTT ATTTTGGTT ACTCATCTAA TCGAATAAAC	840
ATCATGGCAT TTAACAAGTA TATGAGTGAG ACCGTGTTTA TATTATTTGA ATAGATGAGT	900
CTCTTATTTT CAATAGGAGG AATAATAAAA TTAGAAATAA TGATATCATA AGGTGAATCT	960
TCTAAAGATT CCTTTGATAA TTCTAATCA GTCCAAACTT CCAGTTCAAA ATTATTGCTA	1020
CAATAATAAG AAAGTGTCTC TGCAACGAAT TTGTCATGAT ACTGATCAAA ATTACTCATA	1080
ACTAAAACCT TTAGTTTAGG CTGATTTTGT AGCAAATTAA TCACCAAATG TTTGGTATGA	1140
GTGATGAAGG TATAAGATAG ATGATTTACC ATCATTGAAC TAGAACAAAC CTCAAGAGTC	1200
TCTAAATAGT GAGAAAGCTC TTTTTTTATA TCTGAAACAA ATTTTGGAAA AATATTTTGA	1260
AAGTTCCCTGA TTGTATTCCC TTTTGTATCA AATAAAATAA ACTCAGTAAA CAACTCTTGA	1320
CGATACAGAT GTGCGGTATT ATGCAGATGC CAAATCAGAT TATCCTTATT CTCCATTTCA	1380
ATCTGATACT TGACTGAAAT CTGATCAATA AAATCACTCA ATAGATGGTA AGATTTTTC	1440
ACATAACTAT CCTTTTTTAC GCATTTTCATA AAGAGACTTT CATCTATGAA AAACATTTT	1500
TGAAAGTAAG ACACAAATAA TTGGCAAACA ACTTCTTCAT CTAAAGAGAT ATTGTATTCT	1560
GATTCAAAAC TCTGAGCAAC ACCTTCTATT CCTTCTGCCT GCATTAAAAA ATCCAAACTT	1620
TGGTCGTTAA AAGAATCTTT ATCTACTTCC ATAAATGAC CAACTTTAT TCTATATAGG	1680
TTGTAACATA GGAGCAACTT TAGCATTCTA TCGGTTGACA AATTCATTGG AAAGCTTGTT	1740
TCCTTATAAA CCAATTCATA CAATTGAGAT AGTGGCTCTG ATGAAAAATT TTCAAATGGC	1800

1139

CATTCTAGGA AATAATATTT TTCTGAAAAA TATTGTGCAA AAAAGTAACG AATGTCTCTC	1860
TCATTTCCAA TGATTTGAAC AGGGGTCAGA CTAACCTCAA ATTGAAATTG CCTTTTAATC	1920
ACTTTATTGA TTTGGCTAAT AATACGATAG AGCGAAGATG AACTGATATA AAATTCTTTA	1980
CAAATACTCT CAGCTTGACA ACCTTCATTA AAGAAGATGA ATTCTAAAAT CGAAAAATGA	2040
GTTGAATGTT TAAAGAAATG ATGGTAAACC ATTTCAATAT CACTATCATC GGTATTAATA	2100
ATGCGTATAC CATTAGTAGA AGAATGAAAA ATCAAGTCAG GAAAAGCAGA TTAAACATGG	2160
GATAGATCAT CTTTGACTGC ACGTTCTGTA CAATTTAATA ACTCTGCTAG TTCAGAACGA	2220
TGAAACCAAC GTTTATGTTT AAATAATAAT TCTAATAATT CTAATTGCCT ATGACTTTTT	2280
TTAGATAATA AATCTCTCAT GAATATCTTT CTCTCTTTAT AAATTATCGG ATTAAACCTC	2340
TTGCAATTAT ACCACAAAGA ATAGGTATAG CATGATATAA CGACTTTTCC TAAAATCTTT	2400
TATTTCTGAT AATAACACTA CGGAGACAAT ATATAAACAA TTTTCTTATT TTACCGTCTA	2460
TTGAGGGCGT GAATACAGAA TCAAATTCAA GTCTAAAGAT TATATTTTAA ATTTTAAAAA	2520
TTATATAATA GCAACAATTA AAGAATTTGA TTTTTTAAAA TTATATAATA ATAACAATCG	2580
AAATAATTGA CTTTTCTATA TTAAAGTTAT ATAATAGTAA TAATCAAAGA AATTGATTTT	2640
TTGATATTAA AATAAAAAAG GAGGGTAGGC AGTGTGTGTA TCAATTATTG CTGGAGGTCT	2700
TATTGGTCTC TTGGCAGGTA AAATCACTAA AAAAGTAGTT CTATGGGAAT CATCGCAAAT	2760
GTATTCGCTG GTTTAGTCGG GGCATATGCA GGACAATCTC TTTTAGGTAG TTGGGGTCCA	2820
GCAATCGCTG GAATGGCTTT GCTCCCATCT ATTGTAGGTG CAGCGATTGT GATTACTGTA	2880
GTGTCATTCT TTACAGGTAG AAAGTAACT TTTGCCAGT AAAGTTAGCA AACTATTTTT	2940
AAATCAATGA CGGGAAAAAT AGTTTAAATG TTAAATCGAA AGGATTGTAT ATGTCAAAAG	3000
CAAAGAAAAT ATGTTTCATT ATTTTCTGTA TTTTAATCTT GACAATTTTC CTTCTGTTT	3060
TGATAGATTA TCATCAAGTT AGTGATCTAG GTATTCATCT ACTTAGCTGG AGACAGAACT	3120
CCGTAGTTGA ATTCTATCTT GCTAGATATG TCTTTTGGGG GACAGTGGTT CTATCAACTT	3180
TAGTTTTATT ATCCATTTTA GTTGTGATGT TTTATCCTAA ACGTTACTTG GAAATCCAAC	3240
TTGAACTAA AAACGATACA TTAAATTAAG AGAATTCGGC AATCGAAGGT TTTGTTAGAA	3300
GTTTGGTGAG TGATCATAGA TTGATCAAGA ACCCAACTGT TCATGTAAAT TTACGAAAAA	3360
ATAAATGTTT CGTTCATGTA GAAGGTAAAA TTCTTCCTTC AGACAACATC GCTGACAGAT	3420
GCCAAATAAT TCAAAATGAA ATAACATAAT GATTGAAGCA GTTTTTTGGT ATTGAGCGTC	3480
AAGTAAACT TGAAGTTGCA GTAAAAAATT ACCAACCAAA ACCTCAAAAC AAAAAGACTG	3540

1140

TTAGTCGTGT GAAGTAAGGA AGTAAAAAAT GGAATGGCTT AAACAATATC GATATCCAAT	3600
TATCGCTGGT CTCATAGGCG TATTCTGGC TTGTTTGATT GTCTCCTTTG GCTTCTTCAA	3660
AACAATATTT GTATTGATTT TAGGAGCACT GGGAGTTGCA GCTGGATTAT ATATCGAAAA	3720
AAACTATATA GATAAATAAA AAAATAAAAA TTAATAATTT AATTAAAGGA GTTTCATATG	3780
TCAAACGAAA AAAACACAAA CACTAACGTA GAAAAGAAAG ATGCTACTGT TGTAGCTCAC	3840
GAAATCAAAG GGGAACTTAC TTACGAAGAT AAAGTTATCC AAAAAATCAT TGGTCTTCA	3900
CTAGAAAACG TTTCAAGTCT TTTGGGAATC GATGGTGGTT TCTTCTCAA TCTTAAAGAA	3960
AAAATCGTTA ACAGCGATGA CGTAACAAGT GGTGTTAACG TAGAAGTTGG TAAACACAA	4020
GTTGCAGTTG ACTTAAACGT TATTGTTGAG TACCAAAAAA ATGTTCCAGC TTTATATTCA	4080
GAAATCAGAG AAATCGTATC TTCAGAAGTT GCTAAAATGA CTGACTTGG AATTGTTGAA	4140
ATCAACGTAA ACGTTGTCGA CATCAAAACT AAAGAACAGC ATGAAGCAGA CTCAGTAAGC	4200
CTTCAAGATC GCGTATCTGA CGTTGCTGAA TCAACAGGAG AATTCACCTC AGAACAATTC	4260
GAAAAAGCTA AATCTGGTCT TGGATCTGGT TTCTCAACTG TTCAAGAAAA AGTTAGCGAA	4320
GGTGTAGAAG CTGTTAAAGG TGCAGCAAAT GGTGTAGTAT CTCACGAAAA CACTCGTGTA	4380
AACTAAGATA AAATAAATAT AACAGGAGAA ATTATCATGT CAGTAGAAGA AAAATTAAAT	4440
CAAGCTAAAG GTTCTATTAA AGAAGGTGTT GGGAAAGCCA TCGGTGATGA AAAAATGGAA	4500
AAAGAAGGTG CAGCTGAAAA AGTTGTTTCT AAAGTAAAG AAGTTGCCGA AGACGCTAAA	4560
GACGCTGTAG AAGGTGCTGT AGAAGGTGTT AAAACATGT TGAGTGCCGA CGATAAATAA	4620
GGTTAAAAGT TACTTTATCT TTTTAGTAAT ATTAGTCAA AGAGTCTGAG TCAAGATGAT	4680
TCTCAGAAAA CAAAAGCTA GAGATTCCCA ATTGCGGAAC TCTAGCTTTT TAATTTTGCC	4740
TCTTCTCTT ATTATATTTC AGCAGGTTGT TGGCCATGAG TACGAATCCC ATGTCAATTC	4800
TCACTTGACG CTTACCTCTC AGATGACATC TCTTATAACC CAAACAAACC TTTATCTGCC	4860
CAAAGACAGA TTTCATATCA ATCTTACGTT TAGCGAAAAT TTGTCTACCC TTGGAAGATA	4920
AAAGTGCCTG ATATTCTTTA GTTTTAAAC ACTGGTAACG TTCATTGATA TACAGTCTCT	4980
TTTGAGGGGC TGATTCAGGT TCATAATCGC AGTCAACATT GATTTCAGG CTGTTTGCTT	5040
TCTATCTCCC CGG	5053

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



1141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATTCTCTTT TTTCCAACAA AATGTATGAC CTGCACTTGA ATACTTCTCA TTGTTTGTAC	60
ATTCATCTAC TTTCATATAA TCTTTTACAA AATCATAATA TGACATAACA CACTATCCCT	120
TTTAGACAAT ATTCCAATTA GCCTTATTAA TTCAAAACTA TTGTATTAGT AATTATAACA	180
GATGTATAAT AGAAAAGCAA TGATAGATAT TATCAATTAA GCGAATTTAT ATCTAAAAGG	240
GATATTAAAG AAAGGAGATA TGCTTATGAA GATTTACAAA AAACATTTTG CTTATGTCCA	300
AGATAAGAAA TATCTTCGGG TTTTGGCCAT AATTTTTTCT GCTATATCTG CTGCACTTAC	360
AGTATATGGA TATTATTTAA TCTACAAATT TCTAGATAAG TTAATAATTA ATTCAAACCT	420
ATCCGGTGCA GAGAGTATAG CATTAAAATC TGTTATTACA CTAACAAGTG GAGCGATATT	480
TTATTTTGTC TCAGGAATGT TTTACATAT CTTGGGATTC AGGCTTGAAA CAAATTTAAG	540
AAAAAGGGaA TCGATGGTCT GGAAAAAGCA AGTTTtaggt TCTTTGACTT AAATCCATCT	600
GGTCAAATAA GAAAGATTAT AGATGpCAAT GCTGCACAAA CTCATCAGGT GGTAGCACAC	660
ATGATTCCCG ATAGTTCTCA GGCAATAATC ACACCCGTAC TTGTACTTGC ACTTGGCTTT	720
ATAGTAAGTA TAAGAGTTGG CATAATTTTG CTTGCTCTTA CTATAATTGG TGGCTTAATT	780
TTAGGGGCAA TGATGGGCGA GCAAGAATTT ATGAAGATAT ACCAAGAATC CCTATCTAAA	840
CTAAGTGCTG AAACGTGTGA GTACGTGAGA GGAATGCAAG TTGTAAAAAT ATTTAAAGCA	900
AATGTAGAGT CTTTTAAAAG CTTTTATAAG GCGATAAAAG ATTACTCAA GTATGCTTAT	960
GATTATTCCC TATCTTGTA AAGGCCTTAT GTTTTGATC AATGGTTATT TTTGGACTG	1020
ATTGCAATTT TAATTATTCC TATAGTTTAT TTTATGACTA GCTTAGCTAG CGCAAAGGTG	1080
ATTTTACTTG AGCTTATCAT GATTTTATTT TTATCAGGAG TTCTCTTTGT TTCATTATG	1140
AGAATGATGT GtACTCCATG TATATTTCTC AAGGAAATTA TGCAGTAGAT ACTTTAGAGG	1200
CGCTTTACGA AGATATGCAA AAAGACAAAT TAGTGCAATG TAATGTCAAT AATTTTAAAA	1260
ACTATAATAT AGAATTTGAG AATGTTAGCT TTGCTTATAA TGATAAAGCT GTCATTGAAA	1320
ATTTATCCTT TAATTTAGAA GAAGGAAAGT CCTACGCACT TGTCGGTTCA TCTGGATCAG	1380
GCAAATCAAC AGTAGCAAAA CTTATATCAG GTTTTACAA TGTTAATAAA GGAAGCATAA	1440
AGATAGGCGG GATAGCAATA AGTGAATATT CTGACGAAGC CTTAATTAAA GCCATTTCTT	1500
TTGTTTTTCA AGATTCAAAA TTATTCAAGA AGAGCATTTA TGATAATGTA GCGTTAGCTA	1560
ATAAAGATGC GACGAAAGAT GACGTTATGA GAGCCTTAAA ATTAGCAGGA TGCGATTTAA	1620

1142  
TATTAGACAA ATTCCCAGAA AGAGAAAATA CAATCATAGG CTCAAAAGGT GTTTATTTAT 1680  
CCGGTGGAGA AAAACAAAGA ATTGCAATTG CTAGAGCAAT TTTAAAGGAT TCCAAAATTA 1740  
TTATTATGGA TGAAGCATCA GCATCTATTG ACCCAGATAA CGAGTTTGAA TTGCAAAAAG 1800  
CTTTTAAAAA TCTTATGAAG GATAAAACAG TTATCATGAT TGCACACAGG CTATCTACAA 1860  
TTAAAGACCT TGATGAAATT ATTGTCATGG ATAGTGGAAA AATTATAGAA AGAGGGTCTG 1920  
ACAAAGAATT AATGTCAAAA GATACAAGGT ATAAGAGCCT CCAAGAGATG TTTAACAGTG 1980  
CGAATGAATG GAGGGTTTCA AATGAAAGAG TTTTATAAAA AAAGATTTGC TCTTACAGAT 2040  
GGAGGAGCAA GAAATTTAAG TAAAGCAACA CTGGCTTCAT TTTTCGTTTA TTGTATAAAC 2100  
ATGCTTCCTG CCATATTACT TATGATTTTT GCTCAGGAAG TTTTGGAAAA TATGGGCAA 2160  
AGCAATGGCT TTTATATAGT ATTCTCAGT TGTATTTTGA TAGCAATGTA TATTTTGCTT 2220  
TCTATCGAAT ACGATAAATT ATATAACACA ACCTATCAAG AAAGTGCAGA TTTAAGAATA 2280  
AGGACAGCGG AGAATTTATC AAAATTACCT CTATCTTACT TTTCTAAACA TGACATTTCC 2340  
GACATTTTAC AAACAATCAT GGCTGATATT GAAGGCATAG AGCATGCAAT GAGCCACTCA 2400  
ATACCAAAGG TGGGCGGCAT GGTACTGTTT TTCCCATTA TATCTGTAAT GATGCTAGCG 2460  
GGCAATGTCA AGATGGGTTT AGCTGTAATT ATTCCATCTA TTTTAAGCTT TATATTTATA 2520  
CCTTTATCTA AAAAATATCA GGTAAATGGA CAGAATAGAT ATTATGATGT CTTAAGAAAA 2580  
AACTCAGAAA GCTTTCAAGA AAATATCGAA ATGCAAATGG AGATTAAAGC ATATAATTTA 2640  
TCGAAGGATA TTAAAGATCA CTTATATAAA AAAATGGAAG ATAGTGAGAA AGTACACTTA 2700  
AAGGCGGAAG TAACTACAAT TTTAACTTTG TCTATATCTT CAATATTTAG CTTTATATCT 2760  
CTTGCTGTTG TGATATTTGT CGGCGTAAAT CTAATTATTA ATAAAGAGAT AAATTCTCTC 2820  
TACCTTATAG GATATTTACT AGCTGCTATG AAGATAACAG ACTCTTTAGA TGCATCTAAA 2880  
GAGGGCTTGA TGGAAATATT TTATTTATCG CCCAAAATAG AAAGATTAAA AGAAATTCOA 2940  
AATCAAGATT TACAAGAAGG CGATGACTAT AGCTTAAAAA AATTTGATAT TGATCTAAAA 3000  
GATGTTGAGT TTGCCTACAA TAAAGACGCA AAAGTTTTAA ATGGTGTAAG TTTTAAAGCT 3060  
AAGCAGGGAG AGGTCACCTG TTTGGTAGGT GCAAGTGGCT GCGGTAAAAC AACTATCTTG 3120  
AACTTATAT CAAGACTTTA TGATTATGAC AAGGGACAAA TCTTAATCGA TGGCAAAGAT 3180  
ATAAAGGAAA TATCAACAGA ATCCCTTTTT GATAAGGTGT CTATTGTTTT CCAAGATGTG 3240  
GTTCTCTTTA ATCAAAGCGT TATGGAAAAT ATTAGAATCG GTAAGCAAGA TGCAAGTGAC 3300  
GAAGAGGTTA AAAGAGCAGC AAAACTTGCA AATTGCACAG ATTTTATAGA AAAAATGGAT 3360  
AAAGGTTTCG ATACAGTTAT TGGTGAAAAC GGAGCTGAGC TATCAGGAGG AGAAAGACAA 3420

1143

AGATTATCAA TAGCCAGAGC CTTCTTAAAA GATGCGCCGA TATTGATCTT AGATGAGATA	3480
ACAGCAAGCC TTGATGTTAA CAACGAGAAA AAGATTCAAG AGTCTTTAAA TAATTTAGTT	3540
AAAGATAAAA CTGTTGTAAT CATTTACAT AGAATGAAAT CCATAGAAAA TGCAGACAAG	3600
ATAGTAGTTC TTCAAAACGG AAGAGTAGAA AGCGAAGGTA AGCATGAAGA GCTTTTACAA	3660
AAATCAAAAA TTTACAAAA TTTAATAGAA AAGACAAAAA TGGCAGAAGA ATTTATTTAT	3720
TAGGAGGACT ACAATGGATA ATAAAAAATT AAAAGTAAAA GATTTAGTAA GCATCGGTGT	3780
TTTTGGCGTA ATTTATTTTG CCTTCATGTT TGGAGTTGGT ATGATGGGCT TGATCCCAAT	3840
ATTGTTCTTA ATATACCCGA CAGTATTAGC CATAGTTGCA GGAAGTGTG TTATGTTATT	3900
TATGGCTAAG GTTCAAAAGC CATGGGCACT ATTTATATTT GGTATGATAT CACCACTTGT	3960
GATGTTTGCA GCTGGTCATA CCTACGTAGT TGTGGTTTTA TCACTTATAG TAATGATAAT	4020
AGCAGAATTA ATTAGAAAGA TTGGTAATTA TAATTCATTT AAATACAATA TGCTTTCTTA	4080
TGCAATCTTC AGCACATgGA TATGTAGCTC TTTAATGCAA ATGCTTTTAG CAAAAGAAAA	4140
ATATATGGAG TGGTCTTTGA TGACTATGGG AAAAGATTAT GTTGATGTAT TAGAAAAGTT	4200
AATAACTTAT CCTCACATGG CTTTAGTAGC CTTAGGTGCT TTCTTAGGAG GAATCTTGG	4260
AGCATATATA GGCAAGGCTC TATTGAAAAA ACACTTTTCA AATGGATTAT ATTGTGTGGG	4320
ATACTTTACT CCTTGCCTAA TTTTATGGTG CTATCTGAAT TAAACCCTAT AGTTAAGATG	4380
TTTTTGAGTA TACCTATTGT TATTAGAATG TTTATTTTAC CATTTATGGC AGCAAGCTTT	4440
ATGATAAAGA CCTCGGATGT AGGCGCAATA ATTTATCGA TGGATAAGCT TAAGATTTCA	4500
AAGAATGTAT CCATACCTAT TGCGGTTATG TTTAGATTCT TCCCATCTTT TAAGGAGGAG	4560
AAGAAAAACA TCAAAATGGC TATGAGAGTA AGAGGGATAA ATTTTAAAAA CCCAGTCAAA	4620
TATCTTGAAT ATGTTTCTGT GCCACTACTC ATTATATCAT CTAATATATC AGATGACATT	4680
GCAAAAGCGG CAGAAACAAA GGCAATAGAA AATCCAATTG CCAAGACCAG ATACATTTCG	4740
GTAAAGATAC AGCTAATTGA TTTTGTTTAT GTTTTAGCGG TTGCTGGACT TATTGTGGGA	4800
GGCTTAATAT GGTGAAATA AAAAATTTAA GTCTTGATTA TGGTGAAGAG CATATATTAG	4860
ATGATATATC ACTATCCATA GCCGAGGGAG AGTGCCTGCT ATTTACAGGA AAAAGTGGAA	4920
ATGGTAAGTC ATCTTTAATA AATTCAATCA ATGGACTAGC TGTAAGGTAT GATAACGCAA	4980
AGACAAAGGG CGAAATAATT ATTGATGGTA AGAATATAAA AAATTTGGAA CTTTATCAAA	5040
TCTCAATGCT TGTTTCAACT GTTTTTCAAA ATCCTAAGAC ATATTTTTTT AATGTCAATA	5100
CGACATTAGA ATTATTATTT TATTTGGAAA ATATCGGTCT TGCAAGAGAA GAGATGGACA	5160

1144

GGCGTTTGAA GGATATACTT GAGATATTCC CGATAAAAAA TCTTTTGAAC AGAAATATAT	5220
TTAATCTATC CGGCGGTGAA AAACAAATTC TTGCAATTGC AGCTTCTTAT ATAGCAGGTA	5280
CAAAGATTAT AGTTATGGAT GAGCCTTCAT CGAATTTAGA TATTAAAAGC ATAAGTGTTT	5340
TGGCAAAGAT GCTAAAGATA TTAAGAGAGA AAGGCATAAG CATAATTGTT GCAGAGCATA	5400
GAATTTATTA TTGATGGAC ATAGTTGACC GTGTATTTTT AATAGATAAA GGAAAGCTTA	5460
AAAAAACTTA TACTAGAAGT GAATTTTTAA AGCTAGATAA AAATGAATTA AATGCTTTAA	5520
GTTTAAGAGA TAAAGAATTA AGTAAATTAA AAGTTCCTTA TTTAAAAGAA GGTGGAGAGT	5580
ATCAGATAAA AAATCTTAGT TACAAATTTA CTGATGATGA GTGTTTAAGC TTAAGAGATA	5640
TTTCGTTCAA GCTTGGGAAA ATTTATGGCA TAATAGGATC CAACGGACGA GGAAAATCAA	5700
CGCTTTTAAG ATGTTTAATA GGTCTTGAGA AAAAATCAAA AGAAGAAATT TATTTTAAGG	5760
GAGAGAAGCT ATCTAAAAA GAAAGACTCA AAAACTCTTC ACTTGTATG CAAGATGTAA	5820
ATCATCAATT ATTCACAGAT GAAGTATTCA ACGAGCTTAG ATTAGGAGTA AAGAATTTG	5880
ATGAAGAAA GGCGAAAATC ATTTTAAACC CCAATTATTC ACCCCAAATC TAAAAACCAT	5940
CCAGAATCCT TGCCTTAGCT TAGATCCTGG ATGGTTTCTT TTTTCACCCA ATGGGTGTTT	6000
TTTACTAGAC AAAAAGAGT TTCCCTTTA TGGTATAAGT GTAGAAAAA ACACAAAAAG	6060
AAAGGAACT CACATGAACA GTTTACCAA TCATCACTTC CAAAACAAGT CTTTTTACCA	6120
ACTATCTTTC GATGGAGGTC ATTTAACCCA GTATGGTGGT CTTATCTTTT TTCAGGAACT	6180
TTTTTCCCAG TTGAACTAA AAGAGCGGAT TTCTAAGTAT TTAGTAACGA ATGACCAACG	6240
CCGCTACTGT CGTTATTCGG ATTCAGATAT CCTTGTCCAG TTCCTCTTTC AACTGTTAAC	6300
AGGTTATGGA ACGGACTATG CTTGTAAAGA ATTGTCAGCT GATGCCTACT TTCCAAAATT	6360
GTTGGAAGGA GGGCAGCTTG TTCACAGCCA ACCTTATCCC GTTTTCTTTC CAGAACTGAC	6420
GAGGAAACAG TCCATAGTTT GCGATGCCTC AACCTTGAAT TGGTCGAATT CTTTTTACAT	6480
GTTTACCAGC TG	6492

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AACTGAAGGT AAAGGCTTCG ACGCAGAACG TGACGCTGCC CAAGCTGCCC TTGATGACCT	60
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1145

TAAGAAAGCT CAAGAAGACA ACAACTTGGA CGACATGAAA AAAAACTTG AAGCATTGAA	120
CGAAAAAGCT CAAGGACTTG CTGTTAAACT CTACGAACAA GCCGCAGCAG CGCAACAAGC	180
TCAAGAAGGA GCAGAAGGCG CACAAGCAAC AGGGAACGCA GGCGATGACG TCGTAGACGG	240
AGAGTTTACG GAAAAGTAAG ATGAGTGTAT TGGATGAAGA GTATCTAAAA AATACACGAA	300
AAGTTTATAA TGATTTTGT AATCAAGCTG ATAAGTATAG AACATCAAAA GATTTTATTG	360
ATAATATTCC AATAGAATAT TTAGCTAGAT ATAGAGAATT ATATTAGCTG AACATGATAG	420
TTGTATCAAA AATGATGAAG CGGTAAGGAA TTTTGTACC TCAGTATTGT TGTCTGCATT	480
TGTATCGGCG ATGGTACCAG CTATGATATC ATTAGAAATA CAAACATATA AATTTGTAAT	540
ACCGTTCATA ATTGGTATGA TTTGGACAGT AGTTGTATTT CTTATGATCA ATTGGAATTA	600
TATAGGCAAA TACTAAGAAG AGACAAAAAT ATATAAATAT TTCTGTACTT ATAGGATATT	660
TAAAATCAAA ATAAAGTTAA TTTACTTATT TGCAGAGGTT GCAACCCAGC CTCTGTTTTT	720
CGATAAAAAG GGACGGAATC TCATTGTGTT GGGTTTTGTC TCATCAATAG AAAGGAACAA	780
AGAGTGTTTCG TAACTGAACA CGGGTTTCAG AATTTCTTAC TAAATATAAA AGAAAGGAAT	840
TGAACCCGAC CTAAATGGTG GTTCGATTCA GAACATCAAT AGAAAGGAAT AAGGGTGTTT	900
GTAAGTGAAC ACGGGCTATG GACTGTGCCA AAAAGATAGT TTTTCTAGG ACGTAAGCGT	960
CCGTCGTCAA AACTCCTAGA TGGCTGTGTC CGTTTGACGC CCTTTGTATC TTGAATTATG	1020
AACAATACTG AATTTTATGA TCGTCTGGGG GTATCCAAAA ACGCTTCGGC AGACGAAATC	1080
AAAAAGGCTT ATCGTAAGCT TTCCAAAAAA TATCACCAG ATATCAACAA GGAGCCTGGT	1140
GCTGAGGACA AGTACAAGGA AGTTCAAGAA GCCTATGAGA CTTTGAGTGA CGACCAAAAA	1200
CGTGCTGCCT ATGACCAGTA TGGTGCTGCA GGCGCCAATG GTGGTTTTGG TGGAGCTGGT	1260
GGTTTCGGCG GTTTCAATGG GGCAGGTGGC TTCGGTGGTT TTGAGGATAT TTTCTCAAGT	1320
TTCTTCGGCG GAGGCGGTTT TTCGCGCAAT CCAAACGCTC CTCGCCAAGG AGATGATCTC	1380
CAGTATCGTG TCAATTTGAC CTTGAAGAA GCTATCTTCG GAACTGAGAA GGAAGTTAAG	1440
TATCATCGTG AAGCTGGCTG TCGTACATGT AATGGATCTG GTGCTAAGCC AGGGACAAGT	1500
CCAGTCACTT GTGGACGCTG TCATGGCGCT GGTGTCATTA ACGTCGATAC GCAGACTCCT	1560
CTTGGTATGA TCGTCGCCA AGTAACCTGT GATGTCTGTC ACGGTCGAGG AAAAGAAATC	1620
AAATATCCAT GTACAACCTG TCATGGAACA GGTCATGAGA AACAAGCTCA TAGCGTACAT	1680
GTGAAAATCC CTGCTGGTGT GGAAACAGGT CAACAAATTC GCCTCGCTGG TCAAGGTGAA	1740
GCAGGCTTTA ACGGTGGACC TTATGGTGAC TTGTATGTAG TAGTTTCTGT GGAAGCTAGC	1800

1146

GACAAGTTTG AACGTGAAGG AACGACTATC TTCTACAATC TCAACCTCAA CTTTGTCCAA	1860
GCGGCTCTTG GTGATACAGT AGATATTCCA ACTGTTACAG GTGATGTTGA ATTGGTTATT	1920
CCAGAGGGAA CTCAGACTGG TAAGAAGTTC CGCCTACGTA GTAAGGGGGC ACCGAGCCTT	1980
CGTGGCGGTG CAGTTGGTGA CCAATACGTT ACTGTTAATG TCGTAACACC GACAGGCTTG	2040
AACGACCGCC AAAAAGTAGC CTTGAAAGAA TTCGCGGCTG CTGGTGAAGT GAAAGTAAAT	2100
CCAAAGAAAA AAGGCTTCTT TGACCATATT AAAGATGCCT TTGATGGAGA ATAATACTCT	2160
TCGAAAATCT CTTCAAACCA CGTCAGCGTT GCCTTGCCGT ATATATGTGA CTGACTTCGT	2220
CAGTCGTATC TACAACCTCA AAACAGTGTT TTGAGCAGCC CGTGGCTAGT TTCCTAGTTT	2280
GCTTTTACT TTATAGATTT TTTAAGACTT TCCTAAGTAA TGACGGACGG TAGTGACCTC	2340
CTTCGAAGTT CCATACCTAA ACTTTGAACC TAAGTTTAA AGTTTCCGGA CAGCTGAAAC	2400
CAAGCTGTTT CAGGTGTTTT CATTACGGCA GAAAGTCTC GATTTAGTTG TGAAATGGTG	2460
AATGATACTC TTCAAAAAT TCTTCAAACC ACGTCAGCGT CGGCTTGTC TGGGTATGGT	2520
TACTGACTTC GTCAGTTCTA TCCACAACCT CAAAACAGTG TTTGAGCTGA CTTGCTCAGT	2580
TCTATCCACA ACCTTAAAC GGTGTTTTGA GCAGTCTGTG CCTAGCTTTC TAGTTTGCTT	2640
TTTGATTTTT ATTGAGTATG AATTACCTAA ATTATGATGC ATAGTTGATG GGATATATAT	2700
AATAGATTGA AATAGAATAT GAACAAATTG ATAAGAGGAT TTTAAAGTAA TCTCTAACAA	2760
TGCTTTAGAA ACTATGGTGT GCTATTCTAA ATTCAATTCA CTATAACTTG TTTACGTTTT	2820
AAAAAAGAGC CGTCGGGCTC TTTTACTTA TCTTCAGTTC CCTGCATTTT TTTTATCACA	2880
GCTAGTCTAG TCTGGATATC CTTTCCAAG ACCTTAAACT TGTAAGTCAA GTCTTCTTG	2940
TATTCCTTGA TAAGTTCTTT TTGCTGGTTA ATGATTTGCA GGCTGTTTTG GATAATATCC	3000
ACATCGTCCT TGATAGCTTG AACGCGGTCA GTGGTATTCA AGACTTCATC TGTGATGGTT	3060
TGGCGATTTT TTGTAACCAG ATAACCTCCG GCTGCAGCTC CTGCAAATAG CAGTAGGTTG	3120
GATAATTTCA TAGCAACTCC TTAAGCGTTT TTGATGGTTT CAGCGACTTG AGCAAGTTTG	3180
TCAAAGTCTG GTTCGTGGGC GATAAAATCA ATCTTGAGGT CATCGTCAGC ACTGTAGCGA	3240
GGCACAAGGT GAACGTGAGT ATGAAAAACT GTTTGACCAG CGACTTCTTC ACAGTTGGAA	3300
ATGATATTCA TACCAGCAGC CTTAGTGACT TTCATGACTT TTTGAGCTAC TTTTGGTACT	3360
TGGGCAAAGA GTTGGCTGGC GCTCGTAGCA TCCATCTCCA AAAGATTGCG ATAGTGTTCT	3420
TTTGGCACGA CCAAGGTGTG TCCTAGTGTT ACTTGAGAGA TATCAAGAAA GGCAAGGACC	3480
TGCTCATCTT CATATACTTT TGAAGCAGGA ATTTCCCTCG CGATGATTTT ACAAAAAATG	3540
CAATCTGACA TAAATCTAC CTCTACTGTA CTGAATTTTG ATATAATATA GCTACATTAT	3600

1147

ACCAGATTTG GAGAAAATAT GTTAGAAATT AAAAACCTGA CAGGTGGCTA TGTTTCATGTT	3660
CCTGTTTTGA AAGATGTGTC CTTTACTGTT GAAAGTGGGC AGTTGGTCGG TTTGATTGGT	3720
CTCAATGGTG CTGGGAAATC AACGACGATC AATGAGATTA TCGGTCTGTT GGCACCTTAT	3780
AGTGGCTCCA TCAATATCAA TGGCCTGACT CTGCAAGGAG ATGCGACTAG CTACCGCAAG	3840
CAGATTGGCT ACATTCCTGA GACGCCTAGT CTGTATGAGG AATTGACCCT CAGAGAGCAT	3900
ATCGAAACGG TTGCTATGGC TTACGGTATT GAGCAAAAAG TGGCTTTCCA ACGAGTAGAG	3960
CCCTTGTTAA AAATGTTCCG TTTGGAACAG AAATTAGACT GGTTCCTGT TCATTTTCA	4020
AAAGGGATGA AGCAGAAGGT CATGATTATC TGTGCTTTTG TGGTGGATCC AAGTCTTTTC	4080
ATCGTGGATG AGCCTTTCCT TGGTCTTGAT CCGCTGGCTA TTTCTGATTG GATTTCAGCTT	4140
TTGGAAGTGG AGAAGCAAAA GGGCAAGTCT ATTCTCATGA GTACCCACGT GCTGGATTCG	4200
GCGGAGAAGA TGTGTGATGC CTTTGTGATT CTTTACAAGG GAGAGGTGCG TTCCAAAGGC	4260
AATCTCCTGC AACTACGTGA AGCCTTTGAT ATGCCTGAGG CTAGTTTGAA TGATATTTAC	4320
TTGGCTCTGA CCAAAGAGGA GGATCTATGA AAGACTTGTT TTTAAAGAGA AAGCAGGCCT	4380
TTCTGAAGGA GTGTCTTGGT TATCTGCGCT ATGTGCTCAA TGACCACTTT GTCTTGTTCC	4440
TGCTTGTCCT GTTGGGCTTT CTAGCCTACC AGTACAGTCA ACTCTTACAA CATTTTCCTG	4500
AAAATCATG GCCTATCCTT TTGTTGTAG GAATTACGTC TGTTTTACTT TTACTTTGGG	4560
GAGGAACTGC CACCTATATG GAGGCTCCAG ACAAGCTCTT TCTCTTAGTT GGAGAAGAGG	4620
AAATTAAGCT CCATCTCAAG CGTCAAACG GCATTTCCCT AGTCTTTTGG CTCTTTGTAC	4680
AGACCCTTTT CTGCTGTTA TTTGCGCCTT TATTTTTAGC AATGGGTTAT GGCTTGCCAG	4740
TTTTTCTGCT CTATGTGCTT TTATTGGGGG TAGGAAAATA TTTCCACTTT TGTCAAAGG	4800
CCAGCAAATT TTTCACTGAA ACTGGACTGG ACTGGGACTA TGTTATTTCT CAAGAAAGCA	4860
AGCGTAAGCA AGTCTTGCTT CGTTTCTTTG CCCTCTTTAC GCAGGTCAAG GGAATTTCAA	4920
ACAGCGTTAA GCGTCGTGCC TATCTGGACT TTATTTTAAA GGCTGTTTCA AAGGTGCCTG	4980
GGAAGATTTG GCAAAATCTC TATCTGCGTT CTTATCTGCG AAATGGCGAC CTCTTTGCTC	5040
TCAGTCTTCG TCTTCTCTTG CTTTCTTTCG TGGCGCAGGT TTTTATCGAG CAAGCTTGGA	5100
TTGCGACAGC AGTGGTAGTT CTCTTTAACT ACCTCTTGCT CTTCCAGTTG CTGGCCCTCT	5160
ATCATGCCTT TGAATACCAG TATTTGACCC AACTCTTTCC GCTGGACAAG GGGCAAAAGG	5220
AAAAGGCTT ACAGGAGGTA GTTCGAGGAT TGACCAGTTT TGTTTTACTT GTGGAATTAG	5280
TTGTTGGGTT GATTACCTTC CAAGAAAAAC TAGCCCTTCT AGCCTTACTA GGAGCTGGTT	5340

1148

TGGTTTTACT AGTCTTGAT TTGCCTTATC AGGTAAAACG TCAGATGCAG GACTAACATT	5400
GCTGATACGA CACTAAAAAA GAAGTTGAGT TCAGTCTGTC TCAACTTCTT TTTTGTACT	5460
ACAGGATAAT GGTGGTCCG TAGAGACTTA TACTCTTCGA AAATCTCTTC AAACCACGTC	5520
AGCGTCGTCT TACCGTACTC AAGTACAGCT TGCGGCTAGC TTCCTAGTTT GCTCTTTGAT	5580
TTTCATTGAG TATTAACCTG GTCTTGACTT GGTCAAAGTG GAAGCGGTCA TAGGCCCGCC	5640
AAGCGGCGCG AGTTGGAGCA TCTGGATCAA GAGCGCTGAG TCCCATGAGA AGACTGGAAG	5700
TCTGGTAAAA TTTTCTAGT TCAATCAAGA ATCGATTATC CACTGTTTCA GCCTTGGCTA	5760
GAAAACCAAG AATAGAGTTT AATTGCTCCT GAAAGCGGAC GTCGTCAGCG CTTGCCTGTT	5820
TGCATGCTTG GTAGGCTTTG TTTAAGTCAG TAATCAAAGT ATGAGCTCTT TTGATGGGGT	5880
CTGTATCTGT CATGGGAATG CCTCCTTFAA TCTGGGTGCC AGTCTTACTT CTGGCAACTG	5940
TGTTTTGATA CTGTTAGTTT ATCACTTTTA ATTCTTTTTT TTTATTCAA TCTTTAATTG	6000
TCATTGAAAT GTCTTGAATT GCGCTGAGTG AATTTTATGA TAAATAGTT GTAAGCTCAT	6060
CATGATGTTG TAGAAAATAA TCCTTTTAGG AGTTTTCAA GACTGTTTAG GATTGGGTGT	6120
GCTTGGGCTA GACCTTTTCT GTTATTCTTT TCTTAGGAGG AGAATCCAAT GAAATATATG	6180
ATTATTCAGA CGCAGAAAAC AGTCTATAAA GTAAACATCG ACGATATCTA CTATATCCAA	6240
ACACATCCAA CTAAAGCCCA TACCGTACAG ATTGTTACAG AAGAAGCTAG TTTTAATATG	6300
CTTCAAAATT TAAGTAATCT TGAGAACCAA TGTGGGGAAA CCTTGATGAG ATGTCATCGA	6360
AATTGTTTGG TTAATCTTGA TAAATTAAAA TCGATTGATT TTCAAGAAAG AATCCTTTTT	6420
CTCGGAGAAG AAGGTCAATA CGCTGTCAAG TATGCCAGAC GTCGCTATAG AGAAATTCGT	6480
CAAAAATGGT TGAAAGAGGG AGAGTAAGAA GATGAGAATA TTTGTTTTAG AGGATGATTT	6540
TTCCCAACAG ACTAGAATTG AAACGACGAT TGAGAACTT TTGAAAGCAC ATCATATCAT	6600
TCCTAGCTCT TTTGAGGTAT TTGGCAAGCC GGACCAACTG CTGGCTGAAG TGCATGAGAA	6660
GGGGGCCCAT CAGCTATTCT TTTGGATAT TGAGATTCGA AATGAAGAGA TGAAGGGACT	6720
GGAAGTGGCT AGAAAGATTC GGGATCGGGA TCCTTATGCC CTGATTGTCT TTGTGACGAC	6780
TCACTCGGAG TTTATGCCCC TGTCTTTTCG CTACCAAGTG TCTGCTTTGG ACTACATTGA	6840
TAAGGCCTTG TCAGCAGAGG AGTTTGAATC TCGATCGAG ACAGCCCTCC TCTATGCCAA	6900
TAGTCAAGAT AGTAAAAGTC TGGCGGAAGA TTGCTTTTAC TTAAATCAA AATTTGCCCA	6960
ATTTCAGTAT CCTTTTAAAG AGGTTTACTA TCTCGAAACG TCGCCAGAG CCCATCGTGT	7020
TATTCTCTAT ACCAAGACAG ACAGGCTGGA ATTTACAGCG AGTTTAGAGG AGGTTTCAA	7080
GCAGGAGCCC CGTCTCTTGC AGTGCCACCG CTCTTTTCTC ATCAATCCTG CAAATGTGGT	7140



1149

GCATTTGGAT AAGAAAGAAA AACTGCTTTT CTTT

7174

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CCACCAGGGA AAATCATTGA AGTTGGTAGT CACCAAGAGT TAATGCAGGC GCAAAGTTTC	60
TACCATCATC TATTCAATAA ATAAGGAGAA TGTCATGAAT CCTAATCTTT TTAGAAGCGT	120
CGAGTTTTAT CAGAGACGTT ACCATAACTA TCGACAGTG TTAATTATAC CTCTTTCATT	180
ACTATTTACT TTCATCTTGA TTTCTCCCT TGTGCCACA AAAGAAATTA CTGTTACTTC	240
CCAAGGAGAA ATCGCCCCTA CAGTGTCAAT GCCTCCATTC AGTCAACCAG TGATAATCCT	300
ATCCTAGCTA ATCATTTAGT GGCAAATCAA GTAGTTGAAA AAGGGGACTT ACTCATCAA	360
TACTCTGAAA CAATGGAAGA AAGTCAGAAA ACTGCCTTAG CAACTCAATT ACAAAGACTT	420
GAGAAGCAAA AAGAAGGACT TGAATTTTG AAACAAAGCT TAGAAAAAGC GACTGATCTT	480
TTTCTGGCG AGGATGAATT TGGTACCAT AATACCTTTA TGAATTTTAC TAAACAATCC	540
CATGATATTG AACTGGGTAT CACAAAGACT AACACCGAAG TTTCAAATCA AGCTAATCTT	600
TCCAATAGCA GTTCATCAGC TATTGAACAA GAAATTACAA AAGTTCAACA ACAAATTGGA	660
GAATATCAAG AGTTGAGAGA TGCTATCATA AATAACAGAG CACGCTTACC AACTGGCAAT	720
CCGCACCAGT CAATTTTGAA TCGTTATCTT GTAGCCTCAC AAGGACAAAC ACAAGGAACT	780
GCAGAGGAGC CATTTTATC TCAAATTAAT CAAAGTATTG CAGGTCTTGA ATCATCTATC	840
GCAAGCCTCA AAATTCAGCA AGCTGGTATC GGAAGTGTAG CAACTTATGA TAACAGTTTA	900
GCAACCAAAA TTGAAGTACT CCGCACTCAG TTTTACAGA CAGCCTCACA GCAACAATA	960
ACTGTGGAGA ATCAATTAAC AGAATTAAAA GTACAAC TAG ATCAAGCCAC ACAGCGTTTG	1020
GAAAACAATA CCTTAACCTC CCCAAGTAAA GGTATCGTTC ATCTGAACAG CGAATTTGAA	1080
GGTAAAAATA GAATTCCAAC TGGTACAGAA ATTGCTCAAA TATTCCCTGT CATCACAGAT	1140
ACAAGAGAAG TACTAATCAC TTAACGTA TCTTCTGACT ATCTACCTCT ACTAGATAAA	1200
GGACAACTG TAAGATTAAA ACTGGAGAAG ATTGGAAATC ACGGCACCAC CATCATCGGC	1260
CAACTTCAGA CAATTGATCA AACTCCTACC AGAACAGAGC AAGGAAATCT CTTTAAATTA	1320

1150  
ACCGCTCTTG CAAAACATC TAACGAGGAT AGTAAACTCA TCCAATATGG CTTACAAGGT 1380  
CGCGTCACTA GTGTAACAC AAAGAAAACA TATTTTGATT ATTTCAAAGA TAAAATTTTA 1440  
ACACATTCTG ATTAATTTTC AGATAACACT CTATAACTAT TTATTATCTT ATCAAAAAGG 1500  
AGAATCATAA CATGGATAAG AAACAAAACC TAACTTCATT TCAAGAACTA ACAACTACCG 1560  
AACTCAATCA AATTACAGGT GGAGGATTGT GGAAGATTT ATTATATAAC ATTAATAGAT 1620  
ATGCTCATTA CATCACATAA GAACTTCATC ATCCAATACA ACTATAAAAA AATAAGACCG 1680  
AGAAACAAGT ACTCTCGGTC TTATTTTTC TCACTCTGTA TGTATCACAG TAAGTACCTG 1740  
ACGAAAGACT TGATTTTGAC AGGTGGTATT TAGACTGGTA TTAGGATGGC TTTCCACAAT 1800  
CTTCATGACG GTATAGAGAC CAACTCCTCT CTCCTCCCCCT TTAGAAGTGG CTCCAAAGGA 1860  
GAAGATTTCA GAAATATCGA TGCCCTCTTC TTTGATGGAG TTTTCGATGA TAAAGGTCTC 1920  
CTGTGCTCCA TTTTTTAAAA AGGCGATTGA AACATGAGGT TGAAGTCTT CCACACTGGC 1980  
TTCAATAGCA TTGTCACAAA GGATAGACAC AATGGTTAGA AAATCAAGTA GACTCATCCC 2040  
CTCGACCTGA ATCTCCTCAG GAACTTCGAC ATTAAAGACA ATGTTCTTAT CTCTGGCTTT 2100  
TAAAAATTTT CCTGCTAGAA GACTTTTGAG GGCTTTATCA CGAATATTTA CCAATCTGCC 2160  
CAGGTCATAT TTATTGTTCT GCAATTTCTG ACTGGAATCC TTTAAGACGG AGCCATAGAC 2220  
CTCTTTTATC TGCTCCATAT CCTCCTCTTC AATGCCCAGA CGTAAGCTAG TCAAGAGGTT 2280  
GGTATAATCA TGACGAAAGC TCCGTACTTC CTTGTAAAGC TCCTCTATAT GCCGACTATA 2340  
GCGTTCCATA TCTCTATAGC GCAGGGGCTG CTCTTGTTCC AATCTCTCAT AGAGTTTTTC 2400  
CTTCAAATAG GTATCCAATT TCTTGATAAC CCCCATAAAA AAGAGTAGGT AAAAGACTAG 2460  
GATGAGATGG CGAACAGTCT TTGATTGAAT ACTTTGTTCA TATTCAAAAA AAGACAGACT 2520  
TTCCATGACT AGATAGTAGC CACCCATTAT CCAGTTAATC TGAGTCAGGG ACTTTTGAAA 2580  
GGCTTTATCG AGAATCTCCT TTCTCAAGCT AGTAAATCG TAGTCCAACC ATTTCAAAAA 2640  
AGCTAGAGAA ATGAAGAAAT TGAAATTAT TATACATAAC CCAGTAAATG AGTAGCCATC 2700  
ATATACTTGC CCTTGTCCTA AAAATGGAAG CACAAAATAG GAGACTCCTC TATAAAAGAG 2760  
ATTCACCAAT ATCATTGGAA AGAGACCATA AAAGAAAAGG AGTTTTTTAG GAAGCCCTCT 2820  
CAATAATAAG AAAGATAAGC CTATGCCGTA CAAGGGTTCC ATAAAATAAG ATAGGTAAAC 2880  
ATTTCTACT ATATAGCTAA TCATCACAAA AACAAAGGCC AACAGTATCT TCAAAAGAAA 2940  
GGCCTTAAAA ATCTCTCGA AAGTAAGATC AATTCATCC ACCTTAAAGA AGATGACAAT 3000  
TTCTAGTCCA TTAGTAACAA GTGTATACAA CAATATCCAA GCAATGTTCA TAAATTCTCC 3060  
TAGCTCAGTG TAATTTATTG ATGGCCTCAG ACACTTCCCT GACCTTATAA CGGGCGATTA 3120

1151

GACAACTTCC ACCATTGGGA GAGAAGAGCA GTTTTCTTT CTTATCCAAA TGCACCACAT 3180  
TTGCAGGATT GATGAGAAAA GAGCGGT 3207

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTGAATCAAG TGTACTGCAC CAGTTCGTGC ATCAGGCATA ACAACATCTA CAGATATAAT 60  
ATTGTTTTCT GAGTCCGCCT CATAAGTTAA AATCATAAAT TTTTCGATAT TCGAATTTTT 120  
AGTAGCTTGT TCAATTTCTT GAATCATTTT ATCAGAAACT AACTCCATCT GAATTGGAAA 180  
GGAATGACTA TTTTCATCAT TTTTGTAGGA AGAATGTTGA TTAAGATAAA GTGTATTCAT 240  
CTGAGCATAT TCAAATAAGT AGCCACTCTT ATTTTTTGT ACCAAAGGAA ATTGGTTTGT 300  
AAGTCGCTTC TTACCCTTTA TAATTAACAA TACTTTCCCA TATTTTTCTG TATTTGTTTC 360  
AAATTCTAAA TATCCCCAAG TCTGTCTGTC TAATTGTAAT TTATACTCAA ACAAATCTGC 420  
TGATGCAAAT GCAGTATCAA TATGATTAGG TCGCGTCCAT GCATAACCAT TCGACACTAT 480  
CATTGTCTCT CTTTTTCTA GACGTCATC TACATAATCT TTTTGCCCTT TCATCAAAGT 540  
ATCTACAATT TTTTGTGCCT CAAGCGAATC AAAGAGATCC TGATTCAACA TAATCTTCC 600  
TCCTCCAAAT ACTTTTAAAT GAATTATACC ATTTTCTTAA AGAAATTAAT ACAATAATTA 660  
TCTTTTTCTT AAAGTTCTGT GTCAGAGTAA TTTAGAAAAT TATATCTTCT ATAGTAAAT 720  
CAATTAAAAA CTGAACAAAT TTATTGGGAA ATTCAAATCG CTTTCTGAAA ATATTTTAGG 780  
AACCGTAGTG TAATATTCCA GATTCAATTC ACTATAAAAC TGACCTTTCT CCTGCAAAAG 840  
AAAAAGGAAA GACTTCCTTT CGTGCCCTTC CTCTTACTTG CTAATTGTTT GATTATTTTT 900  
GGTAAGCTAC TGCTTGTCTG ATAAAATCCT GAATCGGCTC TCCTTGGTGG AGAGCTTTTA 960  
CTATTTTCGA ACCGACGATA ACACCATCTG ACACCGCATT GAAGCGTCC AGATCGGCTT 1020  
GACTAGATAC ACCAAAACCT GTCAAGACTG GGATGTCGGC CACTTGATGA AGTTGCGCCA 1080  
AGTGCTTGTC CAAATCTGCA CGGTAATTGC CTGATTTCCC TGTCACCCA TTGATGGCAA 1140  
CGGCATAGAT GAATCCCTCC GCCCCCTCAA TCAACTCTTT CTGGCGCTCA ATTCCTGTGG 1200  
TCAAGCTTAC TAAAGGAATC AAGGCGATAT CTGTATTTGC CAAAAATGGT TCTACAAAGT 1260

1152

TGGCATGTTT	ATGAGGCAGG	TCTGGGATAA	TCAAGCCCTT	CACAGCTGTA	TCAGCCAGAT	1320
CTTTGACAAA	GTTCTCCACA	CCGTACTGAA	AGAGGGGGTT	GAAGTAGGTC	ATGATGACCA	1380
GTGGAATCTC	TGTTTCAATG	GTTTTCAAGG	TTTCAACTAA	AGCCTGGGTA	GAGGTCCCGT	1440
GGGCTAAACT	GCGCAAGCCA	GCTTCTTCGA	TAACAGGTCC	ATCTGCAACA	GGGTCTGAAA	1500
AGGGAATACC	CACTTCAATT	GCAGAGACAC	CCAAATCTTC	TAAAAAGTGA	ATTGTTTCAG	1560
CAAGACCGTC	CAAACCTTTC	TCGTGGTCAC	CAGCCATGAT	ATAGGGAACA	AAAATTCCTT	1620
TTCCAGCTGC	TTTAATAGCA	TTTAATTTTT	CTGTTAGTGT	CTTAGGCATG	AGCTTCTCCC	1680
TTCTTTGCTG	CATCTGCTTC	CAAGCGGTCC	TTGACTTGAA	CCACATCCTT	GTCCCCACGA	1740
CCTGATAGGC	AGACAATCAT	AGACTTTTCT	GGTCCAAGTT	CTTTGGCCAA	TTTCACCGCA	1800
AAGGCGATAG	CATGGCTAGA	TTCCAAGGCT	GGGATAATCC	CTTCCACACG	AGACAAGAGT	1860
TGGAATCCTT	CCAAGGCTTC	TTCGTCTGTC	ACAGGGACAT	AGCTGGCACC	TTTAATATCG	1920
TGGTAGTGAG	AATGCTCTGG	ACCGATACCA	GGATAGTCCA	AACCTGCTGA	GATAGAGAAG	1980
GCTTCAAGAA	TTTGACCATG	GGCATCTTGG	AGCACATCCA	TGAGGGAACC	GTGAAGGACA	2040
CCTGGACGAC	CCTTGGTCAA	GGTAGCTGCG	TGGTGCTCTG	TATCCACACC	AAGCCCTGCT	2100
GCTTCAGTTC	CATACATAGC	TACTGACTCA	TCTTCTACAA	AGGGATGGAA	GAGCCCGATA	2160
GCATTCGACC	CACCACCAAC	ACAGGCTACT	AGGGCATCTG	GCAGATCTCG	ACCTGTCAAG	2220
TCACGGTACT	GTTGTTTAGC	CTCTCGACCG	ATGACACTTT	GGAAGTCACG	AACGATTTCT	2280
GGAAATGGAT	GAGGCCCCAA	GGCAGAACCA	AGGATATAGT	GGGTATCGTC	GATATTAGCC	2340
ACCCATGAAC	GAAGGGCTGC	ATTGACCGCA	TCCTTGAGCA	CGCGCGAACC	ATCTGTTACA	2400
GCCTCGACCT	TGGCTCCCAA	AAGCTCCATG	CGGAAGACAT	TGAGGGCTTG	GCGTTTGACA	2460
TCTTCCTCAC	CCATGTAGAT	GGTACATTCC	ATGTTAAAGA	GGGCTGCAGC	AGTTGCAGTT	2520
GCCACACCGT	GCTGACCAGC	ACCCGTTTCT	GCGATAATTT	TCTTTTACC	CATGCGTTTG	2580
GCAAGCCAAA	CTTGTCCTAA	GGCATTGTTA	ATCTTGTTGG	CTCCTGTATG	GTTAAGGTCT	2640
TCCCGTTTGA	GATAAATCTT	GGCTCCGCCA	ATATGCTGGG	TCAAGTTTTT	TGCGTAATAA	2700
AGAGGAGTTT	CACGTCCTAC	GTA CTGGCGC	AAAAGCTGGT	TTAATTCCTC	TTGGAAACTT	2760
GGGTCTGCCT	GACTTTCACG	GTAGGCCTTC	TCCA ACTCCA	AAACTGCTGT	CATCAATGTT	2820
TCTGGGACAA	AACGTCCGCC	GAATTTTCCG	TAAAATCCAT	CTTTATTTGG	TTCTTGATAT	2880
GCCATGCTTT	ACCCTCTCTA	TAAATCTTCT	AATCTTTTCA	TGATCTTTTT	GTCCATCTGT	2940
CTCCACTCCG	CTCGATACAT	CTACTGCATA	GGGAGTAAAG	TGTTGAATTG	CTTTTACTAC	3000
ATTATCTTCA	TTAAGGCCAC	CTGCGATAAA	GAAGGGCTGT	GCTAGTCCAG	TCGTATCCAG	3060

1153

TTGACCCCAA TCAAAGGGCT GGCCACTTCC TGCCACAGGG GCATCAAAGA GTAGATAATC	3120
TGCCTGAGAA TTGGGGACAT GCCCATTTC ATCTACCTGC ACAGCCTGAA TACTGGCACA	3180
AGGCAAATTC TCAAATAAAT CATCTGCCAC CTGACCGTGA ACTTGAACCA AGTCCAAGCC	3240
AACTTTGTCA ATCGCTTCCA GCAGTTCTAC CCGACTTGGT GAAACAAATA CTCCAACCTT	3300
TTTCACATCT GCAGGAATAA GCTTTGCCAA CTCAGCTGCC TCTTCTAAAG TCACCTGTCT	3360
TTTACTAGGT GCAAAGACAA AACCGATATA GTCGGCTCCT GCTGAAACGG CTGTTTCCAC	3420
CGCTTCTTTG GTCGATAGTC CACAAATTTT AACCTTTGTC AATCTGCAAC TCCTTGATTC	3480
TCTGGGCCAC ATTTTCTGCC TGCATAAGAG CTGTCCCTAC CAAAATTCCG TTAAAGTATG	3540
GGGCTAGTCG TTCCGCATCC TGCCCTGTGA AAATGGCAGA TTCAGAAATG TAATAGCGAC	3600
CTTCCTCAAA GTAAGGGGCT AAATCTACAC TGGTCTGCAA GTCGACCTCA AAGGTAGTCA	3660
AGTTGCGGTT GTTGACCCCG ATAATCTCAG CACCAAGTCT GTGGGCTACC TCTAGTTCAG	3720
CTAGATTGTG AGTCTCCACT AAGACTTCCA GACCAAGCTC TGTCGCGTAG TCATACAGTT	3780
CCTTGAGGCG TTCTTCGGAC AAGGCTGCCA CAATGAGCAA GATAACTGTC GCACCTGCAT	3840
TGCGAGCGCG GATGATTGC TTTTCATCGA TGATAAAGTC TTTGTTGAGC GTCGGAATCT	3900
CTACCTGACT GGAAATTTCC CGTAGATAAT CCAAATGCCC TTTAAAGAAA ACCTCATCTG	3960
TCAACACCGA AATCATCACT GCTCCGTTTT CTTCATAAGT CTGGGCCTGT TGCACAATAT	4020
CCACATCGAG ATTGATATCT CCCAACTAG GGCTAGCTTT CTTGACCTCA GCGATTACCT	4080
GCAAGCGGTC CTGATGATTC TTCAAAAATT CTGCCAAGCG ATAGGTCTGG CGCAGAGGCT	4140
GGATTTGCTC CAGCTTCATC TGCTCCACCT CACGCGCCTT CTGCTCTAAG ATTCTGTGTA	4200
AAAATTCCTG ACTCATTTTT GGTACTCCTG TAACAGTCTG AGTTTTTCAA GGGCCTTGCC	4260
TCTAGCAATC ACTTGACGGG CCAAGGCAAC CCCTTCCTTG ATGCTATCAA TCTTACCATT	4320
AGCATAGAAA CCAAGACCAG CATTCAAGAC TGTCGTTTCC AAGAATGGAC TTGCTTCGTT	4380
TTTCAGAACG CTAAGCAAAA TTTCTGCATT TTCCTGAGCA TTCCCACCAC GAATATCTTC	4440
CATAGCATAG CCTTCCATTC CCAAATCCTC TGGAGTAAAG CTTGACAAGC TGATTTGCCC	4500
ATTTTCAAGA AGTGCAATCT TGGTTGTTCC GTTCAAGCCA GCTTCATCCA ACCCTTCTGG	4560
TCCAGCAACC ACGATGGCAC GTTTGCGACC CATATTTTTC AAAACCTGAG CTGTACTTTC	4620
TAGGAGTTCT GGACGACTAA TTCCAAGAAG CTGTGTTTCT AAAGCCATTG GATGAATCAG	4680
TGGACCAGTC AAGTTCATAA TCGTTGGAAT TCCCAATTCC AAACGAGCTG GCATGATGTA	4740
TTTCATAGCT GGGTGATAT TTTTAGCGAA GAGAAAGACG ATTCCAGTTT TATCAAAGAC	4800

1154

CTTACCTAGT TCAGCTGGTT TGAGGTCAAG ATTGATTCCC AAGGCTTCGA GGACATCTGC	4860
GGAACCAGAT TTAGAAGATA TCGAGCGGTT ACCGTGTTTG GCCATGTGAA TACCGCCACC	4920
AGCCAAGACA AAGGCTGCAG TTGTGGAAAT ATTAAACTG AAAGACTTGT CCCCACCTGT	4980
ACCACAGTTG TCCATGGCAT CATGAATCTC AGTTGGAATA TGCTGGGCAT GTCTCTCAT	5040
GACTTGGGCA ATGGCTGTGC GTTCTTCAGG TGTTCCTCCC TTCATCTTAA GAGCTAAGAG	5100
GAGAGAAGCA ATCTGCCCTT CAGTTACACG CCCAGTTACG ATACGCTCAA TGACATCCGT	5160
CATTTCCACA CCTGATAAAT TTTCAAATTT TGCTAGTTTT TCAATAATCT CTTCATCCT	5220
AGTTTCCTCA CTMTACAACC TCCTCGATAA AATTCCGAAT AGAAGACAAG CCGTCTGGCG	5280
TTCCAATGCT CTCTGGATGG TACTGGAAGC CATAAATCGG TAGGTTTTTA TGTGAATCC	5340
CCATGATGGC TTGGTCATCA GTCGAACGAG CTGTCACTTC AAAGTCTTCT GGCATTTCT	5400
CAATCAAAAT ACTGTGATAA CGCATGACCG CACGGCCATC CTCAATACCT TGATACAAA	5460
CAGATGGCGC TTCAAAGTTG ATATTGCTCT GTTTCCTATG CATGACTTTT GGAGCCAAAC	5520
CTAGCTTACC ACCAAAGACT TCTGCAATGG CTGGTGGCC CAAACAAATC CCAAGAATCG	5580
GCTTCTTGCC TGCAAAATCA CGAATCATGT CTTCCATCTT TCCAGCATCA ACTGGCCAAC	5640
CAGGACCAGG AGAAAAGACC AGACCATCTG CTTTTTCAGC TTCTTCATAC AGCTTGAAT	5700
CATCATTTCT CAGAACCTGA ACTTCTGCAA AATTCCCAAT GTATTGGGCC AAGTTATAGG	5760
TAAAAGAATC ATAGTTGTCA ATCAATAAAA TCATGGTCTT AGTTCTCCAA TTCTAGTCAT	5820
AGATTTTGCT TTGTTAATGG TTTCTTGTA TTTCTTTTGG GCGATAGAGT CGTAGACAAT	5880
CCCTGCCCCA GCCTGCACAT AGGCTCTTTG ATTTTGTAGA ATCATGGTTC GGATGGCGAT	5940
GGCCAAATCC ATATCACCCG TCGCAGACAA GTAGCCGATT GCCCCAGCGT ATACTCCCCG	6000
TTTTTCCGTT TCCAGTTCAI AGATACGTCT CATCGCTCGA ATCTTTGGTG CTCCAGAAAC	6060
GGTTCCAGCA GGAAGCGTTG CTTTCAAGGC ATCCATGGCA GTGAGTTCTG GAAGCAAACG	6120
CCCCTTGACT ACGCTGGTCA AATGCATGAC GTAGCGGAAG AGCTCCACTT CCATATACTT	6180
AGTGACTTGG ACACTGGTCG TTTCAGAGAT GCGGCCAATA TCGTTACGCC CCAAGTCTAC	6240
CAACATTCGA TGTCTGCTG TTTCTTCTC ATCAGAGAGG AGGTCAGTCG CCAAGGCCTT	6300
GTCTTCTTCA TCCGTAGCCC CTCTTGGTCG CGTCCCTGCA ATCGGATTGG TTGTCACGAT	6360
GCCATTTTGT ACAGAAACCA AACTTTCTGG ACTAGCTCCG ATGATTTGAT AATCCCCAAA	6420
ATCATAGAAA TAAAGGTAAT TAGAAGGATT AGTCACGCGG AGATTTCTGT AGAAGTCAA	6480
TGGATTTCCA GTAACCTCTG CTGAAAACG CTGGCTGAGT ACACATTGGA ACATATCTCC	6540
GTTACGAATC AAGTCACGAG CTGTTTCTAC CATTCCTCA AACTTATGTG GAGCGATATG	6600

1155

CGGTTTGAAG TCTAACGGAG ATAGATCCAA ATCTTCAAAT TCATTTGGAG CAGGAATGCG	6660
TAATTCCTCA AGCACTTGGT TCAAGGATTT TTCCAAGGCC TCTTGACTGC GCTCACTATA	6720
AAGTGCATCC TCTATGACAT GTATCTTCTC CTTCTTGTGG TCAAAGACCA TATAGCTCTC	6780
ATAGACAAAG AAATGCATGT CTGGCGTCCC AATTGTATCC TCAGGGATTT GACCAATTTT	6840
TTCATAAAGC GAAATCATAT CGTAACCCAC AAAACCAATG GCTCCACCAC CAAAAGGTAG	6900
CTCTGAGTGG TGCTGACTCT TATGAATCAC TTCATAAAGG AAATCCAAGG GATCCCGATC	6960
AATCACTTGA CCATTTTGAT AGAGAACCCC ATTTTCAAAC TTAATCTCAA AAATGGATT	7020
ATAGGCTAGG ATAGAAAAAC GAGCTGTTTC CTTGTCTCTC GGAATACTCT CTAAAATAAC	7080
CTTATGTTGC CCCTTTAAGC GCATATAAGC CAAGATTGGT GATAAGACAT CTCCATGAAT	7140
GATTCGTTCC ATTGTAATTT CCCTTTCAGT TCTACTTCTA GTCCGTGGTG ACTGTATGAA	7200
AAATCCCCAC GCAAAATAAC TTGCGTGAGG ACGAAATTCG CGGTGCCACC TCAATTATAG	7260
GATTTCTCCT ATCTCTCATT CCTGTCTCAG ATATCTCCTG TAACAGGCTG TCGGATAAAG	7320
GGCACTCCCT TGAGAATGAT GTTTTCTTCT CTCGTTTCAG ATGAACCCAA CTTTACAGCT	7380
TTCTCTGCTT GTTTTCAGCA ACCACAAGCT CTCTGTGAGA GAAAGAACTG TAATTTTTC	7440
ATCTATTATT TTTTAGCTTC TAGTAGTCTG CAATCGCAGC TAGGTCCTTG CCTCCACGAC	7500
CAGAGACATT GATGAAGAGA TGTTCACTC GGTACACCTT TATACTCTTC GAAAATCTCT	7560
TCAAACCGCG TCAACGTCGC CTTGCCGTAG GTATGGTTAC TGACTTCGTC AGTTCTATCT	7620
GCAACCTCAA AACAGTGTTC TGAGCTGACT TCGTCAGTTC TATCCACAAC CTCAAAACAG	7680
TGTTTTGAGC TGACTTCGTC AGTTCTATCC ACAACCTCAA AACAGTGTTC TGAGCTGACT	7740
TCGTCAGTTC TATCCACAAC CTCAAAACAG TGTTTTGAGC AGCCTGCGGC TAGTTTCCTA	7800
GTTTGCTCTT TGATTTTCAT TGAGTATTAC TAGCTTTTTT CGTATTAGTC CAGCCTTTT	7860
GTTTGCTTTT AGTAGTAGGC ATGGAGCTGT AGATAGAACT CAAGTTCATC AAAGCGACTT	7920
AAGGCCCTAA TAAAAGATA ACCAAACGAC GGATAGAAAA AAGCCACAC ACAGAAATATA	7980
CTTCCGTGTG AGGGCGTTGG TAACGCGGTG CCACCTCAAT TATAAAGGGA CTATCCCTTT	8040
ACATCTCTGC CTTGTTTAAC AACAAGCTGC ACTGTAAGGT GTGCGCACCG AATTTTCATT	8100
GTTTCAAATT CATTTTCAA ATCAGCCCAC TTTCACTACT TCCAACCACC TATTCACAAT	8160
CACCACAGGC TCCCTGAAGA TCAAAAATAG TTACTTTTCT GATTTGTTGA ACTTATTTTA	8220
ATACTTTGTT TTTCTTTGT CAAGACTTTT TTACGATTTT TTTGAAAATA TCATTGGAAT	8280
ATGACCATGT CTTCTTAGA TCGAACATGA ACATGTCCCA CTTCTTAGAA ATTGGATCCA	8340

1156  
ACTCAATAGA AACTGAATGG AGGCTAAACA GAACTTATTT TAGAACAATC CATCTTTTCC 8400  
ACTAGGATTT TCAAGAATTA AACAACTA GAACTCTGT CTCCTAACAA ATTTAGGAGA 8460  
AACTTCAACA GATGTGACAC TTTCCCTTTT AATAATTGCT AAAACACCTT CTATCATTTT 8520  
TTTAGCCAAT TTAACATAAT TGGGAGCAAT TGTAGACAAA GCTGGAGTAT AATACTGAGA 8580  
AATAGGAATA TTATCAAATC CAATGATAGA AATATCATCT GGAATAAGAA TTCCTTTTCTC 8640  
ATAGCACGCA CGAATCAAGC CCTGAACCTT TTCATCTCCT GAAACAAAAA TAATGTCCGG 8700  
ATAATTTTGG GTAGTCAAGT GCTGCATTGC ATAAGAATAA ACTGAATCAA TTGTAGATAA 8760  
GCCATAAATG ACTTTTAAAT CCATAAAGTA ATTTTATCA TTCAGAAAAG AACGCACACC 8820  
TCTTTCACGA TCCTTATTAA CATGGGATTC TCCTCCATA AGCAACCACA TATTTTAAA 8880  
TTTTTCTTCA GTTACAGCTT TCATCATATC ATAAGTAGCT TGAAAATTAT TATTAGATAC 8940  
ATAGACTACT CCAGACGTTT GAGATTCACC GAAACAAGA AAAGGCATAT GGTCTTCTT 9000  
TAAATACTGA ATTCTGATAT CATCTACACT TTCATAAAAA ACAATAACAC CATCTACTAG 9060  
GCTACCTGTG CTTGATATAA TTGAATTACT AATTGTATCC TCCTCTCCAA AGTACTCAAC 9120  
TATAGCATT AACCACAAAT CTTTACACGT CCGTAACACT TTATCTAACA GCGTATGAAA 9180  
CCAAATTAAA GGAAAAGAGT CGATTTTTTT TACAGAAATC AATATATTTA TAGCTTCTTT 9240  
TTTAGTTAAA TTTTTGTCAT ACGCATTTGG AATATACGAC AATTCCTCTA TAACTTTTTG 9300  
AATCGCTTGA TAAGTTTCTT CTTTAACATT TACTCCACCA TTAATAACTC GTGAAACTGT 9360  
TTTTGGAGAA AAACCTGATA AACGTGCAAT ATCATAAATA GTTACCTTTT TCCCATTAT 9420  
ATTTTTCATT TCAGTCTTCC ATTACGAACA TTCTAATATT ACTATACAAT ATTTAATTTT 9480  
TTTTAACAAG AGAATTTAGT AAATTATTTA AGATCCACAA ATTCACAAAA TTAATTTTAC 9540  
AAATATTCTT CCCCTTCAA AAAGTTTAAA TTGCATTTC CACCTTTATT TTTAAGAATG 9600  
TTTCCAACCT CACGACAAAT AAATTCATAT GAGAAAAAAC TGCCATAAAA TTGTAGATTA 9660  
ACTTTTTCAG TAAAATGTGT AGGATTTATA AAAACATATA ATAGCCTGTC AATGTAACAT 9720  
TTTAACATAG AGTTAATTTT TTCTTTAAAG ATAACATTTG TTATCAACTC ATCAGGAGGT 9780  
AAATGAAAGG CAAACACCAT TTCACAAATA TCATAAAAAG AAATAAATTT GTATACTTGT 9840  
ATCAAACAAT TATTATCAA ATATTCTATT TTACCTAAAT CAAAATTGAT TTTATAATCT 9900  
TTCATAAAAA CCTCTGAGCA AAAATCTACT CAAAAATTAG ATGATTAAAA CATCTAAAAA 9960  
GCAAAAGGAC AAAACATCT GTCCCTTTGT TACTAAATT TCAGCTAATT TCTTCGACAT 10020  
AAATAACACC TACAATATTA GCAATTTCTT CCATCAGTCG AAGATGTTCA AATCTACCTG 10080  
ATAATTCCAG AGTAATAAAT GACGCTATTT TTTGTCCGG AACATCAAAG TATTCAATTC 10140



1157

TGTCAGAATT AACATCTCCA AACGCTGTTT TTGAATCGGT CATTCTGATA CCATTTTCTG 10200  
CACAATAAAC CAATACACGA TTATAGGCTT CTGTAGATTT AACCACATA TACAATTCAA 10260  
TCATTTTAGA ACGATTTTGC AGATATTTTT TTAGTGGTTG GAACATGGAT ATCACACCCC 10320  
AAACAGAAAT GGCTACTAAA AGAGCTCCCT CATAAGG 10357

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

CGGGACATTC TCAATCTTCT GTCTTTTGTT TTTCTCTTCT TTCTATGATA CAATGGAAAA 60  
AATAAATCA AAAGGAGTTT TTTTATGACT TATCCAAATC TCTTGGACCG CTTCTTAACC 120  
TATGTTAAGG TCAACACGCG CTCTGATGAA CACTCTACTA CTACTCCAAG TACACAGAGT 180  
CAGGTGACT TCGCAACAAA TGTCTAATT CCTGAAATGA AACGTGTTGG ACTGCAAAAT 240  
GTTTACTATC TACCGAATGG TTTTGCTATT GGAACCTTGC CAGCCAACGA TCCGTCTTTA 300  
ACACGTAAGA TTGGTTTTAT ATCGCACATG GATACTGCTG ATTTTAATGC TGAAGGAGTC 360  
AATCCACAGG TAATTGAAAA CTACGATGGT GGTGTGATTG AACTAGGGAA TTCTGGTTTC 420  
AAACTCGATC CAGCTGACTT CAAGAGTCTT GAAAAATATC CAGGACAAAC GCTCATCACA 480  
ACAGATGGAA CAACCTTGCT AGGTGCTGAT GACAAGTCAG GAATTGCTGA AATTATGACA 540  
GCCATTGAAT ATCTAACTGC TCATCCTGAA ATTAAGCACT GTGAGATTCTG TGTGGTTTTT 600  
GGTCCAGATG AAGAAATCGG TGTGGTGCC AATAAATTTG ATGCAGAAGA TTTTGATGTG 660  
GATTTTGCCT ACACTGTTGA TGGTGGTCCA CTAGGTGAAC TTCAGTACGA GACTTTCTCA 720  
GCCGCTGGTG CTGAATTGCA TTTCCAAGGT CGTAATGTCC ACCCTGGTAC TGCCAAAGGG 780  
CAGATGGTCA ATGCCCTTCA GCTAGCAATT GATTTTCATA ATCAACTTCC AGAAAATGAC 840  
CGACCTGAGT TAACTGAAGG TTACCAAGGT TTTTACCATC TAATGGATGT GACAGGTAGT 900  
GTTGAGGAGG CGCGTGCAAG CTACATCATT CGTGATTTTG AAAAAGATGC CTTTGAACCG 960  
CGTAAAGCAT CCATGCAATC TATCGCTGAT AAGATGAATG AAGAACTTGG GAGCGACCGT 1020  
GTCACCTCA ACTTGACAGA CCAGTACTAC AATATGAAAG AAGTCATTGA AAAAGATATG 1080  
ACTCCAATTA CCATTGCTAA AGCCGTTATG GAAGATCTAG GTATCACGCC TATTATCGAA 1140

1158

CCAATCCGGG GTGGAACAGA CGGCTCTAAG ATTCCTTTA TGGGAATCCC AACTCCGAAT	1200
ATCTTTGCAG GTGGCGAAAA TATGCACGGA CGTTTGAAT ACGTTAGCCT TCAGACTATG	1260
GAACGTGCAG TTGATACCAT CATGGGCATC GTAGCTTATA AAGGCTAAAA AGACGAGGTA	1320
GCTCAGCTAC TTCGCCTTC TTTTATTCT ACTGGTTTTT CTTGATTTCC AGTAGTTGTA	1380
GAAGATTCTG TTGTTTCATT TTCTGAAGTT GATTGAGCAG GTTTAGAATC TCTTGATTG	1440
CTTGGTTTGT TTTGTCGCT AGCAGTTTCA ATGTTAGATT CTGCAGTTGC GTTTGGTTGG	1500
TTCTCAGCAC TGGTGTATC ACCATTGCT TCAGCATTTT TTGCTGGACT TGTTCCTTCA	1560
CTTGCGCTAG CTTTGACTG GATTGATGA TTCAAACTA GAATAGCTTT TGTCGATTCA	1620
AGTAAAGCTG TTTTGTCTTT ACTCTTAGCA GAAAGTTGAT CTAATAATGC ATCCACCTTA	1680
TCAAAGTCCG CATCAGATCC ATTATTACTT TCTAAATAAG AGTGAAGCGA CATGAGAATA	1740
TCGTAGAGTT TTTGATAGAG TACAAGTGTG TGAGGATCTT GCTCAGCATT TTCCTTTTCT	1800
TGTTGAAGGG CGCTAGCGAT ACGAGTCAAG ACATCTTTTA CCTGACTGTT TACTTCATCC	1860
AAGTCTGCAT CAGCCTTGT TGTGGCAGCT TTTAGATTTT CTACTTCTTC TGCCAAGGAT	1920
TGTCTGATTC CTTCTCATG GATTTGTTCC AAGAGTTGAT TTGCCTTGCT CAAAAGACTT	1980
TCTACTTCTT CCTTGCTATC TGTCGCAGAT TATTGGTTGC TATCTACCAT GTACTCCTAA	2040
AACAGGAGAG TTATAATCCA AGATTACAAG GCCTTACAGA AATAAGAAAT CCAGATAAGA	2100
CAATGTTTCT CCAAGACGCT ATTCGCTTCG CACAGCAGCA CGGATTCAAT ATGCTTTAAT	2160
TTTAAAGTTT AGGTGTCAAG ACCTCTTTTT AGTGTGCCCA AAATTTAGAG AAGTAATCAA	2220
TCAACTAACT TTTATTTTTT TCAAACCTTC AGTAACTGA CCTAAAGCTA ACTCAATCTG	2280
TCTTTGTAGA TGCTTCTGCT ATCAGCTAGA AGTTGATCTA CTTTGCCAA GACTGCCTTC	2340
TCATCAAAAG TTCCAGGTTG ATAGTTGGAT TGCAGGGATG GAATCTTGTT TTTCAAAGCC	2400
GCTTCATATC CCTTAGTTTG AACCTTGATG TAGTGATTGT GGTGCGCATG AGGAATCACA	2460
AAACCTTCTG AATCTTCACT TATAATTCGA TTGGCATCAA AACCATGACC ATCTTCTTCC	2520
TCATGATGGA CATGTAGTGA CGGATTACTT AATACAGAAC TAGAAGAACT TCCTACCTCT	2580
TCCGTGTTAG AGTGTGATGG GGGATTGTTA AGAGATGACT TAGGAATATA GTGATAGTGA	2640
TCCCCATGTC TTAATATATA AGCATCACCT GTATCTCTGA CAATATCATT AGGGTTAAAG	2700
ACATATGTGG CTGCTAATTC ACCTGCCGAC AAGTCACTCT CAGGAATGAA ATGATAGTGA	2760
CCACCATGTG GTACTATAGT AGATTGAAAT AGAATATGAG CAAATTGATA AGGGGATTTT	2820
AAAGTAATTT CTAACAATGA TTTAGAACT ATGATGTGCT ATTCTAAATT CAACTCACTA	2880
TATATAACCA TCATCGGTAG TATAACGTCC CTGTAATTTT GCTACAGATA CTTCTGCACT	2940

1159

AGCTCCTTTA TCGTCTTTAC CATGTTCTTG TTTTGGCGA TTGATTTTCAT CTTTGTTCG	3000
TACATTTTCT GCATGAGCTT GATCTTTAAG GTAAACATAA TACTTTCCAT CTACCTTAAT	3060
AATATATCCT CCCTTAACCT AACTGACGAT ATCTTGATCT TTCGGCTGAT AGTTGGGGGC	3120
TTTCATTAAT AGCTCTTCAC TAAAGAGCGC ATCAAAAGGA ACTTTACCAT TATAGTAGTG	3180
ATAATGATCG CCATGAGAAG TTACATAACC TTGATCTGTA ATCTTAATAA CAATTTGTTT	3240
TGCTTGAATT CTTCTTTTTT GACTAACCTA GTCTGGAGTC AAATTTTCAG TCTTCTTAGT	3300
GTCTTTATTA CTGTTTACAT ATGAAACACG ATTTTATCT GTATTGGCCT GTTAGCTATG	3360
TTGGTTCAGA GCATAAACAC ACAGACTTAA GGAAAGGATA ACAACAGATC CAGCTGCTAT	3420
ATATTTCTTT TTAAATTTCA TAATTACCTC ATTTCTATAA TTATTTATAT GATGTCTTCA	3480
TTATTAAATG ATTAAATAAA TTAATTAACC AATTAATTAA CTAGTAAATA TTCCACCTCT	3540
TTTTAAGTTG TATGTCAAGA AATTTTATAT ATTAATAATA AAATGAAATT CTCCCAAAGT	3600
CAGAGTTTTA TTTCTAACTT TTGAGAGAAC TTCATTTTGT ATTCAGACTT TTTCTACTGC	3660
TATTCCTTAC GCTATGAGAT CAGATAAATT CTTTTTATC ACTTCTCCAC TTGGCAATCT	3720
TAATTCAATC GTTCCATCCA TATTGAATAT AACACTATCT AAGCCTAATC CGTAACTAGC	3780
TGTAAATTTT TCTAATTTT CTTGTACAGG ATCTACTGCT GGAGCTTCCT CTAATGCTGG	3840
ATCTAACATA GGGTCACTCC CCACATTCCC TTCTGGATTC AACATTCCAT TATCCGTTGA	3900
GTTTTCTGGT TTTACAGGTT TTTCTTTGG TGCTCTGGT AAAGAATCTG CTGGTTTATT	3960
TTCTGTTGGT TGGTTCTCAA CTGTCCAGT AGATACTTTT CCATTTTCAG ATGGTTTATT	4020
TTCACCATTT CTTGAGGTG CTTCTCCTGT AAAATCTGCC ATATTCTTTT TAATGACTTC	4080
TCCCGATGGT AAATATAATT CAATTGTTCC GTCCATATTA AACAAGACAT TTTCTAGCTT	4140
CATCCCATAA CTTTCAGCAA ATTTTGCTAC TTTTCTTGT ACAGGATCCA CTGTAGGAAC	4200
TTCTTCTAAC GTTGAATTAC TAGTACTATT CCCAGTTTCA GAAAGTTTTT CTTTTCTAC	4260
CTTCTCACTA GTCTTTGGTT CTTCTACCTT TTCATCAAGT TTTAAGTTTT CTTGTGCTTT	4320
ATTCCTTTTA AATTGTGGTA GAATACTTGG TTTATCAGTT TGATTTTCTT TTTCCAAGAT	4380
AGGTACTTCC ACAATATAAG TCGATTGATT GTCCAAATAA GCATTTGCCA TGAAGGTTAC	4440
AGGAATTTTA TTTCCGGCCG TTCTGGTTGT TCCTTGGTTT AATTTCCGAA TCGGTAATTT	4500
GATTTACCA ACTTTATAGT TATTTTCTAA ATAAGCATTT CCATGAAATT CATCAAACAC	4560
TCTGACTAAA GCATCAGTTC CTTTAGGCAC TGCAAATTGA GGGTTCACCTC TTAAATAAGT	4620
ATCCCCTGCA TGGAAAGGAT AGAAAATCGT TTGACTGGCC ATTTTGTAAG CTAAAGAGGT	4680

1160  
TGGAACTGTA AATGTACCAT CATAACTTAC TTCTGGATAA TCTTTTGAAG CGATAGTATA 4740  
CTTAAATGTT TGTCTGGTA AATAAGGTTG ATCTAATTCA AAGTTTGCAA TATTCCCTAC 4800  
TCCTTCTCCA AATACTTTAC CAGATACTTT CTCCAATACT TTTCCATCTG GTGTTATTAA 4860  
TTTACTAGC ATATTGATAC CTAATTTTTT CTCCAATTCA GGCGGAAAAC TAAAAGAAAC 4920  
GCGTTTTTGA CCATTGGCTA GAGTAAAGTT TTGATTATTA AACGTACTAT TTTTAAACAA 4980  
ATTAACAACA TTCGTTAATT CTTCTCCAGT ATAAACTTTA TTCCCTTCTT TTTTAGCAAC 5040  
TCCTTCTTCG GGTTTAAACA GTTCATAGTT ACTGTGAGAA TGACCAATTC CAACCGGTTT 5100  
ATGTTTCATCA ATCGGATCTG CATGATGGTG ATCTCCATGC GGATAAATAA TCGCATTTTT 5160  
TTCTTTATTC ACGACAATAC TTTCACGTTT GACACCATAT TGTTTCATAA TGCCAGCAAT 5220  
TTTTTCTTCG ATTTTTTTAT CTAAATCTTT CATTTCTTTG GCATTACTTG GATAATCCTG 5280  
TTCATGAGAT GACAAAGAAT CTAATCCATT ATGACTAGTT TTAACCTCCT CTAAATGTTT 5340  
TTGCGCAsCT TAATTTGCTC TTCTGTCAAG TCCTTCTTGA AGAAATAATG ATTGTGGTCT 5400  
CCGTGACTCA TGACAAAACC TGATTCATCT TCAGCGATAA TACGATTAGC ATCAAATCCG 5460  
TATCCATCTT CTTTCATGTT CTCATGTGAA GTTCCTGGAT TGATTGGAAG AGATGGAGAA 5520  
GGTGTGCTA GACTATTGTT TGGAAGAGTC GGTGCCCCAA TTTGATTGA TTTTGAATG 5580  
TAATGGAAAT GATCACCATG TCTTACAATA TAAGCTGTAG CCGTTTCTTC AACGATATCT 5640  
TTTGGATTAA AAATATAACC ATCAGATGCT GAAGAGAGCT CCTTACTTGT CGTTAAAGAA 5700  
GAAGGATTGC TTGAAAGACT GCCTAGACTA GACACTACTT CATTAGGTTT TGCAATTGTA 5760  
GAAACTGTAG AACCAGTTCC ACTGATAGGC ACCATTCTGG CAATCTTTTC TTCTAAGGCA 5820  
GAAAGCTTGC TGTAAGGAAT AAAGTGGTAA TGGTCGCCAT GCGGAATCGC AACTCCATTT 5880  
GGGTACGAC TGATAATCTT AGCAGGGTCA AAGACCAGGC CATCTGATTC ACTGTAACGT 5940  
TGGGCGCTAG GTGAATCATA GAGTTCCTTC AAAAGACTCT GGAGATTTTC AGATTTATTT 6000  
GCTGGCTTGC TAGTTGATCC TTTTGCTACA GATTGCGTGT TATTGTCACT AGCTGTTGAA 6060  
GAATAGCTTA ACTGACTCGG TTGCATATTT TTTCCAGCCA GATGTGCTTT AGCTGCTGCT 6120  
AATTCACTAG CAGATAAATC GCTTTTGGGA ATGTAGTGAT AGTGACCTCC ATGAGGAACG 6180  
ATATAAGCAT TACCCGTATC TTCGATAATA TCAGCTGGAT TAAAGACATA ACCATCATTT 6240  
GTCGTATATC GTCCCTGAGA CCTTGCTACA GCAACATTAG AGTTAACCTT CTCATTATCT 6300  
TTGACATGTT CTTGTTTTTG ACGATTGATT TCATCTTTAG TTCGAACATT ATCAGCATGA 6360  
GCTGCATCTT TCAGGTAGAC ATAATATTTT CCATCGACCT TGATGATATA ACCACCCTTG 6420  
ACTTCATTGA CAATATCAGC GTCTTTAAGT TGATAGTTTG GATCCTTCAT CAAGAGTTCT 6480

1161

TCCTAAAGA GGGCATCATA AGGAACTTTC CCATTATAGT AATGATAGTG GTCACCGTGT	6540
GACGTTACAT AGCCCTGATC TGTAATTTTG ATTACAATTT GCTCAGCCTG AATTCCTTCT	6600
TTCTGGCTAA CCTGGTCTGG TGTCAAGTTT TCACTTTTCT GACTTGACTG GCTGCCATCC	6660
ACATAAGAGA CACGATTATT GTCCTTATTT TCCTGCGAAC GATGCTGGTT TAGTGCATAG	6720
GCACATAGAC TCAAGGATAC GATAACAGCT GATCCAGCTG CTATATATTT TTTACTAAAT	6780
TTCATAAATC CCTCATTTC AATAATGATG AAGTTTTTTC TCAACTTCTT TTACTTTATT	6840
AAATAGTTTT CTAAACCCGG GGGTACC	6867

## (2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CGTTCTAAAA ATGCAGTACG TTTGATTGAG AAATCAGTTA AAGGTATGCT TCCACACAAT	60
ACACTTGGAC GCGCTCAAGG TATGAAGTTG AAAGTATTTG TTGGAGCTGA GCACACTCAC	120
GCTGCACAAC AACCAGAAGT TCTTGACATT TCAGGACTTA TCTAAGGAAA GGAACAATAA	180
AGTATGTCAC AAGCACAATA TGCAGGTACT GGACGTCGTA AAAACGCTGT TGCACGCGTT	240
CGCCTTGTTT CAGGAACTGG TAAAATCACT GTTAACAAAA AAGATGTTGA AGAGTACATC	300
CCACACGCTG ACCTTCGTCT TGTCATCAAC CAACCATTCG CAGTTACTTC AACTGTAGGT	360
TCATACGACG TTTTCGTAA CGTTATAGGT GGTGGATACG CTGGTCAATC AGGAGCTATC	420
CGTCACGGTA TCGCTCGTGC CCTTCTTCAA GTAGACCCAG ACTTCCGCGA TTCATTGAAA	480
CGCGCAGGAC TTCTTACACG TGAATCACGT AAAGTTGAAC GTAAGAAACC AGGTCTTAAG	540
AAAGCTCGTA AAGCATCACA ATTTAGTAAA CGTTAATTCG AAAGAATTAC TATACTTATA	600
CAGAGCACCT TTCGGGGTGT TCTTTTTTTA TACTTTCTTA CTAAATGGT GCAATTGACA	660
CAGTTGTTGC GACTTTAGTC GCTTACAAAT GTGGCTGCAA CCTGACATGG TCAGTTGCCT	720
CAAAACGTTA ATCAATACGA TTATATCAAC GTTTCAAAGC ACTCAAGGGT TTACCCTATG	780
GGTGCTTTTT TCTATACTTT CTAAAAAAGT TTACCCTAAA ATTTGCCCTA AAATTACCCT	840
ACTTATTTTT AAGATGTTGG TAGGCAACTT GTCCAGCAGA TAATGGAAC ATGTTTGAAG	900
TATTAACATA AGTCTTAGTT GTAACGGTAT CGCTATGAGT TAATGCTTCA GAAATGGCTT	960

1162  
CTAAGCTCAT TCCTGCTTTT TTAGCAAGTG TCGCTCCTG 999

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2315 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATATTATCA CTGTTCTTGA AGGCAGAACA CAAGCTGTCA TCCGAAATCA CTTTCTTCGC	60
TACGATAGAG CCGTTCGTTG TCAAGTGAAA ATCATTACGA TGGATATGTT TAGTCCTTAC	120
TATGACTTGG CTAAACAGCT TTTTCCGTGT GCTAAAATCG TTCTAGATCG TTTCCATATT	180
ATCCAACATC TCAGCCGTGC CATGAGTCGT TTTCGTGTTT AAATTATGAA TCAGTTTGAA	240
CGAAAATCTC ATGAATACAA GGCTATCAAG CGTACTGGA AACTCATCCA ACAGGATAGT	300
CGTAAACTCA GCGATAACG TTTTATCGC CCTACTTTTC GCATGCACTT AACAAATAAA	360
GAAATTCTTG ACAAGATTTT AAGCTATTCA GAAGACTTGA AACACCACTA TCAGATCTAT	420
CAACTCTTAC TTTTCACTT TCAGAACAAA GACCCTGAGA AATTTTTCGG ACTCATTGAG	480
GACAATCTGA AGCAGGTTCA TCCTCTTTT CAGACTGTCT TTAACCTT TCTAAAGAAC	540
AAAGAGAAAA TCGTCAACGC CCTTCACTA CCCTATTCAA ACGCCAAATT GGAAGCGACC	600
AATAATCTCA TCAAACTTAT CAAACGCAAT GCCTTTGGTT TTCGAACTT TGAAACTTC	660
AAAAAACGGA TTTTATCGC TCTGAACATC AAAAAAGAAA GGACGAAATT TGTCCTTTCT	720
CAAGCTTAGC TTTTCTTCAA CCCACTACAG TTGACAAAGA GCCTATTTTC GCTGATTCTC	780
CACTACATTT GACTGGATTC TAATTTTFTA GAGAAATACA AAAGAGCTAG CTTTAGCTAG	840
CTCTTTTCCT ATGCGGAGAG AGGGACTTGA ACCCTCACGA CCTAAAGCGG TCACAGGATC	900
CTTAGTCCTG CGCGTCTGCC AATTCGCCA TCCCCGCGTC GATTACTTTA CTAGTATATC	960
AACTTTTGGG ATGCTTGTC AACTTTTTT TCAAATTTTT TCATTTTCAC CAACCAGGTT	1020
ACTCAAAAAG TTCATTTAGA TTTTCATCTA CTAAGTAGC TCCGAGTGTA TTTTGAAAT	1080
GACCTAGGGC AAATTGATGA TTTTCAGGCC AGATGGAAGC AACAGCTGGT TTAACAATCT	1140
CGATGTCATA TCCTAGATTA TAGGCATCTA TAGCTGTATG TAGGACACAG ATATCCGTCA	1200
AGACACCTGT TAAGATAACG GTAGACACTC TACGCTCTCT CAAACGAATA TCTAGGTCAG	1260
TCCCTGAAAA AGCTGAGTAA TGGCGTTTAT CCATCCAAA GACACGACTG TCTGAACCAT	1320
GCTCTTGATA AAAGATCCCC AAATCTCCAT ATAAATTCGG TCCACTCGTC CCAATCAGAT	1380

1163

TATGAGGAGG AAATAACTTA CTTTCCGGAT GGAAACAATC GTTTTCTTCA TGAGCATCAA	1440
TAGTAAAGAA GATATAATCT CCTCGTTCAA AAGCTAATCG AGTTACCTTG CTGATGGCAT	1500
CCGAAATCGC CTGAGCTGGA GCACCTGCTG TTAGTTTCCC ACTATCAGCA AAAAAATCTT	1560
CTGTATAATC AATCGAAATT AAAGCCTTTG TCATTAGTAA TCTCTTTTCT TCACTTCTTC	1620
AAAAATATCT GAAATCAAGA CCTTAAGATA GGTTCCTTTC ATTCCAAGTG AGCGACTTTC	1680
AATAATCCCC GCAGACTCAA GTTTACGAAG AGCATTGACA ATCAGAGAGC GAGTGATTCC	1740
GATACGATCT GCAATCACTG ACGCAGTCAA CTTCCCTTCA TTTCCATTTA ATTCCCCTAA	1800
AATTGCTGAA ACAGCACGGA GTTCGGAGTA AGAAAGGGTA TTGACCGCCA TGGTGACAGC	1860
AGTACGACGA CGAATATTTT TCTCATCTTC TTCACGTTGG AAGTTAAGAA GCTGAATCCC	1920
AACAACGGTA CTGGCAATCT CAACAAGAAC CAAGTCCTCA TCTTCGAATT TTTTATCATT	1980
ACGCCAAATA ATCAAAGAAC CAAGGCGAAT CCCCAGTACA TGAATCGGTG CAATAGTCGT	2040
CAAGCCATCT GGAAAATCAT CTCTACTCTC AATAGGGAAA ATACTCATAT CATGCTCAAC	2100
AGGCAAGTTT GCTTCTGTTT CGTAAATCAT ATTAGCCCCCT TGAACGTAGT CATCTGGGAA	2160
AATCTTAGTT TGGAAGAATT GCTACGCGA TCTGTATTTG TTTTATAACG CATAAAATAG	2220
CCAAGCAGAC GTCCCTTACT ATTGATAATG CAGGCATTGC AATGAATAAT ATCCGCTAAC	2280
TGACGCGTAA TAGCGTTGTA AGGGAGCTCA TCTCG	2315

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6693 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CGATTTCTTC CATTTCTTCA AATAAGAATA CTTCATCTGA CATATGTGTT ACCTTCTTCA	60
TCAAAAATTA TTTTGTAATC GATTACATTG CAGATCGTAA CATAAAGAAA AACAGATGTC	120
AAATATTAAA CGTAAAAACA TGGTCACTAA AGAACTATAA GAGAAAAGGT AAACCTAGCG	180
ACGCGATGAA CGCTGGGTCG TTTGGTTTCG ATTGCTCTCT TCCTCTTGTT TTTTCTGTTT	240
TTCTTCTTGT TTTTCTCAG CTTCCCTGGC CTCTTGTTTG GCTTTTTCCT CAGCTTCCAT	300
AATTAATTTA TCCGCCACAG TGTAAGCTGA GATTCCAGCT TCCATGTGCA CCACACTCGG	360
TTCTGACAAT TGAGGCTTAA TCTTACTGTA ATATGGCAGT TTCTTACTCA TTTCAGATAG	420

1164

AGGAACCAAG	ACTTCGTCCG	AATCATTTCAT	GGTCAATCGA	ATTAAATCGG	ATGTCACCTT	480
GCTTGGGGCT	AATTCACCT	TTTGATAGC	CGCCTTGAGT	TCTGGGCTAA	TTTGAGCAAG	540
TTCTGAGACA	AAAACTTGA	TTGTTCACCT	ATCATTAAAG	AGAACTGATA	AATAAGTTTC	600
TGGTAAACTG	TTCAGACTCA	CAGAACTAGT	CTCAAGCTGA	CCACTGGAAA	GAATAGGATA	660
ATGATTTTCA	CCAGAAATAT	AGTAGGCCAC	AATATCATAT	TCCTTGACCT	TAATAGTGAA	720
CTTAGTTGGA	AATTGATAGA	CAAGTTGAGC	TGATTCAACC	CAATAGTTAG	ACTTAATCTG	780
CTTTTCATAT	TTTGCCCTGT	CTAGCAGAAG	GTAAATCGTA	TAATCCGAAT	CCTGAATGCC	840
TGAAGCCTGT	CGAATATCAT	CAGCTGTAGT	TTGCACCGTT	CCCTCAACAC	GAATATCTTT	900
CATGGTCGCA	TAAGGACTGA	GCAAGTAGGC	AGAGACAAAC	AATAGAAGCA	GACTTGGAAG	960
TAAATCGTG	AAGGCTCGCA	AGATATGGAT	ACCAGGAATC	TTTGCTTTGG	CTGGTTTTTC	1020
CTTTGTAGCC	TTTTTAGCAA	GCTTTTATC	CTGTTCTCC	TTCTCTTTAG	ACTCTGGTTC	1080
TTCTTTCTCT	TCTTTCTCTT	TGTCAGCCTC	TGAGGATGCT	ACTTTTCTTT	CAGACTCTTC	1140
CTTAGCTGAT	TCTGAATCTT	CCTGGTCTGT	TTCACTCTCC	TGGTCCTGTT	TATCCTCTGA	1200
CTTCTCAGAT	TCTTCTCCCA	TTGAGCTTG	TCTTTCTTTT	TCCTTCTCCT	CAGCTAGAGC	1260
CGCCTCTTCT	TCAGCCTTCT	TTTTAGATA	TTCTTGGTTT	CGTTTCTGCC	ATTCTGATAA	1320
CTCTTTCAAT	TCTTCGAGGG	TTCTTTGTC	CTCATTTTTT	TTATCTTTTG	ACATTTACTT	1380
TCCTTATGAT	AAATCTTTTT	TCAACAATTG	ATAAAAATCT	GCTAGAGATT	TCAATTCCTT	1440
AGAAGCTTTC	ATCTTAGCTT	GGTAATCTTC	CTTGTGACTT	AGTAAGTGAG	AAAGCTTCTC	1500
TTCCAAACTA	TCCAAGGTCA	AATCGCTTTC	TTGAAGGTCT	TCTGCATAGC	CTTTCTTAAC	1560
AAAGTAAGCT	GCATTTTCAA	TCTGGTCACC	ACGACTAGCT	TCACGACCAA	GCGGCACAAT	1620
GACATGCAAT	TTTGCTATCG	CCAAGAGCTC	AAAAATCGTA	TTGGCACCAC	CTCGTGTAC	1680
AACAATATCA	GCCAATTCCA	TCAAGGGTTG	ATAGAGATCG	GTACATAGT	CAACACGAAA	1740
AAGATTTTGC	CTCAACTCAT	TCAGACTAGA	ATCTCCAGTT	AGATTGATAA	TATTGTAGCG	1800
CTCTGTAGT	TCTTTCTTAT	GGTCTGTCAC	CAATTGGTTA	AAGACACGAG	CGCCTGCAGA	1860
ACCGCCAACA	AACAATACAG	TTGGCAATTT	GGGATTAAAG	TGGGTTTGAA	TATCCACCAA	1920
TTCACTCTGGT	TCTGGAGTGT	TTTGTCCGA	AACCTTGGTC	ACCGCTCCCA	CATGCTCAAC	1980
CTTAGCCAAA	CTCGAAGCTT	GTTCAAAGGT	TGAATACATC	TTAGTCGCAA	ATTTATAGGC	2040
GATTTTATTG	GCCAAGCCCA	TAGACAGGTC	AGATTCTGTA	ATAAGACAG	GCACTCCTGA	2100
CACACGCGCA	GCGATAACAG	GCGGTACTGA	GACAAAGCCC	CCCTTTGAAA	AAAGGGTCTG	2160
TGGACGCAGT	CGCAACATGA	TAAAGAGCGA	TTGGACAATT	CCCCAACCAA	CTTTGAAGAC	2220



1165

GTCCAGCATA TTTTGCCAAG AGAAATAGCG ACGCAATTTT CCAGTCGCAA TAGAATGGAA	2280
GGTGACATCC AAACCTGACT TAAGGATTTT TTGGTGTTCG ATACCACACT TGTCCCCGAT	2340
ATAGTGGACT TCCCAACCAT CTTGATGAA CTTGGGCATT AACAAAAGAT TGAGGGTAAC	2400
GTGTCCAACC GTCCCCCAC CTGTAAAGAC AATTTTTTTC ATATTATCT TTTAACTCCG	2460
CTACTGTGTC GATAAAGAGG TCGCCACGTA CTTCAAAGTT AGCATACATA TCCCAGCTAG	2520
CATTGGCAGG ACTAAGAAGA ACCACATCTC CTTGAGTCGC AAGCTCATAG GCCTTGCGGG	2580
TCGCATCTGC AATATCTGTC GCCTCCACAT AAGCGACACC AGCCTTGTCT GCTGCCCGTT	2640
TGACACGTTT TGCAGATTGA CCCAGGATGA CCATCTTCTT GAGTCCAGTA ATGTCTGGCA	2700
CCAATTCGTC AAATCATTG CCACGGTCCA AACCACCTGC AATCAAGACG ACCTTGCTGT	2760
TGTCAAATCC TGACAAGGCT TTTTGAGTAG CCAAGATATT AGTTGATTTA CTGTCGTTAT	2820
AGAATTTAAC ACCCTTGATG TCATCCACAA ACTGGAGACG GTGTTTGACA CCACCGAAGG	2880
CTGAAAGAGT TTCCTTGATG GTTTGATTGT CCACATCAGC AAGCTTGGCT ACAGCAATAG	2940
TCGCAAGGGC ATTTTCCACA TTGTGGCTAC CTGGAACACC GATTTTCATT GCTGCCATGA	3000
CTACTTCACC ACGGAAGTAG AGTTGACCAT CTTCCAGATA AGCTCCATCA ACCTTTTCAA	3060
GTGTTGAAAA TGGTACAACA GTGGCTTCTG TCTTGGAAGT CAAGTCTTTT GCCAAGTCTT	3120
GATTAAAGTT CAAGACAAGG AAATCAGCTG CTGTCATCTT GTTCTGGATA TTCCACTTGG	3180
CTGCTACATA TTCCGAAAAT GACCCATGGT AGTCGATATG AGTTGGCATG AGGTTGGTAA	3240
TAACCGCAAT CTCTGGATGG AATCTTGAA CACCCATGAG TTGGAAAGAA GAAAGTTCCA	3300
TAACAAGCGT GTCCTTATCT GATGCTATTT GAGCAACCTG ACTAGCTGGA TAGCCGATAT	3360
TCCCTGATAA AAGACCATGT TGGCCAGCAG CAGTCAAAAC TTCCCCAATC ATAGTCGTTG	3420
TGGTTGTCTT ACCGTTGAT CCTGTGATAC CAATAATCGG TGCTTCTGAA ATCAAATAAG	3480
CCAATTCAC CTCAGTCAAG ACTGGAATTC CCTTGGCCAA AGCCTTTTCA ATCATGGGAT	3540
TGTTGTAGGG GATACCTGGA TTTTTCACCA TAAGGGCAAA CTCTTCATCC AAGAGTTCCA	3600
AAGGATGGCC ACCTGTAATG ACCTTGATCC CTTCTTCCAG CAACTTTGG GCAGCTGGAT	3660
TGTCCTCGAA AGGTTTCCCA TCATTTACTG TCACAATGGC ACCTAGCTTG TCCAACAAAC	3720
GAGCTGCAGA TTCACCAGAC TTGGCCAAAC CTAAAACAAG GACTTTCTTA TTTTAAATT	3780
GATCTATTAC TTTCATGTCT CGAACTCCAT TTCTACTCCT ACTATTTTAC CATTTTATG	3840
GAAATAAAAA AGCCACAAAG TGTGTTTGTG ACTCTTCTT CTAAGTGAAT CTTACCATAT	3900
CATCTATGTG ATAAATCGGT AACTCGAATG ACCTGATCCA CTTGCTCCCA AATCAGAGGA	3960

1166

TTATGGGTCG CAATAATAAT GGTCCGATTC GGATTTTPTA AAGATTCTAG GATGGAAAGT	4020
AATTCCTCAG AGTTTTTGGG GTCTAAGGAA GCGGTTGGTT CATCTGCGAG GATCAAAGGT	4080
GGATCCTTTA AAATTATCTT CGCTAGTGCA ACACGTTGTG CTTCTCCTCC TGATAACTCA	4140
AATATAGGTT GCTTCAAATC CAAATAAGAG AGGTTTACAC GGTTTAGAGC TTGTTTCATC	4200
AAAGAGATTT TCTCTTTTTC CTTCAACTTT TTACCAACTA AACCCAGATT GAGATTCTCT	4260
TTGACGGTTT GGCTTTCAAT TAAGCCAAAA TCTTGAAATA AGTATCCTAA GTAATCTCTA	4320
AAGAAAACAG AAGGCTTGAT GTCCTTAAGA GAAGTGCCAT CATAGATGAT TTGCCCTTTG	4380
TCATATGGCT CCAATCGTCC AATCATATTC AAGAGTGTTG TCTTACCACA GCCACTTGTA	4440
CCGATTAAGG CATAAATTTT CCCACCTTCA AAATGAAGAT TCATATCTGA AAATAGCTGA	4500
CGGCTTCCAA ATTTTTTAGA TATATTCTTT AGTTCAATCA TCCTATTTTC CTTTCATAAT	4560
TGTCATAGAA ACACGAGATT CTTTCTGCGC TTGACGGTAA AGCGTCAAAA CTGCACTAGC	4620
TAGAAAGACC AATAAAGTGA GCAAGCCAAT CACCAAGTCT CGACTGCTTA AAATAAGAG	4680
ACTAGCACCA AATACAAAAC TAGCAAATTG GCTAACCATA TACTGAGCAT GTGTTTCAAA	4740
AAATCGTAAA CCTGAAATTC GTTTAATCAA GATATCTCGG CGGAATTGCT CGAAATATAG	4800
AAGATTGACA GAATAAAGA GTAACAAGGA ACTGGCTATT CCAACAATAG CTCCTAAGAT	4860
TAAAGTTGCT GTTTCAGTTT GAACTTCATT ATAACGAGTT AGATAAACAC TTCTTCCTTC	4920
TTTAAGATAG GATACTTGCT CATAAATTCC AGCTTTCTTC AAGAGTTCTA GCCCACTCTC	4980
ATATCCTTTG ATAAAGAGTT GTTTTCCAGC ATTGATAGAC CAACTAGATA AGGATATAAA	5040
ACTATCACCT GTAGAAGTCG GCGTGAATAC CACTAAATC GGATCAGTCA AATACTGAGT	5100
AGATACGGGA TTCTCACCGT TATTATAAAC AAACCGCTTT TCTCCCATTC AAAGATAACT	5160
AACGTGCGCT TTCATCTCAT AATCCAAAGG AGCACTTGCC TCCTCACCAG ATTTTCCATA	5220
ATAACTCAAT CTTTCTTCAA AAACCTTTCTT AAGTTCTGCT TCTCGAGAGC GCAAATGTTC	5280
TGGGAGCAAG AGGATAAACT CACCTTTTTG GAGATGGGCT AACTTCTGTT TGGTCTCAGC	5340
ATCTACCACG ACCTTTTCCT TGTCCAAATA ACTGGGACTA ACATAGAGCG TATTAGCATC	5400
TGAACTATAG GTATCCAGTG TCTCTCCCTG TTCATTTTTT CCTTGTGGAT TGGCAAAATG	5460
GAGCAGATTA TCCTTTACAT AAAGAGCTTG TTCTTCTTCG ATTGCTTCCT TGGCAAAGGC	5520
ATACCACTTG CTCTGATTTT CTGTATCTTT TCCTCTATCA CCTAAGCCAA AGGAAATCTG	5580
GTAATAGTCT GCTCTGTCCT GCCATGCTTG TTTTGAAATT TCAAGTTCTT TCAATCGTTG	5640
GTAAGACGTC AAACCTGTCT TAACAGCGTA GCCTACTGTA AAAACAGCTA CTAAGTACA	5700
CAATAGGGTT AAAGCCATCA AGCGTTTAAG GGGTAATCTT CCCTTAATAA CGGGAACATA	5760

1167

TGCTTTGTAA CTCAAACCTCA TTAGGTAAAG GAGCATTAGT AAAATTGAAA TCGCCAATAA	5820
AAACAACAGA TAGAACTAA TCCCAAAACC ATAGGTGGCT AACAAGATAG GATAAAACAA	5880
ACCTTGACTA AAAAGAACGA CTCCCCCACC TAGGAAGGAA AGGAGGGCTG ATAGAAGGAG	5940
CCATTTGATA TCAGTAGATA AAGAATGCCC CATGATGGAT AAGAGAGTCT GACCAGAAAA	6000
GAGTTTATA CTGCTGCTC TCATTTCTT AATCCGAGTG ATAATCACTA AAGCAAAGAA	6060
AGATAAGCCA AATATTGCTA AACTAATTAA AATAAGGGGA TTTAGTAATA TTCGAAAAGC	6120
AAGAAAATAG GGCGGTATCT TTCGGTCAGC ACTTGCTTTA TAACCCAAAT CTCCTAATTT	6180
ATCGGCAAGC TTTCTTTTCG TCAAGGAGCC TGACAAAAGG AGATAACTAT TTAGCGGANT	6240
ATACGTTTAC GACTTTCTTG GCTAGCTTCT TGGAATTCCT TTGGTAAAGT TCCCTGACCA	6300
TAAGTTGCAT AAGTAAAGTG AGTCGTCCCA TCCTTACTCG GCTCTACAAT TCTTCTAGCT	6360
ATTAACTCT GTTCTGAGTT TGCAAAATTC TCCAATTCCT GTTCAAATAC CTCACGCGTC	6420
GGTTCCTGAG TATCTTTTTT GACACGAAGT AAAGAAACGG AATCATAGCT TGCATATAAA	6480
TATTGTGGCG CACGTAAGAC AATAATCCAA GCAAGGAAGA AGCTGAGAAA AAAAGTTGAT	6540
AATAATATGA ATAGTTTCTT CATAGTAGAC TCCTTGTAAG CAAAATTCCC CCTGTAATTT	6600
CTTACAAGGG GAACGATTTA AATCAATGAA CGATTAGTCA TAATCACAGT AAAATGCTAC	6660
TTGTTCTCCC CATTTAGTCC AAATCCATGC AGG	6693

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1847 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CCGGTCTATG TACCCACTAC TTTGGGACAA TATGGGGATC AGCTACCCAA AACTAATCGA	60
GCGTTTGGTT GACCTTGCCA AGGAAAGTTT TGACAAGCGC GACGATTGTA TATAAATGA	120
AAGAGAGGGT AGAAGCCAGA ACCATCACTG CACGGTGACT AGAGTTCTCG GACTTCAGCC	180
CTTTTAAAG GAGTAGAAAT GAAATTAACA ATCCATGAAA TTGCCCAAGT TGTGGAGCC	240
AAAAATGATA TCAGTATCTT TGAGGACACC CAGTTAGAAA AAGCTGAGTT TGATAGTCGT	300
TTGATTGGAA CTGGAGATTT ATTGTGCCA CTAAAGGTG CGCGTGATGG CCATGACTTT	360
ATTGAAACAG CCTTTGAAAA TGGTGCAGCA GTAACCTTGT CTGAGAAAGA GGTCTCAAAT	420

1168

CATCCTTACA TTCTAGTAGA TGATGTTTTG ACAGCCTTTC AATCCTTAGC ATCCTACTAT	480
CTTGAAAAAA CGACTGTTGA TGTCTTTGCT GTTACAGGTT CAAATGGCAA GACAACGACT	540
AAGGATATGT TGGCGCATTT ACTGTCAACA AGATACAAGA CCTACAAAAC ACAAGGCAAT	600
TACAATAATG AGATTGGCCT TCCTTACACA GTTCTTCATA TGCCTGAAGG AACAGAAAAG	660
TTGGTTTTGG AGATGGGACA GGATCACTTG GCGGATATTC ATCTCTTGTC TGAATTGGCT	720
CGTCCAAAAA CAGCCATCGT GACCTTGGTT GGAGAAGCCC ATTTGGCCTT TTCAAAGAC	780
CGTTCAGAGA TTGCTAAGGG AAAAATGCAA ATTGCAGACG GAATGGCTTC AGGTTCCTTG	840
CTTTTAGCGC CGGCTGACCC TATCGTAGAG GACTATTTGC CAACTGATAA AAAGGTGGTT	900
CGTTTTGGGC AAGGGGCAGA GCTGGAAATT ACTGACTTGG TTGAGCGCAA AGATAGTCTG	960
ACCTTCAAGG CCAATTTCTT AGAGCAAGCC CTTGATTTGC CAGTAACTGG CAAGTACAAT	1020
GCGACAAATG CTATGATTGC ATCCTATGTT GCCTTGCAAG AAGGAGTTTC AGAGGAGCAA	1080
ATTCGTTTGG CCTTCCAAGA TCTTGAATTG ACGCGTAACC GTACCGAGTG GAAGAAAGCA	1140
GCCAATGGAG CAGATATCCT GTCAGATGTT TACAATGCCA ATCCAAGTGC TATGAACTG	1200
ATTTTAGAGA CTTTCTCTGC CATTCCAGCC AATGAAGGTG GCAAGAAAAT TGCAGTGTG	1260
GCGGATATGA AGGAGCTTGG TGACCAGTCT GTTCAACTTC ATAATCAGAT GATTTTGAGC	1320
CTTCTCCAG ATGTGCTTGA TACCGTGATT TTCTATGGAG AAAATATTGC TGAATTAGCC	1380
CAATTGGCCA GTCAAATGTT CCCAATCGGC CACGTTTACT ACTTCAAGAA AACAGAAGAC	1440
CAGGATCAAT TTGAAGACCT AGTCAAGCAG GTCAAGGAAA GCCTTGAGC CCATGACCAA	1500
ATCCTGCTCA AAGGCTCTAA CTCTATGAAT CTAGCCAAGT TGGTAGAAAG TTTAGAAAAT	1560
GAAGACAAGT GATTTTGTCA AGTATTTGCA AAGAATGATT GCCATTACAG ATACTGGCTT	1620
AACCTTTACA AAAGATCCGT TTGACCGTGA GCGCTACGAA GACTTGCGAA GTCTGTTATC	1680
TGAAATGTTG AATCAAGCAT CAGACCTTGA TTCCGAAGAA GTGGCAGAAG TCTTGAAGCC	1740
AACTTCTGCT TATGCGACTC CGTTAATGGA CGTCCGTGCT TGGATTGTTG AGGATGAGAA	1800
GATTTGTCTG GTTAGGGGAC AAGGAGAGGA TAGTTGGCCT TTGCCGG	1847

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1062 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

1169

CAAGCGAAAA CATTCTTTAT TCCAAATAAA CAGAGCATT TAGGAGAACA AGAGATTTTG	60
AATGCCAAGT CGATCTTGGC CTTGCTAGAC GGTTCGGAGT CACATAGCTA TGATGTAGTC	120
TATCTCCGTC AGCCTCTTAA TCGTCTCGAA TATATCGAGT GTGCGATAGT GGGGCAATCA	180
CAATTTCTCT TTAAGGTCAG TTATGCTGAT GGTCAAAAGG CTTACCGTGT CGATCTTCCT	240
GACCTACTAA CAAAGACAGA CTGGCAGATT ATCAAGTCAT TTTTAGATGC TTTGCTTGCT	300
TATACAGGGA CTGATATTGA AGGGCTAGAT GGTTCGTGATT TTGAAGCTTA TTTCCAAGCA	360
AGTATTCAAG CCTATCTAGC AGACCCTGTA GCTCGTTTAA CGATTTCGCA AGGAATTTTT	420
AATCCTATTT TCTTTAGTCG TGAGAACTTG AAAAGCTTTT TAGAGGCAGA TGGCTTGGCT	480
CAGTTTGAAG CGCGTGTGCG TGCGGTTCAA GAGACAGATG CCTACTTTGC GAGAGTTTCC	540
TTCTATCAGG ATGGAGAAGG AAAAGTGCAT GCGGTTTACC ATCTAGCTCA AGGAGTCAAG	600
ACAGTTTAC CGAGAGAACC GTTTGTTCTT GCAGCCTATA TTGAGCAATT GGTGGATAAG	660
GAAGTCCAGT GGGAGATTGA CTTGGTTCAA ATCACAGGAG ATGGCTCTAA ACCAGAAGAC	720
TATGAAGCCA TTGCTCGCTT GGACTATGCA AAATCTTAG AGGTATTACC CCCATCTTTT	780
TACCACCAAC TAGACGCCAA TCAAATAGAA GTGCAACCCA TATTAGACAA AGATTTTAAA	840
ACATTAGCAC AAGAAAAGTA AAGCAGAAGC AGGTCAATCG ACTTGCTTTT TTGACATAGA	900
AAAAATCCTG CCAAGATGAC AGGATTGCTA CTCAATGAAA ATCAAAGAGC AACTAGGAA	960
GCTAGCCGCA GCTGTACTTG AGTACGGTAA GGCGAAGCTG ACGTGGTTTG AATTTGATTT	1020
TTGAAGAGTA TGAAGTTTAA AGAAAAGCCA AGATACGAAG AT	1062

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6846 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TATCTACAAC CTCAAAAACA TGTTTTGawG gCTCGTCAGT cTATCTACAA CCTCAAAAAC	60
ATGTTTTgAa kGctcGTCAG tTCTATCTAC AACCTCAAAA ACATGTTTTG AcaGcCtCgT	120
CAGTTCTATC TACAACCTCA AAAACATGTT TTGAGCTGAC TTCGTTAGTT TCATCTACAA	180
CCTCAAAAAC ATGTTTTGAG CTGACTTCGT TAGTTTCATC TACAACCTCA AAAACATGTT	240
TTGangnChT CGTCAGTTCT ATCTGCAACC TCAAAGCAGT GCTTTgagcG CTTGTCAGT	300

1170

TCTATCTACA ACCTCAAAAC AGTGTGTTGC GCAGCCTTTA ATCAGCCGCC TAGTCCGCTC	360
TATGGTATTC ATTAAGTCAA CATCTCTTGT TTAAGAGCAC CAAATCAGGA AATCTTCTCG	420
ATTCCCTGAT TTTTCTATT TACGTTTTCG TGTGAGCTA CGTTCTGTCA AACCATGAGG	480
TAAGAGAACT TCACGTTCTT CCAACTCTTC CTTATGCATA ATCTTGGTCA ACATACGCAT	540
ACTAATGGCA CCAAGGTCAT AAAGAGGTTG GGCAATCGTT GTCAAGTTTG GACGGGTAAA	600
GCGTGAGATT TGTGAATCAT CACTAGTAAT AATTTCAAAA TCTTCTGGCA CAGAAACACC	660
CTTATCAGCC AAACCGTTCA AGACTCCTGC TGCCAACTCA TCACCTGTCA CAACTGCTGC	720
AGTTGCATTT GATGAAATCA AACGCTCTGC TAAGGCGTAA CCATCATCAT AGCTATATTT	780
AGATTCAAAT ACCAAACCCT CACTATAAGT GATTCCTGCT TTTTCAAGG TTTCTTGTA	840
GCCAACTAAA CGAACCTTAC CATTGATGTC ATCCACTAGC GGACCGCTAA CGAAAGCAAT	900
ACGCTCATTT TCTTTAGCAA GGTAACCTAC TGCATCAATT GTTGCTTGCT TATAGTCAAT	960
ATTGACACTT GGCAACTGGT GCTCAACATC GACAGTTCCT GCGAGAACAA TCGGAGTACG	1020
TGAACGCGAA AATTCTGAGC GAATTTTATC TGTCAAGTGA TACCCCATAT AGATAATGCC	1080
ATCTACCTGC TTTGAAAAGA GGGTATTGAC AACAGAACT TCTTTCTCGT TATCTTCATC	1140
GCTATTAGCT AGGACAATAT TGTACTTGTA CATTTCTGCA ATATCATCAA TCCCCTTAGC	1200
CAAACCTGAA AAATAACCAT TGGTAATATT TGGAATCACG ACACCGACAG TGGTTGTCTT	1260
TTTACTTGCA AGACCACGCG CAACTGCATT TGGACGATAA TCCAAACGAT CAATTACCTC	1320
TAGCACTTTT TTACGGGTAT TCTCTTTTAC ATTTTATTG CCATTGACCA CACGGCTGAC	1380
CGTCGCCATG GAAACACCTG CTTACAGAGC GACATCATAA ATGGTTACTG TATCATCTGC	1440
ATTCATTCTT TTTCTGTCC TTTCTATCTC ACACATTCTT TTACAAGTAG AGGTACTGAT	1500
TGAAGCTCTA TATCTACTTA CAAAAGTGAA GATGTGAAAA TTTCGTTTTT ATATTTCTAC	1560
TTATTCCATT CTATCACTAA TTGTAAACAC TTTCAAGTGT TTTTGAAGA TTGATTGAAA	1620
AAATTTTATA GAAAACCTAG GTTTAGCTCC TTGCTACCAC CTTAGACTAA AAAAAAGGA	1680
GGAAACTAAG CCCTCCTAAA GTTATAGTAA AATGAAATAA GAACAGGATA AATCGATCAG	1740
GACAGTCAAA TCGATTTCTA ACAATGTTTT AGAAGTAGAG GTGTACTATT CTAGTTTCAA	1800
TCTACTATAG GTATTGTTCC ATTCACTACC GTCAATTTTA GCACATAGTC TTCATGAAAA	1860
TATTATATCA TCATAACCAA CCAGATTCTT TCGCGATATT AGCTGCCTCT GTTCGATTAC	1920
CTGCATCTAG TTTCGAAAGA ATATTGGTGA CATAGTTTCG GACTGTTCCG TTGGATAGAT	1980
AAAGTTTGTC TGCAATTTCT TGGTTAGAGA AGCCCTGAGC AATTCCTTTT AAACTGCGA	2040
TTTCTTGCTC CGTTAATGGA TTGGGATGCA TCATCACCAC TTCCATCAAT TCAGGCGAAT	2100

1171

ACTCCTTGCG TCCTTCGAGG ACGGTGTGCA AGGTTTGCAT GAGGTCTGCA ATGTTTCTTT	2160
CTTTTAATAC ATAAGCATCT ACTCCAGCCT TGACCGCACG TTCAAAATAC CCAGGACGCT	2220
TGAAGGTCGT CACCACAACC ACCTTTGTTT CAAGCTTTTC TGCTCGTATC CACTCCAAGA	2280
CTTCAAGACC TGTCTTAACA GGCATTCTA CGTCAAGGAT GCGGATATCT ACAGACTCCT	2340
TTTCTAATAG TTGGATTGCT TCTTGCCCAT TCTTGGCTTG AAAGACAGAC TCTACATCCG	2400
GTTGAAGCAT GAGCAACTGG CACATGGCAT CTCGCAACAT ACTTGATCT TCTGCGACTA	2460
ATACTTTCAT CTACTTTCTC TCCTTATAAA GTAGTCGAAC CTGCATTCA GTTGGATGTT	2520
TCTGACTGAT TACACTTACT TCTCCTGAAA ATGGAAAAAC ACGATTTCGG ACTGTATGGA	2580
GCTCATCCCC GCTTATAGAG GCAAAGCCAC AGCCATCATC TCTCACTGTT AGAATGAGTT	2640
CTTCTCTGT CCGTTCTAAT TTCAAGTAGA CTTTAGACGC TTTAGCATGT TTGATGATAT	2700
TGGTCACTAA TTCAAGCAAA ATCATGGAAG CCGTTGACTC CAATTCCTGA GTTAAGCTAG	2760
ACTTGTCCAA GTGATTCTCA ACTTGAACCT CAATTCAGC AATTCTAAC ATCTTTTCA	2820
CAGTCTCTAG TTCGGATGTC AAAGTTCTAG ACTTAAGATT TTCCACAATG GTTCGCACTT	2880
CATTCAATGA CCTTGCTGA TCTGGTGAAT TTCTTTAAT TCCTTTTCCA CCTGTGGATA	2940
AGCCTCCATC TGAAATAACT GCAAGGCTAA ATCTGTCTTG ACACTCAGCA TAGCAAAGGT	3000
ATGTCCCAGA CTATCATGCA AATCCTGACC GATACGACTA CGTTCATTTT CAGCAAGCAA	3060
TAGATTTATC TGAGCATTTT GCTTGACCTG AGCTTCTTTC AAATCCTCGA CAATACGAAT	3120
CCGAACCAAT CCAAAGTCA TTAAATCGAC AAAAGTAAGA ATTACAAGTA GATAGAATAG	3180
AAACTCAACT TCGATTCTCT GAAAAATCAA CAGTTGCCCC ACAACAAGGA CTTGAGCAAG	3240
AAGAAAAGTC CAGACATGTA AAGACTTTAA ACTACGTACG CTGAAATGAT AACTTAAGAG	3300
ATTGGATAGG AAAAAGAAAA ACCAGATATA ATTAACAGCA ACAAAGGCAG TATTCCTAAC	3360
TACATAAGTC AGCATGAGGC CCCAATATAG CCAAGATAGG CGCTGGCTCT TAGTTGTTAA	3420
AACACCCAAA TATGCCACTA CAAATAGAAT ATCAATCAAT AAATGCCAGG CAGAAAGCCA	3480
CCCAGTCACT ACAGACAGGA TGGGGAAAAT CATAAAAATT AACTGATCC AAAACATATA	3540
ATGTATTCTT TTCAGTCTTT CAAGCATTA GCATTCTCCT TATGACCTTG AAGGTAAATG	3600
GTCAAACCAA ACAAACCTAC TGAAAAACA AGTAAATAAA CTGTGGCTGA TAGATTGATG	3660
CCACCCTCAT TTAAGAAGGT CTTGAGCAAC TCCATCAACT GATAGGTCGG GAGACACTTA	3720
CCTACTACTT GCATCCAGTC TGGAAATAAA GAGATAGGCA TCCAGAGTCC ACCTAAAACA	3780
GCCAACCCTA GATAAAGAAG ATTGCCCACG ACAGACATCA ACTGACTAGT TGGTAAGAGA	3840

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GTCAAGGTCA AACCAAGCGC TACGAAGGCA ATACTTCCTA CTATCAGCAA AAGTGCAGCC	3900
CCAATCCAAT TTCCAAGAGA CATGTCCACA CCTCTTACAA AATGCCCAAC TGAGAAAACC	3960
ACCAAGATTG AAACCAAATA ATCAACCAGC ATACTTGTTA TCTTTGATAG ATAATATTCT	4020
ACCATATTTA CAGGGCTATG ACGCAATGTT TTCTGCCAGT TGTGATCTT GTCGGTATGT	4080
AAAACAAC TGGAATGAGAA GATAGCTGTT GACATCATGG AAAATGCAGT CATGGAGATA	4140
AGATAATCAC GCATAAAATT CGCGAGTTCA CCTGGTGTGT CCTGATAGAT ACCAGAAAAA	4200
AATAAATAGA AAGCCGTCGG CATCCCTACT GACAATAGAT AATAGATCAA TTGTCGTTTG	4260
GTCAATAAAA ATTCTATCTT ACTAAGTGCT AGCCATCGTT TCATCTTAGT TATCTCCCTT	4320
CTGCGTTTCT TCAAAGATTG TATCCAACAA ACTACGATTA TTAACCTCAA TTTCTTGAT	4380
GCCACATCCT GCTTGAAC TAACAGTTCCCA AAAAGCATCT GCTTCGCGTG TGACTACTTG	4440
TAGAGCATCC TGTTTTTG TGACAGTTTTC AACCAAGTTA GACTGCTCAA TGACTTCCTT	4500
GTATGCCAGA GGAAGGATAA AATGCTTTTC AATTCCTCA CTACGCATAG CTAGAGGCGT	4560
CGTATCACGA ATCAACTCTC CCTTATTTAA AACCAAAATC CGGTCAGCCG TATGCTCTAC	4620
CTCTTCAATA TAATGAGACG AATAGAGAAT CGTGACTCCT TGCGCTTTTA GGTCCCGAAC	4680
GATTTCCCAA AAGCGTTGAC GAGTTGAAGT ATCCATGGCA GCAGTTGGTT CATCTAAAAA	4740
GACAAGCTTT GGTGCGCCAA TCAAGGTCAA GACAAAAGAG AAGAGACGCT TTTGCCCCGC	4800
TGACAATTTT TCTGCGAATT GCTCTTTT TGCTGGTCA AACTGCAATA GTTGATCGAT	4860
TTCTGATCG CTCAAGGAAT TTGGATAGAT ACGTTGAAAG AAAGCAATCA ACTCTTGAC	4920
CTTTAATTTT TGAACGATGA CATTTTCTTG AGGCAGATAA CCTCTAATAT AGTCTAACTG	4980
AGAACTCGTC ACTGACAAGC CTTGGATGGA TACTTGACCG CTTGTGACCA GTTTATCTCC	5040
AAGCAGACAG TCCAAGAGTG TGGTCTTCCC AGCACCATTG GGCCCAATCA AGGCGACGCA	5100
TTACCTTCA GCTACCTCAA AGGAAATACC CTTCAAAATA GCCTTGCCCT TGATGTTTTT	5160
ATTTAGGCTT TCTACCTTAA TCATATTCAT GATATCTCC TTTCAACCAC TCCATTCTCA	5220
TAAGGAAAAC GACGAAAATC ATAAATCCAA ACCCCAAAGC ACCACGAATG AATTGGCGAA	5280
GCAAGGTTTG GTCAAACCAA CCTGTAAACA TTTCCACTAA CCATACCAAG AGTGACAGGC	5340
CGATAAAGAA ATAGATGATC CCTCTCTTCA TTCCTCAAGC TCCTTTTTCA CATCTCCGAC	5400
TAATTTCAAA CCTTCTCTAA CAAGCCAAGA CATCATTTCA AAGCCAGCAA AGAGCTCCCA	5460
AGGAAAATGA TAGAACTCT CATCCAATCC CGAAAACATG AGTTAGGTCA TAACTCCTGC	5520
TACTACTAAA CTCACTGCGA TAATCATTTT ATTTCTCATC TCTTCTTCTT CCATTTCTTA	5580
CTACAATTAT AGTCTTTTGA AATCAGAGGA GACAGAAGCT TCTGTCACTA GAAAATATGA	5640



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CAAATGTCAT AAAAAATTCT GTTCAAAACA AGCAAGATAC ACTATACAAT AAAACACAAT	5700
TAGAAAAATC TAAGGCAACT TCCTCAAAAG AGATATCAAA CCCAATTCAC ACCATAATGT	5760
AACTAATAC TTATTTAAAA TCAAAAAGAG TAGAAATTTT TATCAGACAA ACACATATAT	5820
AGTGTATTGA ATCTATAACA GTAGGCCTTA AATACTAAAA TATTTCTATA AATTAATTTA	5880
ACTTTCCTGA TAGAGCTGTT CATATCTTAT TTCAATTCTC TAAATTATAC GTTGAACAAA	5940
ACCCTTCTAT TTCTTTCTTA AAGATTTATA AGAGTTATAA AATCTGTAA ATTTCAATGT	6000
GTATACCTAA ACTACGGTAT TTATTGAAAA GACTGGAGAC AAAAAGTATA CGCTGCCAAA	6060
ATGAATTACT GAAAATCAAA AAAGAGAGAA CCAAATGAT TCCCTCTTAA TGTATATAAT	6120
ATCTAGTTTT AAAAAATACAC ACTCACATAT CTCTGTAATG AATCGGGAAG ACAGGATTCG	6180
AACCTGCGAC ACCTTGGTCC CAAACCAAGC ACTCTACCAA GCTGAGCTAC TTCCCGAGTT	6240
AAATAGAAAA ATGCACCCTA GAGGAGTCGA ACCTCTAACC GCCTGATTCTG TAGTCAGGTA	6300
CTCTATCCAG TTGAGCTAAG GGTGCTCCAT ATTATGCCGA GGACCGGAAT CGAACCGTA	6360
CGATCGTTAC CAATCGCAGG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC	6420
CTCTCTAAGC GAACGACGGG ATTCGAACCC GCGACCCCA CTTGGCAAG GTGGTGTCT	6480
ACCACTGAAC TACGTTGCA CTGTTTTCTT CTATCTAAAA ATGCCGGCTA CATGACTTGA	6540
ACACGCGACC CTCTGATTAC AAATCAGATG CTCTACCAAC TGAGCTAAGC CGGCTCATTT	6600
GTTATATCTT AATGCGGGTT AAGGGACTTG AACCCCCACG CCGTTAAGCG CCAGATCCTA	6660
AATCTGGTGC GTCTGCCAAT TCCGCCAAAC CCGCATATAT GACCCGTACT GGGCTCGAAC	6720
CAGTGACCCA TTGATTAAAA GTCAATTGCT CTACCAACTG AGCTAACGAG TCTAAAATAA	6780
cTTGCGTTAC CTTAAACGGT CCCGACGGGA ATCGAACCCG CGATCTcGCC GTGACAAGGC	6840
GACGTG	6846

## (2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2911 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GAATTCATTT TAAATAAAGA TACGGGAGAG GTAAGTGAAT TAAACCTCA TAGGGTAACT	60
GTGACCATTC AAAATGGAAA AGAAATGAGT TCAACGATAG TGTCGGAAGA AGATTTTATT	120

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TTACCTGTTT ATAAGGGTGA ATTAGAAAAA GGATACCAAT TTGATGGTTG GGAAATTTCT	180
GGTTTCGAAG GTAAAAAAGA CGCTGGCTAT GTTATTAATC TATCAAAAGA TACCTTTATA	240
AAACCTGTAT TCAAGAAAT AGAGGAGAAA AAGGAGGAAG AAAATAAACC TACTTTTGAT	300
GTATCGAAAA AGAAAGATAA CCCACAAGTA AACCATAGTC AATTAAATGA AAGTCACAGA	360
AAAGAGGATT TACAAAGAGA AGAGCATTC AAAAAATCTG ATTCAACTAA GGATGTTACA	420
GCTACAGTTC TTGATAAAAA CAATATCAGT AGTAAATCAA CTACTAACAA TCCTAATAAG	480
TTGCCAAAAA CTGGAACAGC AAGCGGAGCC CAGACACTAT TAGCTGCCGG AATAATGTTT	540
ATAGTAGGAA TTTTCTTGG ATTGAAGAAA AAAAATCAAG ATTAAGATAA AAGCTATAGA	600
AAAAAATGGT TTATGTACTG AGATTAGATA GTGAGGTGAT GACATAGTTT TGTGAAAATA	660
GCCATTTATA ACTCAATTAT TTAGTTTACT TTACTTTACT AGTGATACTA TTTGGAGTTA	720
TTAATGGACT TAGTTTATAT AACTAATGAA TTGATTGAAA GGGTTAGTAT TGACAATATT	780
GGTCATATTG ACTAGAAAAT AGAGTCTATC AAAATTTAAA GGCTAATAGA GGTGATGAGA	840
CAATTCGGC TCTTTGTCAA CTGTAGTGGG TTGAAGTCAG CTAAGCTCGA GAAAGGACAA	900
ATTTTGTCTT TTTTCTTTTG ATATTCAGAG CGATAAAAAT CCGTTTTTTG AAGTTTTCAA	960
AGTTTCGAAA ACCAAAGGCA TTGCGCTTGA TAAGTTTGAT GAGATTATTG GTCGCTTCCA	1020
GTTTGGCATT AGAATAGTGT AGTTGAAGGG CATTGACAAT CTTCTCTTTA TCTTTGAGGA	1080
AGGTTTTAGA GGATGAACTT GATTCAGATT GTCCTCAATG AGTCCGAAAA ATTTGTCAGG	1140
CTCCTTATTC TGAAAGTGAA AAAGCAAGAG TTGATAGAGA TTATAGTGGT GTTTCAGTC	1200
TTCTGAATAG CTCAAAAGTT TATCTATAGT AGATTGAAAC TAGAATAGTA CACCTCTGCT	1260
TCTAAACAT TGTTAGAAAT CGATTTGACT GTCCTGAATG ATTTGTCTTG TTATTATTTT	1320
ATTTTACTAT AAATCCACGT TTACGAATCT CTTCCACAC TTGTTCAATG GGGTTCATCT	1380
CTGGTGTGTA TGGAGGAATA AATGCAAAAC CAATATTAGT CGGAATCTTT AAGGTACTTG	1440
ATTTATGCCA TATAGCATTG TCCATAACGA GTAAAAGATA ATCATCTGGA TAAGCTTGTG	1500
AAAGCTCCTA TTCCTAAAGC CCCTTTATAA CCTCTTGCGA GAGAGACTAT TGA CTCAGCC	1560
CTTACTTCAT GCGGATGAAA CTTCTTATCG GGTCTAGAG AGTCATAGCC ATCTGACCTA	1620
CTATTGGACC TTTTGTCTG GGAAAGTTGA GAATCAAGCA ATCAGCTGT ACCATCATGA	1680
TCAGAGTCGG AGTGGTTCGG TAGTACAAGA ATTCCTAGGA GATTATTCTG GCTATGTTCA	1740
TTGTGATATG TTGCGGCAGT AACTTAGGAC TTTAGTCCTC TAGTTCTGCC TATGCGATAG	1800
CAGTCCAAGG TTTAGGAGCA AGGCGACGCT AAGCTTGGTA AACTGCGAAC CGCTAGAAGC	1860
TTATCGTCAA CTGGAAGAAG CTGAACTTGT TGGATGTTGG GCGCATGTGA GAAGGAAATT	1920

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TTTTGAAGCG ACCCCCAAGC AAGCAGATAA ATCATCCTTA GGAGCTAAAG GTTTAGCTTA	1980
TTGTGATCAG TTATTTTCCT TGGAAAKAGA CTGGGAGGCT TTGCCAGCTG ATGAACGACT	2040
ACAGAAACGT CAAGAACATC TCCAGCCCCT AATGGAAGAC TTCTTTGCTT GGTGCCGCCG	2100
TCAGTCAGTT TTAGCAGGTT CAAAAC TAGG AAGGGCAATT GAATACAGCC TCAAGTATGA	2160
AGAAACCTTT AAGACTATTT TGAAAGACGG ACATCTGGTC CTTTCCAATA ATCTAGCTGA	2220
ACGCGCCATT AAATCATTGG TTATGGGACG GAGTAAAGA GTCCAGTGA CTCTTTTAGC	2280
CTGAGCTCAG TTTAAAAAAG CGAGGGTGGT TATTTTCTCA AAGTTTTGAA GGAGCTAAAG	2340
CAAGAGCTAT TGTTATGAGC TTGTTGGAAA CAGCTAAACG TCATCAATTA TAGTGCGTTG	2400
AATCTATAAC AGTACGCATC GACTGCTAAA ACATTTCTAT AAATCAATTT TCCTTTCCTA	2460
ATCGATTTGT TCATATCTTA TTTCAATCCA TTATAAATAG CGAGAAATAT CTATCCTATC	2520
TTCTAGAATG TCTTCCAAAC GAGGAACTC TCGTAAACAA AGAGGTTTTA GAGGTTTATT	2580
TACCATGGAC TAAAGTTGTA CAAGAAAAGT GCAAATAAGA AATCTCCAGA TTAGGAACTA	2640
TCCGTGAGTT CACTAATCTG GAGATTTTTC AATAGATCG TTATTGGGCG GTTACGATAT	2700
GATCACTACT TCGTCAGTCT TATCTACAAC CTCAAAACAG TGTTTTGAGC AACCTGCGAC	2760
TAGCTTCCTA GTTTACTCTT TGATTTTCAT TGAATATTAG AACAGAAAAA ATGCTTGGAG	2820
TATTTGTTTG TGTGTTTATT TTTATATAAC AAATAATAA CAAATAAAA ATATAAAAAA	2880
AGAGACAAAA AAGAACAGAA AGTAATTGAC A	2911

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6854 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GAAAAAAGT CTTGACAGAA AGCGCTATCA ATGATAGAAT GAATTCAGAT AAAAAGATTT	60
ATTTTAAAA CAAAAATGAA ACGTTTCAAA AAAAGAAATA AAGAGACAGC GCCAAGCGCT	120
ATCTTTTCTA GAAAAAATG AAACGTTTCA AAAAGGAGG TTGCTATGAA TAGCAAAGCG	180
AAGCAAGTTT CTCTTTGGGA AAGAATCAAG AAACAAAAAC TCTTGTTATT GATGACTGTC	240
CCCGGTTTAG TTTTAACCTT TATCTTTAAA TACATCCCTA TGTATGGGGT TTTAATCGCA	300
TTTAAAGATT ACAATCCTTT AAAAGGAATT TTAGGGAGTG ATTGGATTGG TTTTCTGAG	360

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TTTACAAAAT TCATATCCTC TCCCAACTTT GGTATCTTGT TAGCCAACAC ATTAAAAATTA	420
AGTATCTATG GTTTATTGCT TGGCTTTTTA CCACCAATCA TTCTCGCGAT TATGCTCAAT	480
CAACTCTTGA GTGAAAAAGT CAAAAAACGA ATTCAGCTCA TTTTATACGC ACCAAACTTT	540
ATCTCAGTCG TTGTTATTGT CGGTATGATT TTCCTCTTCT TTTCAGTGGG AGGACCAATC	600
AACAATTTTC TTTCTATGTT TGAATGAAG GCTGACTTCT TGACAAATCC AGACTTCTTT	660
AGACCTTTAT ACATCTTTAG TGGTATCTGG CAAGGAATGG GCTGGGCTTC AACGCTCTAC	720
ACGGCAACAT TGGTAAATGT AGATCCAGCC TTAGTAGAAG CAGCCCGACT GGATGGAGCC	780
AATATCTTCC AACGAATCTG GCACATTGAT ATTCCAGCTC TTAAGCCTAT TATGGTTATC	840
CAATTTGTTT TAGCTGCAGG TGAATTATG AATGTCGGAT ATGAAAAAGC ATTCTTGATG	900
CAGACATCGT TAAATTTGCC AACTTCTGAA ATTATCTCGA CATATGTCTA TAAAGTTGGT	960
CTTGTATCAG GAGACTATTC TTA CTCAACA GCGGTTGGTT TGTTTAATGC AGTGATTAAC	1020
G TAGTATTGC TTGTTGCAGT TAACCAAATC GTTAAACGCA TGAATAATGG TGAAGGAATT	1080
TAAGGAGGAA AGTATGAAAA ATTTCGATTAT GGATACAAAA TTTGATAGAC GTATCTTACT	1140
CTTAAATAAA ATCATTATTG TCTTTATCGT TTTGATGACT TTGCTTCCTT TACTTTATAT	1200
CGTCGTAGCA TCCTTTATGG ATCCTAAGGT TCTGGTTAGT AGAGGGATTA GCTTTAATCC	1260
AGCCGATTGG ACTGTAGAAG GTTACCAGCG TGTATTCACT GACCAATCTA TTCTAAGAGG	1320
TTTTATCAAT TCTCTACTAT ACTCTTTTGG ATTTGCAGCT TTAACAGTCT TGCTATCTGT	1380
GTTTACAGCT TATCCTCTTT CTAAGAAAGA CTTGGTTGGA CGTCGTTGGA TTA ACTACTT	1440
CTTGATTGTA ACTATGTTCT TTGGTGGTGG TTTAGTCCCA ACTTACTTGC TCGTAAAAGA	1500
ATTGGGAATG CTCAATACTC CATGGGCTAT CATTGTTCCA GGTGCTGTTA ACGTTTGGAA	1560
TATTATTCTT GCTAGGGCCT ATTTCCAAGG ATTGCCTGAA GAATTAGTTG AAGCTGCTGT	1620
CATTGATGGT GCAAATGATT TACAGATTTT CTTCAAAATC ATGCTTCCTC TTGCAAAACC	1680
AATTATGTTT GTTCTCTTCC TTTATGCTTT TGTAGGACAG TGGAACTCAT ACTTTGATGC	1740
AATGATTTAT ATCAAGGATC CAAACTTGGG ACCATTGCAA CTTGTACTTC GTAAAAATTCT	1800
CATTCAGAGC CAACCAGGTC AAGACATGAT TGGAGCACAA GCGGCTATGA ATGAAATGAA	1860
ACGTTTAGCT GAATTGATTA AATACGCAAC TATTGTCATT TCCAGCTTGC CATTGATTGT	1920
TATGTATCCA TTCTTCCAAA AATACTTTGA TAAAGGAATT ATGGCTGGTT CACTTAAAGG	1980
ATAAAAAAG AAAAAATAAA AGGAGTTTTT TCATGAAATT CAAAACATTC TCAAAATCAG	2040
CAGTTTTGTT GACAGCTAGT TTAGCAGTAC TTGCAGCCTG TGGCTCAAAA AATACAGCTT	2100
CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT TCAAGAAAAG AAAACATTGA	2160

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AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC AAATGAAAAG TTAATTTTGC	2220
AACGTTTGGA GAAGGAACT GCGGTCATA TTGACTGGAC CAACTACCAA TCCGACTTTG	2280
CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC AGATGCTATC CACAACGACG	2340
GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG TGTATTATT CCAGTTGAAG	2400
ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT GGATGAGAAA CCAGAGTACA	2460
AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT TCCATGGATT GAAGAGCTTG	2520
GAGATGGTAA AGAGTCTATT CACAGTGTCA ACGATATGGC TTGGATTAAC AAAGATTGGC	2580
TTAAGAACT TGGTCTTGAA ATGCCAAAA CTAAGTATGA TTTGATTAAA GTCCTAGAAG	2640
CTTTCAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA TGAAATTCCA TTTTCATTTA	2700
TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC TGCATTTGGT ATAGGGGATA	2760
ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA CTTACACAGCA GATAACGATA	2820
ACTATAAAGA AGGTGTCAA TTTATCCGTC AATTGCAAGA AAAAGGCCTG ATTGATAAAG	2880
AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG TCATGATCAG AAATTTGGTG	2940
TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA CGAAAGTTAT GATGTTTTAC	3000
CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG TACAAACGGT ATGGGATTTG	3060
CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT AGAATTGACA GCTAAATGGA	3120
TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA CTGGGGAAC TACCGAGATG	3180
ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAA TAGTCTAAAA CACTTACCAC	3240
TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA AGTAGGAGGA CCACTAGCTA	3300
TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA TGATGCCAAA TGGCGTTTGG	3360
ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT CAATAACTAT CCAAGAGTCT	3420
TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA AGCAGATATG AATGACTATA	3480
TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT TGATACTGAG TGGGATGATT	3540
ACAAGAAAGA ACTTGAAAA TACGGACTTT CTGATTACCT CGCTATTAAA CAAAAATACT	3600
ACGACCAATA CCAAGCAAAC AAAAAGTAGA GGTGATTAT GGGAGATAAG AAATACACAG	3660
TAGAAAAAGC CAATCGTTTT ATAGCAGAAA ATAAACATCT CGTTAATACT CAATATAAGC	3720
CTGAAGAACA TTTTTCAGCT GAGATTGGTT GGATCAATGA TCCAAATGGA TTTGTCTATT	3780
TTCTGGGAGA ATACCATCTC TTTTATCAAT TCTATCCATA TGATAGTGTT TGGGGGCCTA	3840
TGCACTGGGG ACATGCTAAA AGTAAGGACT TGGTGACTTG GGAGCACTTG CCAGTGGCAC	3900

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TTGCTCCTGA CCAAGATTAT GACCGAAATG GTTGTTCCTC AGGCTCTGCC ATTGTCAAGG	3960
ATGATCGCCT CTGGCTCATG TACACTGGAC ATATCGAAGA AGAAACCGGT GTCCGCCAAG	4020
TGCAAAATAT GGTATTTTCA GATGACGGGA TTCACTTTGA AAAGATTTC CAAATCCAG	4080
TTGCAACTGG ATCAGACTTA CCAGATGAGT TGATTGCTGC TGATTTCCTG GATCCAAAAC	4140
TCTTTGAAAA AGATGGACGC TATTACTCCG TAGTAGCTGC CAAACACAAG GATAATGTGG	4200
GCTGTATCGT TCTACTAGGG TCCGATAACC TAGTAGAATG GCAGTTCGAA TCCATCTTTT	4260
TAAAAGGGGG AGAACACCAA GGTTTTATGT GGGAAATGCCC AGATTACTTC GAGTTAGATG	4320
GGAAAGATTG CCTTATTATG TCACCCATGC GTTATCAGCG TGAGGGAGAC TCATATCATA	4380
ACATCAACTC ATCGCTTTTG TTCACGGGTA AGGTAGATTG GAGAGAAAAA CGTTTATCC	4440
CAGAATCAGT TCAAGAAAT GATCATGGCC AAGACTTCTA TGCGCCTCAA ACATTGTTGG	4500
ACGATCAAAA TCGTCGTATC CTGATTGCTT GGATGCAGAC ATGGGGGCGT ACCCTTCCAA	4560
CCCATGACCA AGAACACAAG TGGGCATGTG CCATGACTCT ACCTAGAATT CTAAGATTGG	4620
AAGATGGCAA ACTAAGACAA TTCCCTGTTA AAAAAGGCCA ATATCAAATC CAAATAGATA	4680
AAGATTGTCA TPACCACTTA GGAAATGATA TAGATTATCT TGAATTGCTT TATGACAGTA	4740
ATGCGCAGCA AGTTTACATT GATCGTAGCC ATCTTATTCA AAAAATTCTA GGTGAAGAAG	4800
AACAGGACAC TAGTCGACGG TATGTAGATA TTGAAGCTAA AGAATTGGAA GTTGTCTAG	4860
ATAAAAATTC CATCGAGATT TTTGTCAATC AAGGTGAAGC AAGCTTGACT GCAACTTATT	4920
ACTTAACGGT GCCAGCTGAG CTATCAGGAA TTGATTAAAA ATTAAGTTAT TTCTCCTAAA	4980
GAAAAAGTTC TCTTTCTAAA ATAGTGAAAA GAGGACTTTT TGTGTTTGG GTATATAAGC	5040
TTAGTTTATG GTATTTGTAA AATTGGTGTG GGATTATGAT TTAAGCTAGT TTTCTAAAGA	5100
ATTTGAAAAA AATTTTATTT AAGCAAAAAA ACCTTGGTTC CAAGGCTTTT CCTGTTGTAT	5160
TTAGATGCCC CCTACAGGGA TTGTAGGAGA TATGTTGCTT AGATGTTCTT GATTTTCTGG	5220
TGTTTGTAA CGTTTAAATG AGTTTTTTGA GTTTGTTGGT GGGGCGTTGC CCGGCAATTG	5280
CCCGACTTAT TGCTTGAAAA AGAATTTAAA ATATAGTATA GTTAATTATA GATTAACACT	5340
TGCTTGAGAG AACTGATGAA GAACAATGAA AGATTAGGTA TTAAATTAAG TAGAGATAGC	5400
GTTTTAGGAT TGAGGGAAGT TAGAAGGCTT TATTTAGGCA GTTCAGATAT CCCAGTTTCT	5460
GATGGCTATG TGATTGAAGT TGCTTATAAC CAGATATCAC ATGAGATTGA TATTATTGAT	5520
TGGGTAGAGT TGAACAAGTC AAAAATTAAG ATAAGTGAAA TTAGTGAAAG CGTGATATA	5580
GATGCCACTA GCTTGAGAAC AACTTTGACT TTAGACACAT TAGTATATGA AGGTATGAGA	5640
GATATACAGT TAAAGTTGAG AGAGCTTACA AAGGGGAGAG TATTCTTTTC ATTTGTAGTG	5700

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AAGTTAGTTT TGTTCGCTTC TATTTTAAAG AAAAAAGATT TACTAGAAAA ATTTCAAGAA	5760
AAGTGTTAAT CAAGTATTGA CACTTTATCT GGATTTCCGT ATAATATGCT TAGAAAGGAA	5820
TCTTCTAAA TTTTTTCGT CCTTATGTGT TAATCAAAGA CGAATACAAA AACATATTTT	5880
TTTACTCTAA AAAGTGTTAA TCAATGATGT ATTTGTTAGA GAGGTAGATA AATGGAATTG	5940
AGAGCACCAC CAGTTATAAT AGTATAAAC GTATAATAA AATATTTTAA CTTGAATTAT	6000
AGAAAAGGAG AAACAAATCA TGAAACAAA ACAACCGATT GTTCTAGAA CGAAACAACA	6060
TACATTTGAA GAGCTTATTC AAGACCAAAA GTTAGAAAGA TTGGCTAAGT TGTCGCCCGA	6120
TTTGGTTGGA AGGTATGGTT TTAGTGCTAG CTGTGCGTCT TCATTTGCGA ACTTGATTAA	6180
AGAAGCGTAT GGGGGTAAAA ATCTAAACGT AGTTTATGCG AGTCGGATGT TGGCTCTCTG	6240
GAATATTGCT TGCAGTTGTT ATCATAAGGC TGATGGGTAT TCTTTAGCAG ATGCGCTTTT	6300
TAGTGATAAA AAAATTTGTC TAGATTCTTA CTATTACCAC AAGAATACCT CTAATACCAT	6360
AACTAGTGAT GTGATAAAG ATGTTTACGA TAATTATAAT AATTATATGG TTTTAACTCG	6420
AGAAGCGACA CCTGAATACA TTTATGTGT ACAAACTGAA ATGCCAAAAG ATTCAGATTT	6480
ATATTTTAT ATTAGAGAAG TTCTGGGATT ATCGTTTAGT ACCATGCATT ATGCATTTT	6540
AGTCAAGGTT CTTGCAGGAG CGCTTGCTAG AAAATATAAG CCATATCGAA ATTGAATTAT	6600
TTAAATTTAT ACTCTTCGAA AATCAAATTC AAACCAAGTC AGCTTCGCCT TGCTGTACTC	6660
AAGTGCTGTC TGTGGCTAGC TTCTTAGTTT GCTTTTGTAT TTTCAATTGAG TATTACTCTT	6720
ATGGTAGTTA TTTATGGCAT AATAATATTG ATTTGGGAGT TATAGCGAAA ATTTTAGGTT	6780
CTATAATATT TGTAGTGGT AAACCACTAT AGATATTATG GAGCCTATTT ATTGTAGAAA	6840
AAAGTCCCAT ATGA	6854

## (2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3895 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

TCCTTGCTAA GTTTATACTC AATGAAAATC AAAGAACAAA CTAGGAAGCT AGCCACAGGT	60
TGCTCAAAGC ACCGCTTTGA GGTTCAGAT AAAACTGACA CGGTTTGAAG AGATTTTCGA	120
AGAGTATTAA TTTACATAAA TAGCCAGTGT TTGATAGGTT TTGAGTAGAA TTTTCTCAGA	180

1180

CACTTCTGCA TCTTCATAGT TTGATATCAA AATCTGTCCA TTTTGGTAGA CTGCTGGCAA	240
GTCGATTTcA CTTCTTTAGC ATAAAAGTTA TTGAGCACTA GTAACTTTTG ATCCTCAAAC	300
TGGCGTTCAA AAGCGTAGAC TTGTTTGCTA TCTTCAAAGG CTGGTTTGTA ACTTCCTTCT	360
GAAATGATTG GCATTTCTTT ACGCATCGAA TCAAGTCTTG ATAGAAGGTA AAAATCGGAC	420
CCTGGATTTC ATTTTCTACA TTGATGTATT TATAGGATTT ACCAGCTTTC AACCAAGGAG	480
TGCCTGTTGA AAATCCTGCA TTTTCCGAAG CATCCCACTG CATGGGAATG CGTGAATTAT	540
CACGCGACTT AGCTTGAATA ATCTGGAAGG CTTCTTGCTG ACTCTTTCCT TCTTCTAAGA	600
GCATCTGATA GGCATTAAGC GATTCGACAT CCACATAATC AGCCATAGAA TCATAGTCTG	660
GGTCAATCAT CCCGATTTC TCACCCATGT AGATATAAGG TGTCCACAGT GACAGGTGAA	720
TGCTGGCTGC TAGCATGGTG GCTCCTTCCT TGCGGAAGTT TTGAATATCG ACAAACGGT	780
TCAAGGCACG TGGTTGATCG TGATTATTCC AAAAGAGGGC ACTCCAACCG TCTTTATCAC	840
TCATTTCTTT ACCCCAATA TGGTAAAGAC TCTTCAACTC TTCAAATCA AAGGGAGCCA	900
AGGTCCACTT TTGTCCATCC TTATAGTCCA CCTTGAGGTG ATGAAAATTA AAGGTCATGG	960
ATAATTCCTG ACGATCAGGC GACGAATAGA GGACACAGTT TTCCATGGTG GTAGAAGACA	1020
TTTCCCCAAC TGTCATAAAG CTATCGTCGG ATCCAAAAGT GGCTTG GTTC ATCATACGCA	1080
AATAGTTATG AACGATGGGT TTGTCTGTAT AAGCTGGCTT CCCTTCATTT TCAGGACAGT	1140
CCACTGAAAC CTCGTCCTTA CCGATCAAAT TGATCACATC AAATCGGAAA CCTTTGACAC	1200
CCTTGTCGCG CCAGAAATTA ACAACCTGA AAAGCTCCTT ACGGACATTG GAATTGCGCC	1260
AGTTAAGGTC AGCCTGGGTC TCATCAAATA GGTGAAGATA GTATTTCCCA GTATCCCCGA	1320
AAGGCGTCCA TGCAGAACCA CCAACTTAG ACTGCCAATC TGTGGTTGG TCTTGATGA	1380
AGAAAAAGTC TTGATAATAC TTATCACCAG CTAGGGCTTT CTGAAACCAT TCATGCTCTG	1440
TCGAACAATG ATTAAGTACC ATGTCCAGCA TAAAGTCAAT CTTGTGCTCT TTACCGACAC	1500
ACACCATTTT CTCAAATCA GCCATATCAC CAAAAGAGG ATCCACTGCC ATATAATCTG	1560
AAATATCGTA ACCATTATCC CGTTGAGGGC TTGGATAGAA TGGATTGAGC CAGACCATAT	1620
CCACACCTAG TTTGGCTAAA TAGGGAATTT TTTCGATAAT CCCACGAAA TCCCCAATAC	1680
CGTTTTCAGT GGTGTCTTG TAAGATTTTG GATAGATTTG ATAGACTACT TTTCTTTAT	1740
CAAGTGTCAT CTGTTCTCC TTTTCTGATA AAAGGGAGGA AGCAGTCTTC CGTCCCTATT	1800
TGTGCTATTT CAATTATACT CAATGAAAAT CAAAGAACAA ACTAGGAAGC TAGCCACAGG	1860
TTGCTCAAAA CACTATTTTG AGGTTGCAGA TAGAGCTGAC GTGGTTTGAA GAGATTTTCG	1920
AAGAGTATTA GATTCGTGTA GCGACCATGA GAGATGCTCC AGCTTGGATC GTTGTCCGAT	1980



1181

AAGTTCCGGG AATAGTCGCT GTATAAGCAT CTTGGTTGGT GATGATAACA GGAGTTTCTG	2040
TCACCAGACC TGCAGCCTTA ATGACATCCA TATCAAAACG AATCAGTTGC TGACCAACTG	2100
TAACGTGATC TCCTTGGACT ACAAGACTTT CAAAACCTTT GCCATCAAGA CCTACTGTAT	2160
CCATACCGAT GTGGATGAGC AATTCAACTC CCTCGTCAGA GACAATGCCG ATGGCATGCT	2220
TGGTAGGGAA AAGAACCGTC ACTGTCCCAT TAACTGGAGA GGTCAACTCA CCTTGGCTTG	2280
GTTCAATGAC TAGACCTTGC CCCATGACAC CTGATGCAAA AATAGGATCC GTCGCTTGAC	2340
TCAATTCTTT CACTTGGCCA GTTAGTGGGC TGATAATTTT TACCGAAGTA AGTTCTACTG	2400
GTTTCATGGT CACAAATTCT GCTTCTTCTT GAGCAACGAA TTCTGCCTGC AAGTTCTGAT	2460
CGCCCTCTGT TTTTGTAAG AGACCAGCCT TGC GGAAGAA GAAAGTCAAG AGCATTGGAA	2520
CAACAATCGC AACTAGCATA GTTCCTGCAA ATGGCAGCAT GTATTGAGGT TGAATAGAGA	2580
GAATACCTGG CAAACCACCG ATACCAATAG AAGCCGAGT TACATTAAAA GTAACGGATA	2640
ACATGCCTGC AAGGGCTGAA CCAGTCATCC CAGCAACAAA TGGATAAATA TATTTTACGT	2700
TAACCCCAAA AAGAGCTGGT TCTGTAACAC CGAGATAGGC TGAAATGGTT GCAGGAAGTG	2760
AAACCTGAGC CTCACGCTCA TCATGGCGAT GCATGAAATA ATAGGCAAAC ACGGCTGACC	2820
CTTGAGCAAT ATTAGAAAGA GCAATCATTG GCCATAGGGC AGTGCCACCA GCATCCGCAA	2880
TCAATTGTGT ATCAATGGCA TTGGTCATAT GGTGCAGACC TGTGATGACA AATGGAGCGT	2940
AGAGGGCGCC AAAAATTGCA CCGAAGAGCC ATTTAACTGG ACCAGTTAAA CCTGCCAAGA	3000
CAACTGATGA AAGTCCTTGT CCAATTGTCC AACCGATTGG TCCCAAAACA GTATGAGCCA	3060
AAATCAAGGC TGGAAATCAAT GACAAGAAAG GTACAAAAAT CATAGAAATG ACTTCTGGGA	3120
TATGCTTGTG CCAGAAGATT TCAAGATAAG ACAGACTCAA ACCTGCAAGC AAGGCTGGGA	3180
TAACTTGGGC TTGGTAACCG ATACGATTAA CAGTAAAATA GCCAAAATTC CAAACCCAGT	3240
TTGCCGCGAT ATCAGCTGCT GCGGTTGAAG CAACCGCATA GGCATTGAGC AACTGAGGCG	3300
ATACCAAACA GATTCCGAGA ACAATTCCCA AAATTTGGCT GGTCCCATC TTACGAGAAA	3360
CAGACCAAGT AATCCCTACT GGTAAGAACT GGAAGATAGC TTCACCAGGC AACCAGAGGA	3420
AGTGATTGAC ACCTGCCCCA AACTGAGAGG ATTCTGTGAT GGTCTTGCCA TCCAACATCG	3480
ACCAATGGAC ACCTTCCAAG ACATTACGGA AACCGAGGAT CAATCCTCCG ACTATCAAGG	3540
CTGGAATAAT CGGAGTAAAA ATCTCCGCCA GAGTGGTCAT AACACCTTGG ACCACGTTTT	3600
GATTACTCTT AGCTGCAGAC TTGGCTGCTT CTTTGAAAC ACCCTCAATA CCTGAAACGG	3660
CTGTAAAATC ATTATAAAG ATGGGCACGT CATTCCAAT GATTACCTGA AATTGACCTG	3720

1182  
CATTGTGAAA GGTTCCTTTA ACAGCTGGAA TTGACTCGAT AGCTTTAACA TTAGCCTTCT 3780  
TATCATCTCC TAAACAAAC CGCATCCGTG TCGCACAGTG AGTTACGGCA GTCACATTTT 3840  
CTTGCCTCC GATTGCCTGA AGCAGATCTT TGGCTTCTTG TTCAAATTTT CCCGG 3895

## (2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3936 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGGATCGCCG CTCCAGCTAC TAAGTCTCGT GCAGTGCCGA TTTATCAAAC AACATTTTTT 60  
GTTTTTGATG ACACGTAGGA AGGTGCCGAT CTGTTTGCCT TGAGGAAACC AGGGAACATT 120  
TATACTCGTA TCACCAATCC TACAACAGCT GCCCTTGAAG GTGGTGTGA AGCGCTAgcA 180  
ACAGCATCAG GTATGACTGC AGTGACTTAT ACGATTTTGG CGATTGCCCA TGCTGGTGAC 240  
CATGTAGTGG CTGCTTCGAC TATTTACGGT GGAACCTTCA ATCTTTTGAA AGAACCCCTT 300  
CCTCGTTATG GTATCACAAC AACCTTTTTC GATATTGATA ATTTGGAGGA AGTAGAAGCA 360  
GCTATCAAAG ACAATACCAA GCTTGCTCTG ATTGAAACCT TGGGTAACCC CTTGATTAAT 420  
ATTCCAGACC TGGAAAACT GGCAGAGATT GCTCATAAAC ATCAAATCCC ACTTGTGTCA 480  
GACAATACTT TTGCAACACC TTATTTGATT AACGTCTTCT CTCATGGCGT TGACATTGCC 540  
ATTCACTCTG TGAATAAGTT TATCGGTGGG CATGGTACAA CTATTGGAGG AATAATTGTC 600  
GATAGTGGTC GTTTTGAAGT GACGGCTTCA GGGAAATTCC CTCAATTTGT TGACGAGGGT 660  
CCAAGCTGCC ACAATTTGAG CTATACTCGT GATGTGGGTG CAGCAGCCTT TATTATAGCT 720  
GTTTCGAGTC AATTGCTTCG TGATACAGGT GCAGCCTTGT CACCATTCOA TGCTTTCCTC 780  
TTGCTACAAA GACTTGAAAC CTCTTCACTT CGTGTGGAAC GCCATGTACA AAATGCTGAG 840  
ACAATTGTTG ATTTTCTTGT CAACCATCCT AAGGTAGAAA AGGTAAATTA TCCAAAACCT 900  
GCAGATAGTC CTTATCATGC CTTGGCTGAG AAATACTTGC CAAAAGGTGT CGGTTCAATC 960  
TTTACCTTCC ACGTCAAAGG TGGCGAGGAA GAAGCACGCA AGGTCATTGA TAATTTAGAA 1020  
ATCTTTTCTG ACCTTGCAAA CGCGGCAGAT GCTAAATCGC TTGTTGTCCA TCCAGCAACA 1080  
ACCACTCACG GTCAATTGTC AGAAAAAGAC CTAGAAGCAG CAGGTGTCAC ACCAACTAA 1140  
ATTCGTTTGT CAATCGGTCT TGAAAATGTA GAAGATTGTA TTGAAGACTT GCGCTTGGCC 1200  
TTGGAAAAAA TTAAAGTAA AAGAAGATAA ACAGTGGGCT TCGACTCACT GTTTTGTATT 1260

1183

TTCCCTCAGG CATGATATAA TGGTTACAGA AGTCTAGAAA GAGGAACGAT ATGAACGAAA	1320
TCAAATGTCC CAACTGTGGG GAAGTCTTTA CAGTAAATGA GAGTCAGTAT GCCGAACCTCT	1380
TGTCCCAAGT GAGAACGGCA GAGTTTGATA AGGAACTACA CGATAGGATG AAGCAGGAAC	1440
TGGCCTTGGC TGAGCAAAAG GCCATGAATG AGCAACAGAC TAAACTGGCT CAGAAGGATC	1500
AAGAAATTGC GCAATTACAG AGTCAGATCC AAAACTTTGA TACAGAAAAA GAATTGGCCA	1560
AGAAAGAGGT TGAACAGACA AGCCATGAGG CTCTCTTGGC TAAGGACAAG GAAGTACAGC	1620
TCTTAGAAAA TCAGTTGGCT ACCTTCCGTT TGGAGCATGA AAATCAACTA CAAAAGACCC	1680
TTTCTGACCT AGAAAAAGAA CGGGATCAGG TTA AAAACCA ACTACTTTTG CAGGAAAAGG	1740
AAAATGAATT ATCTTTGGCT TCTGTTAAGC AAAACTACGA AGCCCAGCTC AAGGCAGCTA	1800
GTGAACAAGT CGAGTTTAT AAGAATTTTA AGGCTCAACA ATCTACAAA GCGATTGGGG	1860
AAAGCCTAGA ACAGTATGCA GAGAGTGAGT TTAACAAGGT TCGTAGTTTC GCCTTTCCAA	1920
ATGCTTACTT TGAGAAGGAT AACAAGGTCT CTTCCGCTGG GTCTAAAGGG GACTTTATCT	1980
TCCGTGAGTG TGATGAAAAT GGAGTTGAAA TCATTTCTAT CATGTTTGAG ATGAAAAACG	2040
AAGCGGACGG AACAGAGAAG AAGCACAAGA ATGCAGATTT TTACAAGGAA TTGGACAAGG	2100
ACCGTCGGGA GAAGAACTGT GAGTATGCCG TTTTGGTGAC CATGCTTGAG GCTGATAATG	2160
ACTACTTTAA CACAGGGATT GTTGACGTCA GTCACGAGTA TGAAAAAATG TATGTTGTTC	2220
GTCCTCAATT CTTTATCCAA TTGATTGGTC TCTTACGTAA TGCGGCGCTA AATTCCCTAA	2280
AATACAAGCA GGAGTTGGCC TTGGTTCCGG AGCAAAATAT TGACATTACG CATTTTGAGG	2340
AAGATTGGA TGCCTTTAAG CTAGCTTTTG CTAAGAACTA TAATTCAGCT TCGACTAACT	2400
TTGAAAAGC TATTGATGAA ATCGACAAGG CCATCAAACG CATGGAAGAG GTTAAGAAAT	2460
TCCTGACCAC ATCTGAAAAC CAACTCCGTT TAGCTAACAA CAAATTGGAA GATGTCTCTG	2520
TTAAAAAATT GACCCGAAA AATCCAACAA TGAAAGCGAA GTTCGAAGCA CTGAAGGGGG	2580
AGTAGAAAGC AAAAATGAAC GGTATTATTA ACTTAAAAA GGAAGCAGGA ATGACCTCGC	2640
ATGATGCGGT TTTTAACTG CGTAAGATTT TGGGAACCAA GAAAATTGGT CATGGTGGAA	2700
CCTTGGATCC GGATGTGGTG GGTGTTTTCG CGATTGCGGT TGGCAAGGCG ACACGCATGG	2760
TCGAGTTTAT GCAGGACGAG GGTAAGATCT ATGAGGGGGA AATCACTCTG GGCTATTCCA	2820
CGAAGACTGA GGATGCTAGT GGGGAAGTGG TCGCAGAAAC CCCTGTTTTG TCTCTCTTG	2880
ATGAAAAGCT TGTGATGAA GCGATTGCTA GCTTGACTGG GCCTATTACT CAGATTCCCC	2940
CTATGTATTC GGCAGTTAAG GTTAATGGTC GCAAGCTCTA TGAGTATGCG CGTGCTGGTC	3000

1184

AGGAAGTGGG	GCGTCCAGAA	CGTCAGGTGA	CCATTTATCA	ATTTGAGCGA	ACAAGTCCGA	3060
TTTCTTATGA	TGGCCAACTT	GCCCGATTCA	CTTTTCGTGT	AAAATGCAGT	AAAGGGACGT	3120
ACATCCGTAC	TTTGTCACTT	GATTTGGGTG	AAAAGCTTGG	TTATGCGGCT	CATATGTCCC	3180
ATTTGACTCG	TACTAGTGCT	GCTGGCTTAC	AATTAGAAGA	CGCTCTTGCC	TTGGAGGAAA	3240
TTGCTGAAAA	AGTAGAGGCT	GGGCAATTAG	ATTTTCTCCA	TCCTTTAGAG	ATTGGGACAG	3300
GTGACCTTGT	CAAAGTTTTT	CTAAGTCCAG	AAGAGGCTAC	AGAAGTTCGC	TTTGGTCGTT	3360
TTATTGAGCT	AGACCAAACG	GACAAAGAAC	TGGCTGCCTT	TGAAGATGAT	AAATTGTTAG	3420
CCATTCTAGA	AAAACGGGGC	AATCTCTATA	AGCCAAGGAA	GGTTTTTAGC	TAGATCGTTT	3480
AGGAATAAAA	ATCGGGTGAT	AGATAACAAT	TGCTTGATAA	AACCCCATAC	TAATAGTAGA	3540
ATGGTTTTGG	GAATTATAAT	ATTCCAATTG	TTGCGAGTTG	TAGGTACTCA	AATAATCTAT	3600
ATAGAAATTT	AGAGGTGTGA	AATGAAGCAA	TTTAAATTC	TTTCAGATAA	ATATTTAGAG	3660
TCCATTACAG	GTTCTGATGG	GAACCTAGGC	CCAGGATTTG	GTGTGATAAT	TCCATGATGC	3720
GAAATGAGTT	TCGAGAAAGG	GTGGAGCAAC	TTCTTCAACA	AAAAGAAATA	AATGAAAATA	3780
GTGAGTTGAG	TCACCTGTTT	CGTCTTGCTA	TACAAAATTT	AGACAGAAAT	GAAAAATACC	3840
AATCGGTCAT	GGCCAATTTG	AGTCAAGGGT	TGTCACCTTA	CCTCATGACG	CATCATTACC	3900
AGGCACCTAA	GTCTGTCATT	GATTTTGGTT	TATGGA			3936

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CATCCAGCAA	CTGCTCCTCT	GAGCGTTTCA	AAATTGATGT	AATTTTCTA	GTTTTTCTA	60
ATAAATGTGC	CATTTTTCAC	CTCGAATTTA	ATCGCTATCA	TTATAACATA	AAAACGTCTC	120
TTTTTCAATA	ATTATCTGAA	AATTCCTTAT	TGACTTGCAAT	TGACTTACAA	TTTAATTAAA	180
AACCAGAATA	TTTTTAATTA	AATTGTTTCT	TTTCTATTGA	CAAGTTGCCT	ATTTTGTGT	240
ATCATAATAT	TATAAAAGAT	AATATAATAA	TTTTATTGT	CTTTTCACAT	TCGGTCTCCT	300
TATATAAAAA	AGCGATTCAT	TTTGAACCGC	TTTTCTTAT	TTATCGCCTT	TGTTACGAAT	360
AACAAAGCCT	GTTTGCTTTT	CGCTTAAAGT	ATTGCGTGGT	TTTTTATTAT	CCTTACGGTA	420
ACGTTTTTCC	TTATCAAAAC	GATCGTTGCC	ACGACTTCCT	TTTTTGAAC	CATCACGGCG	480

1185

ACCATTGCCA CGGCGATCAC GCTCTCGACG GTCGTCCCCA CGACGGCCTC CACGACCTCC	540
CTTAGCTTTA CCACCGAAAC CATTACCTGA TGGTTTAAAC GGTAGTGGtT TTTCACGTGC	600
AATCTCCACT TCTGGAAGGC TATCTGGGTC TTGGACTGTC AGACTCAAGA TATACATTGC	660
CAATTCTTCT GGAGTAACT CAGCAGCCAA TTTGCGAGCA TCCTTACCAA ATTTCTCAAA	720
GTTGGCACGA ATGGTTTCAT CTGCAAAATC ACGTTTCGATT TTCTTGAGAG CTACCTGTTT	780
TTTTGATTGG AAGGATTCTT CTACACTTGC AGGTTTGAGA CCTTTCATGC GTTCTTAGT	840
CAAGTTTTCA ATGATTGAA GGTAACCCAT TTCGTTTGA GCAACAAAAG TAATAGATTG	900
ACCTGACTTA CCAGCACGAC CTGTACGACC GATACGGTGA ACATAACTCT CAGGATCTTG	960
TGGAATATCG TAGTTGTAGA CATGGGTCAC ACCTGAAATA TCCAAACCAC GCGCTGCAAC	1020
GTCTGTGCGA ACCAAAACAT CAAGATTGCC ATTTTAAAG TCACGAAGGA CACGAAGACG	1080
TTTGTTTTGG TCTAGGTCGC CATGAATTCC TTCTGCACGG AAGCCACGAA TTTTCAAACC	1140
ACGAGTCAAT TCATCCACAC GCGGTTTGGT ACGACCAAAT ACAATAGCGA GTTCTGGTTG	1200
TGCCACATCC ATGAGACGAG TCATGGTGTC AAATTTTCT TGTTCCTTAA CACGGATATA	1260
GTACTGGTCA ACCAATTCTG TTGTCAATTC CTTAGCCGCA ATCTTGACAT GTTCAGGGGC	1320
TTTCATAAAC TGAACACCGA TACGTTTGAT GGCATCTGGC ATAGTTGCTG AGAAAAGCAA	1380
AGTTTGACGG TTCTCAGTA CACGGGAAAT AATGGCTTCG ATGTCTTCAA GGAAGCCCAT	1440
GTTAAGCATT TCATCCGCTT CGTCAAGGAT AAGGGTTTCA ATGTCTTGTA ATTTCAAGGC	1500
CTTGCGTTTA ATCAAGTCCA AGAGGCGACC TGGAGTTCCC ACCACAATAT GGGCACCAGA	1560
TTAAGAGCC TTAATTTGTT TTTCAATGCT TGATCCGCCA TATACTGAAC GGACTTTGAC	1620
TCCCTTACTA CGACCAAAGC GGAAGAGTTC TTCTTGACTT TGGACAGCTA GTTCACGAGT	1680
TGGAGCGATG ACCAAGGCTT GGATAGTCGC TTCTTCTGTA CGGATTTTTT CAAGGGTAGG	1740
CAAGCCAAAG GCTGCAGTTT TTCCTGTACC AGTCTGAGCT TGACCGATAA CATCCTTGCC	1800
TTCAAGGGCC AAAGGAATAG TTTGTTCTTG GATAGGACTA GCTTCTACAA AACCAGCTTT	1860
TTCAATTTCT GCTAGCAAAT CAGCAGACAA GTTTAATTCA TTAAATTTCA CGTTATTCTT	1920
CTTTCTAAAG GTGGTGCGAA GCCACCCTAT AGGGCTTAGT TTATACTTTT CTTTTTATGA	1980
CGTATTTTCA TATAACTAGA TATAAAATCG TGTTGCTTCT TTTCCACAAA AGAAAAGTAC	2040
TGTTTTCTTT GCAACCTATC TAGTATAACA CAAGACCAGA GCAAAAGATA GCCCCATTC	2100
TACAGAAAAT CATGTAAGCG CTTTTGACT TTCTTTTTTG ATTGAACGAC CTAGATAATA	2160
AGACAAAGCC AAGGCGATAC TGTATAAAAT GAGAAAACG AACAAGGTTT GTGTGTACGA	2220

1186

ATGAGCCATT TTATAAGTCT CTGCTAATAA AATAGGTCCC GCTAAACCAG CCATTGCCCA	2280
AGCTGTTAAA ATATAACCAT GCAGAGCGGC CAATTCCTTG GTTCCAAAAA TATCACTGAG	2340
ATAAGCTGGA ATCAAAGAAA AACCAGCTCC ATAGCAAGTC ATCAAAATAG ACATAGCAAC	2400
TACAAATAAA ACGGAATCTG TAAAGAGCCA AAGTGAGAGA GAAAAGAAAA GATTGACAAG	2460
CAGTAATATA CTAAAGGTTA GAGGGCGACC GATATAGTCA GACAACTCG CCCAGAGCAA	2520
GCGACCAAAT CCATTGAAAA TCCCCAAAAC ACCCACCATT ACTGCTGCAT GACTTGTAGA	2580
CAAGCCAGCC ATCTCCTGTG CCATTGGCGA TGCCGCTGAA ATTAAGCCTA AACCACAAGC	2640
TATGTTGATA AAGAAAATAA TCCAAAGCAT ATAAAACCGA TTGCTTTTTA GAGCCTGATT	2700
TGCAGCCATT CCTTGCCTCA AAGAGGCTGT TTTTCTTTC CCTGAAGAAG ATAAAATTGC	2760
AAGCTCTTGC TCATTTGGAC GCTTAATGAA TTGTGAAGCT AGGAGCATGA TAATAAAGTA	2820
ACTTGCTCCT AAAATATAAA AAGTTTCTAC AAGCCCTACC CCTGCGATGA GGTGTTGCGC	2880
TATGGGACTA GTCAATAAAG AAGCAAAACC AAACCCATA ATCGCTAAAC CTGTTGCGAG	2940
ACCACGTTTA TCAGGAAACC ATTTTATAAT CGTCGACACA GGGGTAATAT AGCCTGCTCC	3000
CAAACCAAGC CCACCTAAAA TGCCATAAGC GAGATACAAC AACCACAGCT CTGACGGTCT	3060
ATTGCAAATC CTGTTAAGAT ATTTCCACCT GCGTATAGAA AAGCAGATAG ACTTCCCATG	3120
ACTTTCGGAC CAAATTTTTC TACCAAACGC CCCATAAATG CAGCCGATAA GCCCAAACAA	3180
AAGATTGCTA GACTAAAGGC GAAGGCAACA GAAGCCTGAT CCCATCCCGT	3230

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5096 base-pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CCTATGAAGA CTGTCCCAAC TGGGTGTCCT TCTAGGCTAT CTGGTCCTGC CACTCCAGTC	60
AAACTAATTC CAAAATCAGA CTGGGTCTTG CTTCGTGCCT GCTCAGCCAT CTTCTGAGCT	120
GTAAATTCAG ACACCACACC ATGTTCTTCC AAATTCCTGG CAGGAATATC CAACATCCTT	180
GATTTTTCCT CCAAGCTATA GGTCAAAAA CCACCTTAA ATATACTTGA AACTCCAGAA	240
AAATTCGCCA CGGTAGCTTG GAAAAGACCT GCCGTCAAAC TCTCTGCAGC CGCGATGGTT	300
TTCCCTTGCC TTTTCAGTTC TTCTACCACA ATGCTGGCTA AACTAGTTTC TTCCCCATAA	360
CCATAGCAAA AGTCTCGTAA AGAAATTCCT TCGAAAGTCT GGCAGTCCAA GATTTGATTT	420

1187

TCCAAGATAT CCAGCGCTTG ATTGCCTCT TCTTGACTGC TAGCCTTTGT TGACAGACGT	480
AGAGTGACTT CTCCTGTCTT GGCATAAGGG GCCAAGGTAG GATCGATCTG ATTATCAATT	540
AAATCAGCCA AAATCGTAAC CAACTGGCTC TCGCCAATCC CAAAGAAACG AAGAACTCGG	600
GAATACAGCT TGCTCCCTGT CATCAACTTG GGTAGAAGTT GGTTTAAGAC CATGGGTTTC	660
AATTCACTTG GCGGACCTGG AAGGACGACA TAGGTCACTC CGTCTACTTC TAATTTTCCT	720
CCAACAGCCA GTCCTGTTTC GTTGGCAGT GGAATCGCTC CTTCTACAAT TTGAGCTTGT	780
CTTTCGTTAT TCGGTGTTTC GGCATAGTCT GGTGCGAGGG TAAAAAAGAT ATCCAACTTC	840
TCCTGAGCCT GAGGATCAAA GACTAATGCT TTCCCTAAAA ATTTAGCTAG GGTTCGTTTG	900
GTTAGGTCGT CCTCAGTTGG CCCCAAACCG CCTGTCAAAA TCACCAGACT GCTACGTTGA	960
CTGGCAATCT CAAGCAAAGA CAAGAGACGA ACTTCATTGT CTCCTACAGC CGTCTGAAAA	1020
TATACATCTA CCCCAATCTC AGCTAGTTTT TCCGACAAAA ACTGGGCATT GTGTTGACA	1080
ATCTGCCCTG TCAAAATCTC TGTTCCAACA GCAATGATTT CTGCTTTCAT GTTTCCTCCT	1140
ACCTATCTAT TCGTATTTTT TTGAAAAAAT CGCAGGAATT TTCCTACGAT TGATTTTTTT	1200
ATTTGTATCA AAAGTTAATT ATCTTCATCA CCAACAGGTG CTCTGCCAAA TAAATCTTCA	1260
AATAAAACCG CATGCTTTC AAGCTGAGTA ACTTCTTCTT GTCCCAAAGA ACGTCGGAGT	1320
AGATTTTGCA TTTCCAACAT ATGTGCTCTC GAAACAATCT GGTAAGAAAC ACCTTGAAGT	1380
ATCTCTCCTT CACCCTGCAA CTGCTGAGTT TCAATGGTTT TAAATGAATC TTTATAGCCT	1440
AGCAAGTTAG GGATACTTTT TGCAGACAAA TCAATATTGG TCTGCATATT GTCACCTCAA	1500
GCTTTTAGAA TCTCTTGATA ATGACCAATG CTATTTAAAC TGAGAGCTTT TTCCATGACT	1560
TTTTGAATAA CTTACGTTG ACGTTTTTGA CGACCATAAT CCCCCTCAGG ATCTTGGTAA	1620
CGCATTCGTG CATAGACTAG GGCTTCTTCT CCCCCAATAT GTTGCTCCCC AACACCGATA	1680
GAAATAGTAT TAAATCTTC TTGGTCACTG ATAGAAATTG GGAAACCTAG GATATTATTG	1740
ACTGTAATAC CTCCTACTGC ATCCACTAGT TTTTGCAATC CTCTCATATT GACCATCACA	1800
TAGCGATCAA TATGGATATT CATCATTTTT TGAATGGTTT CTATAGCAAG CTCTGCTCCA	1860
CCATCTGCAT ATGCTGAGTT CAGTTTCGCT TCATGAGCCT GACCATTCCC TGATTCAATG	1920
CGCGTCAGAA TATCCCGCTC TAACTCATC ATTGTTGTTT TTTTCGTTTT AGGATTCACT	1980
GTCATCAAGA TCATGCTATC ACTTCTACCG ACCCAAGTTT CAGTTCGTTT AACATTTCCG	2040
GTGTCCACTC CCATTAACAG AATGGTTAGA GGTTCAGTCG CTTCAATAAC CTTGGTTTCT	2100
TCACCGATTT TTTTATAGGT TTTAGCTAAG GTTCTGTCC CTTGTTGATA AATAGTATAA	2160

1188

GCAAAAACAC	CTACTCCTAC	TACAGTTACA	GAAAGTAAAG	CTAGCACCAT	TCCAATAATT	2220
TTTTTAACCA	TATTTCTACT	AACCTATCAG	TTTACCCATC	AAGTAAACAT	CGATAAATTT	2280
CCCTTCTTCT	ATATATGCCC	CACGCTCTTG	GCTACCTTCA	ATGACAAAGC	CATGCTTTTG	2340
ATAAAGATCG	ACTGCTGCTT	GATTACGAGT	TTGGACAGTC	AGTTGGAGAC	GACGCAGAAT	2400
GCCACTTGCT	TGTGCCCCACT	CTATCGCTTC	TTCTAGCAAC	AACTTCCCA	AGCCATTATT	2460
CCAATATCTT	TTTCCAATCA	CAATGAAGAG	ATCTCCAATA	TGACGGACTC	TCTTACGCTG	2520
ATCAGCTGTA	ATATTTACAA	TACCAGCAAT	TTTGCCATTT	AAGAATGCAA	GTAAGGTTAT	2580
CTGATTGTCC	GAAGTAGCTT	GCTTGTGAG	GAATATTTCC	ATCTCCTCAC	TAGTCAAGAG	2640
AATACCATCT	CCGTCTAGGC	TGGTAAAGTC	TGTCTCCAAA	CTCACACGAT	TTAAAAAGGC	2700
CACTAATTCA	GCTGCATCTT	TGGGCTCTGC	TTCCCTAATG	AGCAATTCAT	ACTCCATATT	2760
GAAGCTCCTC	TAACAATTTT	TCAGCACGCA	AACCTTTTGC	CTGAAAATTT	AAACGGCGTC	2820
CATCTGCTTC	TTTTAGAATT	TCCAATTCTA	AATAAGCATC	TGGCAAGGCA	TCTCCTAAGA	2880
GATTTCCCCA	CTCAATAACA	GTCACGCCGC	CACCAAAGAT	AACTCATCC	AAGTCGATAG	2940
AATCAGCATC	TCCTTCAATA	CGATAAACAT	CTAGGTGATA	AAGTGGAAGT	CGACCTTCAT	3000
ACTCTCTCAC	GATAGTATAG	GTGGGACTTT	TAATCATTTG	AGAAATCTGT	AATCCTTTTG	3060
CAAGTCCTTT	AGTAAAGGTC	GTTTTACCTG	CACCCAGTTC	TCCAGTTAAG	ATTAAAACAT	3120
CATTCTTTGC	TAATAGATGG	CCCAAACGCT	CCCCTAAGGC	TTGCAACTCT	TCTTCATTTT	3180
TTGTGTACAT	ACTCTTATTA	TACCAAAAAC	TTTCTTTTGT	TGTCTATTTT	CCTACTAAAC	3240
TTATCATCAT	AACATCCATA	AAAAACAGGC	TTTCTCTAAA	AGAAAATGAG	CGTAACAATG	3300
ACCAATACAA	GATCTCGGAA	AATATGACCA	TAAAAGGAAA	CTTCCTTCTT	AACCGAATTT	3360
GGGACAAGAT	AGGCTGCAAA	AAACAAGCCC	AGTCCAATAT	AAATCAGAAG	TGAGACAATG	3420
GTCATTGGAT	TTCTTAAGAA	AAGAAGTGTT	GCTAAAATAG	TCACCAACAC	TGTCTTTTTT	3480
CTGTCCAGCA	TAGCAAGAAA	ATCGCGCACG	TATTTTTCAT	AGGGTAAAAA	AATCAGCAAA	3540
TCTAGCCCAA	ATAGGAAAAA	GAAGGATGGC	AATAAAAAGT	CAACTAATTC	TTGCTGCAGC	3600
GTATTTTGA	TGAACAAGTT	ATCTGACAAA	ACAAGAACAG	CTCCTAACAA	ATTAATTAAG	3660
AGTAACATAC	TGTAAAAAAG	CTTCACCGAC	TTCTTACTGG	CTAGGACACT	ATGGACTTCT	3720
TGCTTACGGG	TATAAAGATA	ATTTACTCCA	GCACAGATTC	CTGAAACGAA	AACCATGCTT	3780
CCGATGAAAA	AAGCTGTACT	TTGTTTAAAG	GACAAGATGC	ATTCCTTCCA	TAGGAAACAG	3840
CTACTCAAAC	TGATTTGAAT	TAAAGCTAAC	AAAAATAAGA	TTCTCATTTA	TTTCATCTTC	3900
TCTCTCCCTT	CCTACCAATC	ATTATACTAG	GAGAAAAGAG	AGAACTGTTT	CTAATCTTCT	3960



1189

CAAATGTCTC TTAAAGACGC TAAACAAACA CTAGAGACTA ATACTCAATG AAAATCAAAG	4020
ATCAAAC TAG GTAGCTAGCC ACAGGTGCT CAAAACAGTG TTTTGAGATT GCAGATAGAG	4080
CTGACGTGAT TTGAAGAGAT TTTCGAAGAA TATAAATTTG AAATCATGAA AATCCGTCAA	4140
ACGGGTGGTT GTTTTGTCTC GCACCTCACG GAGCGAGACG GACTCAGAGT CACATAATTA	4200
TAAGGCTGAT AGTATTAATC TAACTATCAG CcTmCAGGTT ATTTAACGTT TCAGAAAAAC	4260
TATAATGTCA AGATTAACTA AACAGTATCT AGTTCCTTCA AATAATTTTC TATCTTCATC	4320
AACATTAAAG GATTGTTATA AATCTTACAT AACTCTCTTG CTTCTATATA ATAATTTTTC	4380
ACTTGTTCTC TGTCTAGAAA TTGGGCTCCA GCATTTCTTA CAAGAATAAG TAGAGGAGCC	4440
AATTGGTAGC TTGCTGTCTT TTGTTTACAG AGTTCAATCG TTTCAAGAGC TTCTTGGATG	4500
GCTTCATTAT ATTTTCTCTT TGATACTAGG TAGTGAGCGT AGTTGTAACG AACTCTGATG	4560
TAGCCAAATA AAAACTCTTG ATGGTCCAAA TTTTTGTCT GATACAACTC TATTAAATGA	4620
GAGTAGTTTG CCTCATATTC TTGTTACGA CCCACTAAGG AATAGAAAT AGATAGAGTA	4680
TTCAACGCCT TTAATAAAT CAGAGTATTT GAAGAGACTT TTAATAATAT ATTTTCCAAT	4740
GACGAAATG CCTCACACTT ACTGTCATAT TGATAGAAGT CAATTATAGA TTTAATCCAT	4800
TCAAGGTAAG TTCGGTCTTC TAATGTTAGA AAAGTGCTTC GTTCTACTTC TATTTTATAA	4860
AGATATTCTA AATCGTCATA ATTTCTGTCA TCTAATAGGC GAGCAGATAG ATGTTTGAAA	4920
TTAGAGAGGT TAGACTTAAC TTCGATTTGT TCATTGAAAA AGTAATCCAA AGGGACTTCA	4980
AGTCGTTGAG AGAGTTTGAA TAACAAGTCT GCGGAGGGAA TAAATGACC TCTTTCAATT	5040
TTACTAATCT GGCTTTGTTT ACAAATTCCT TCTGCAAGAG TTTGTTGGGA GAGTCT	5096

## (2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ACAAGATAAA AATAAAGGAT TACAATGGGG AATATAAAGT AAACCGGTAA ACCTAAAAAG	60
AAAGGAGAAA AGATGAAAAT TGTACTTGTA GGGCATGGAC ATTTTGCTAC AGGGATTAT	120
AGTTCTTTAC AATTGATTGC AGGTAATCAA GAAAATGTGG AGGCGATTGA CTTTGTGGAA	180
GGAATGTCAG CAGATGAACT CAAGCAAAAA ATCTTACTTG CAATTTCAA TGAAGAAGAA	240

1190

GTTTTAATCC TAAGTGATCT CTTGGGAGGA TCGCCATTCA AGGTTTCTTC TACCATAATG	300
GGAGAAAATC CAGCCAAGAC AATGAATGTT CTCTCGGGTT TGAACCTAGC CATGTTAATG	360
GAAGCAGTCT TTGCTAGAAT GGCTCATAGC TTTGATGAGG TTGTTAATAA ATCAGTAGTG	420
GCGGCCCAGG GCGGAGTCGT AAATGGTAAA GAATTGTTTT CAACGGATGC AGAGGAAGAG	480
GAAGAAGATT TCGAATCGGG TATTTAAAGG GTAAAAGAAT GATAAAAAAG GTTACGATTG	540
AAAAAATAAA ATCGCCTGAG CGCTTCTTAG AAGTACCACT TCTGACGAAA GAAGAAGTCG	600
GCCAGGCAAT CGATAAGGTT ATTCGGCAGT TAGAACTCAA CCTTGACTAT TTCAAGGAAG	660
ATTTCCCGAC GCCAGCTACC TTTGATAATG TCTATCCAAT CATGGATAAC ACGGAATGGA	720
CCAATGGTTT CTGGACAGGA GAACTGTGGT TGGCTTATGA ATACAGTCAA CAGGATGCAT	780
TTAAAAACAT CGCTCATAAA AATGTTCTTT CTFTCCTGGA TCGTGTCAAT AAGAGAGTAG	840
AATTGGATCA CCATGATCTC GGCTTCTTGT ACACACCGTC TTGTATGGCT GAATATAAGA	900
TAAATGGAGA TGGAGAGGCT AGAGAAGCAA CCTTGAAAGC TGCAGATAAG TTGATTGAAC	960
GCTATCAAGA AAAAGGTGGT TTTATTCAAG CTTGGGGAGA CTTGGGCAAG AAAGAGCATT	1020
ACCGTTTGAT TATCGACTGC TTGCTCAATA TCCAACCTCT ATTCTTTGCT TATCAAGAAA	1080
CAGGCGATCA AAAATACTAC GATATTGCAG AAAGCCATTT CTATGCTTCA GCTAATAATG	1140
TAATCCGTGA TGACGCTTCG TCCTTCCACA CCTTCTATTT TGATCCTGAG ACAGGTCAAC	1200
CCTTTAAAGG TGTAACGAGA CAAGGGTATA GTGATGATTC ATGCTGGGCA CGTGGTCAAT	1260
CATGGGGAGT CTATGGTATT CCTTGACTT ATCGTCACTT AAAAGACGAG TCCTGCTTTG	1320
ACTTGTTTAA GGGTGTGACC AATTATTTCT TGAATCGTCT GCCAAAAGAT CATGTGTCCT	1380
ATTGGGATTT GATTTTAAAT GATGGTAGTG ATCAATCACG AGATTCTTCA GCAACAGCTA	1440
TCGCCGTCTG TGGGATTCAT GAAATGCTAA AACATCTCCC AGAGGTGGAT GCTGACAAAG	1500
ATATTTATAA ACATGCTATG CATGCCATGC TTCGTTCTT GATCGAACAT TATGCAAATG	1560
ATCAATTTAC CCCTGGTGGG ACAAGTCTCC TCCACGGTGT GTACTCATGG CATTCAAGTA	1620
AAGGAGTGA TGAAGGCAAT ATCTGGGGTG ACTACTATTA CCTAGAAGCC CTTATCCGTT	1680
TCTACAAAGA CTGGAACCTA TATTGGTAGG AGGAGAAATA TGACAATGCC AAATATTATT	1740
ATGACCCGTA TCGATGAACG GTTGATTCAT GGACAAGGAC AACTTTGGGT AAAATACCTA	1800
GGTTGTAATA CGGTCATTGT TGCCAATGAC GAAGTAAGCA CGGACAAGAT GCAACAACT	1860
CTGATGAAAA CAGTTGTGCC AGACTCAGTT GCCATGCGTT TCTTCCCTTT GCAAAAGGTG	1920
ATTGATATCA TTCACAAGGC TAATCCTGCT CAAACGATCT TTATCGTTGT AAAGGATGTG	1980
AAGGACGCTT TAACCTTGGT AGAAGGTGGT GTCATATCA AAGAAATCAA TATTGGGAAC	2040

1191

ATTCACAATG CCCCTGGTAA AGAGCAAGTG ACACGCTCCA TCTTCCTGGG TGAAGAGGAC	2100
AAGGCGGCCC TCAAGGAATT GAGCCAACT CATCAAGTAA CATTTAATAC GAAAACAACT	2160
CCAACAGGAA ATGATGGAGC TGTTCAGTC AACATTATGG ACTATATTTA ACAGAGGAGA	2220
TCGTTATGTC GATTAATGTA TTTCAAGCGA TTTTAATTGG ATTATGGACA GCTTCTGT	2280
TTAGTGAAT GCTGTTAGGA ATTTACACCA ATAGATGTAT TGTTCGTCA TTTGGTGTG	2340
GAATTATTCT AGGTGATCTG TCATGCTCTT GCAATGGGAG CCAATGGTGA ATTGG	2395

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCTTCTTTAG AGGTAAATTT TGCAAAATCG TCGATTGTTA TATAAGGATT ATTATAGAGA	60
CTGTTGCGAA AGAATCTCTG ATATGTTTTT GAATCTTTTG AATACAAAAC TATCTCTCTA	120
ATAGCATTGC CATCTGTTCC ATCAATTGGT AAACATACCG TAACTAGAAA AAGAATTATA	180
TTCAAAATAA AAAATTCTGA TCGGTACGGC ACAAATCCCA AAAGTGCTAA TATTGCGACA	240
ATTAGGTTAG CTCCACCTCC CCCAAAGAAG TAGAACACCA AATTCCTATC ACTATTTTTT	300
TCATTAGTAA TGTTCTATT ACTCATTTGA CAATAACCGA ATGCTAATAA CACTGGAAAT	360
TTGAAATATA TTTTTTTTCT GAAATAGAAG AAAAAGGGAG TAGCAAGCAT CTCTAGTTTA	420
TAAGATAAAC ATCTTCCCAC TAAAAAATGA CCTAGTTCAT GTAATGTAAT TGATATTAAC	480
GAAATTAAAA TCAATCGAAA ATAATAGATT AATGAATCAT TTGGAAAAAT TATCAATAAT	540
AGGAACAATA ACGGAATCAA ACATAAATAT ATGACAGAGT TATTTAATAT TTTCAACATA	600
ATACCATTC TCTAACTAT TAGCTTCAA AAGGCGTTTT TTCTCCCAAT ACATCTTCTC	660
AAAATGTTG GAATCATAAT TTTCTAAAAT TAATTTTATG TCTGGTAAGC TCTTTCTTGA	720
TAATCCGTTG TTTGTACTT AATTTTCCCT TCAAGTACAT CTTCAATTTT ATAAGTTGCC	780
TCCATCAACT GAGCCTCTGC AATATCTTTG AGTGAATTGG TAATTGAAAC TTGGTGTAAT	840
ATCTGTCCtS CCATATATGA AAATATATCT CTAAGATATT CTGACACATT ATCAGAGCCG	900
TTACTCTCAG CAACATCTAA TGTTACAACA AACTTTCCAG CTAATCGAAA AAGATGGCTC	960
CACCCCCCAA TCCTTTCAAT AAAGTTTTTT GTGTCCACAG ATACGTTTTG TAAATATACA	1020

1192

GGAGAAGAGA TAATTATAAT ATCAGACTCT AATAACTCTT TTTTATAAC ACCTCCATCA	1080
TCAGCATTAC TTGCGCTATC AATTCCTTTC TTAAACAACT CTTCTGAATC AGAATTAGAT	1140
ATTTCTAGCT CTGAATTGAA AGGTGTCCTG AAAGATATAT CAACATTATT TCTACTAGAA	1200
ATGATACTTG AAAGTCTCTT AGTATACTCT AAAGTCTTAG AGTTATGATT TCGCACTCCT	1260
GCATATATAA ATATTTTATT CATTTTAATT CATCCTCTCA ATTTGAATTT AGTAGATTTT	1320
TCAAGATAGT ATGGTACAAA AACAGACTTT TGTGACTCA CATTATTACA TATGTTTTGT	1380
ATTAAACCAA AATCAATACT ATTTTGGAG TAATTTTGAT TTTAGTTTAA AATCATTCT	1440
ATAACAGTAG CATATACCTC AAGCCGTTTA GCAATTAGAA TAGAACTTTT CTTTATTATA	1500
TTATTATCTC AACGAAAAGC TACACTATTA AAAATATTTT ATAGAATTAC ATATTAACT	1560
AGTCAATCTT GGTATTTTAA TATTGCTTAA TGAGTGGACA CCTCTATTTT AGAAACAAA	1620
CTATAAATTA AGCTAGATTT CAAGTAATGA GGGGATAACT ATCTTTTTGT CATCTGATT	1680
CAGTGCGATA TACCTTAAAA AAGTATAAGC AATACCAGTC ACACCTGTAT ACAAAGAAAA	1740
ATCTGGGAAA TTGCTTGTTT GGACGATACG ATACTCTCCT TCTTTTGATT TATTCATTAC	1800
AACACTACAC AATAAAGACT CCAATTCCAT ACTAGTATCC ATTTCTTTCA TGTAGTCGAT	1860
GTAAAAATTT ATTATGGCCA TACTTCCATG GCAAAATGTA TCATTATCTA AACTAGCTAC	1920
AATTCCTCTT GGAACACTTT GGGGATGATT AACTAATGTC CCAAATCTC CACTACACCA	1980
CTTCAAAGAA TGAATTTTGA TTTCTCCCT AGGAACTAGT TGTAATAATTA ATTCTTTATA	2040
TTTTTTAAGT CTTGTCACTT TATAAATATT TTTTAATGTA AAAATTACAC CTGATAGTCC	2100
ATGGCCAAAA CTATATCCAA AATTACTATT ATCTCTCTCG CTTACATCAT TATATAGCGT	2160
ATCACCTAAA CTTAATACTA GCCTTAGAAC ACGTTCCTTC TCTATTCTC TCCTATAATA	2220
TCTTACCAGT GTATTAATTA AAGGTAGAAG ACCATTAATA TAGTCAGACT TGTGTGAAAC	2280
ACTTGCAAAA TCAGTCTTTT CAAGCTCAGT TAAAACACTC TTTATATAAT TTAAGCATGC	2340
GAGAGTATTT GTATCGTAAT CCTCTATAAT GGATAGAACA ATGAAATATC CTATATCCCC	2400
AGTTAAACCA AATGTGGTCT TAGATAAAGA AACAGATGGC GGAATTGCAG ATAACATTTT	2460
ATTGTACAGT TGAGTATATG ATGATTTATC TTTCAATAAT TTTACATAGT ACATAAACAG	2520
TAATATTCCA GCTCTACCCC TATACATATC ATTTCCCGTT TGTTCAGAC ACCATTTAGA	2580
ACCTTTAAAA TTAACAGGTA TACTCCAAAT TGGATATTCG TCATAAATAT TATTAATAAC	2640
CAAAGAGTCT GCAATATTTT CTACTTCATT ATGCAGAATA GTAACATAAC TTTCAATTGG	2700
GAGTTTTTTT CTATTAGATA AGTTTAATTT ATATCCTTTT TTTCGCTGAT CAAAGCTTGG	2760
AAAATAAATT TCAATGATAT CAAGTTGCTT TTCTAAATTT TCCAAATTAT TATTAGGTAA	2820

1193

ATATTTTCATA AAATAGTCAT ATCCAGAAAA TTGATGTAGG GAAATAAAAT GATTTCCAAA	2880
ATCATCGTAG ATTCATTGA TATTTGTATC TGTATAAAAA ATCGGAATAT CTAATAACCT	2940
CATTTGTTCA CATTGCTTG CTACAATACC TTGATTAGAA AACTTATTGC TCCAGAGATT	3000
TTCCAATGCT TTTTCTCTAT CTAACATTTT TCATAAAAA TCAGGATGAT ATAAAAAGA	3060
TAGTACTGAA GCATAGCTAT TTGTGTCTCT AAAAAGTACC CTTGTCTTTA AACCATACAA	3120
GTTTGCTTTT AATAGCATTT TAAATCTTTC TGTTTTATTT AACTCTTCAA ATATCAGATA	3180
AAAATCCCTA AAACCTTTTT TGAAATCTTT TATATACTTA TCAAATCTA TATCACCATC	3240
CCGAACAGGC AGGTTTTTCC CACCTTCAA ATCAATTTTC CCAATATCAA ACTTTACCTT	3300
ATCAGTATTT AAATTAATTA AACTTGACC AGGGATCCTC TA	3342

## (2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GAGAAAAGAA TGTAAAGAA AAATGATATT GTAGAAGTTG AAATTGTTGA TTTGACCCAT	60
GAAGGGGCAG GAGTTGCCAA GGTAGATGGT TTGGTCTTTT TTGTAGAGAA TGCTTTACCG	120
AGTGAAAAAA TTCTCATGCG TGTCTCAAG GTCAATAAAA AGATTGGCTT TGGAAAAGTT	180
GAAAAATACC TTGTCCAGTC ACCACACCGT AATCAAGATC TAGATTGGC TTACCTGCGT	240
TCAGGAATCG CGGATTTAGG ACACCTTTCT TATCCAGAAC AGCTCAAGTT TAAAACCAAG	300
CAAGTCAAGG ACAGTCTCTA CAAGATTGCT GGAATTGCAG ATGTAGAAGT TGCTGAAACG	360
CTTGGTATGG AACATCCAGT CAAGTATCGC AATAAGGCGC AGGTGCCCCG TCGTCGAGTG	420
AATGGTGTCT TGGAAACAGG ATTTTCCGT AAGAATTCGC ATAACCTCAT GCCCCTTGAA	480
GATTTCTTTA TCCAGGATCC TGTCATTGAC CAAGTCGTAG TAGCTCTTCG AGACCTGCTC	540
CGTCGTTTTG ATTTAAAACC TTATGACGAA AAGGAACAGT CTGGATTGAT TCGGAATCTT	600
GTGGTGCGTC GTGGTCACTA TTCAGGACAA ATCATGGTCG TTTTGGTGAC AACTCGTCCA	660
AAAGTTTTTC GTGTTGACCA ATTGATTGAA CAAGTTATCA AGCAGTTCCC AGAGATTGTG	720
TCTGTCATGC AAAATATCAA CGACCAGAAT ACCAATGCGA TTTTGGTAA GGAGTGGCGC	780
ACTCTTTATG GTCAAGACTA TATTACGGAC CAGATGTTGG GAAATGACTT CCAAATCGCT	840

1194

GGCCCAGCCT TTTACCAAGT CAATACTGAA ATGGCGGAGA AACTCTATCA AACAGCCATT	900
GACTTTGCAG AGTTAAAAAA AGATGATGTG ATTATTGATG CCTATTCTGG TATTGGAACC	960
ATTGGTTTAT CAGTCGCCAA GCATGTCAAA GAAGTCTACG GTGTTGAACT GATTCCAGAA	1020
GCAGTAGAGA ATAGCCAGAA GAATGCTTCT TTGAACAAGA TTAATAATGC CCACTATGTC	1080
TGTGACACGG CTGAAAATGC CATGAAGAAA TGGCTCAAGG AAGGTATTCA ACCAACCGTT	1140
ATCTTGTTG ATCCTCCACG CAAGGGCTTG ACAGAAAGCT TTATCAAAGC AAGCGCCCAA	1200
ACAGGAGCCG ATCGCATCGC CTATATCTCC TGCAATGTCT CAACCATGGC GCGTGATATT	1260
AACTATACC AAGAGTTGGG ATATGAATTG AAGAAAGTCC AGCCGGTGGA TCTATTTCTT	1320
CAAACGCATC ACGTCGAGAC GGTAGCACTT TTGTCCAAAC TCGATGTCGA TAAGCACATA	1380
AGTGTTGAAA TTGAGCTGGA TGAGATGGAT TTGACAAGTG CGGAGAGCAA AGCAACATAT	1440
GCTCAAATCA AAGAATATGT TTGGAATAAA TTTGAATTAA AAGTTTCGAC ATTATATATT	1500
GCACAGATAA AAAAGAAATG TGAATAGAA TTACGAGAAC ATTACAACAA GTCTAAAAAG	1560
GATAAACAAA TTATTCCACA GTGTACACCT GAAAAAGAAG AAGCCATCAT GGATGCTTTG	1620
AGACACTTCA AAATGATTTA ATAGAAAAGA ATGACAGTAT ATGACTTTCT GCATTTATTA	1680
CATTCTACT TGGTATAGGA ACAGCTATTA TTCCTTTCTT GCAAGGTATC AATTAGAAAA	1740
TAGGCTCAAT ATAAAGATTG ATAGGATCAT TTTTATATTT AAAGGAGCGT TGAAATGATT	1800
GATAAAGGCA ACAAAAAATT TTAGGATAAA TTTGCTAAGT TGTATGCCTC TTTTATGAAA	1860
AAAGATAAAG AGGTTTATGA TAAAGTTTGT GAATATCTTA GTCCTCATTT GAATAAAGAT	1920
ATGGAGGTGC TTGAACTTGC TTGTTGGTTT CGTGTCTATA CAGTTATAGA GGCAAATAGT	1980
TATGTAAATA TAAGGAGTTC AAGACTTCTA CCAAAGTTTA AACTCAAAA AATAAATAGT	2040
TGGTGTGCTG CTTACAATAT CCATTTTAAT AATGGATATT GTAAGCAGCA CCCCcAtGAA	2100
TTTAAAGATT CTTTAAAGAG TCTTATTTTG TGATGAAAAT TTAATATGTA AATCTCAGAC	2160
GATAGAAATT AAAAATCTTA TCGTCTTTTT TATACTCAAA ATTAGGAGGT AAAAATGGTA	2220
AGGATAAGAG GTCCCACTTA AAACAATTTA TGGCAAAATA AGGACGGAAT AACACAACAA	2280
ATTCTCTAAA ACAAATCACT AAATCAATGT AAGATTGAAT GAAATCAATA TTTATGCTAT	2340
AATTAAATAA ATTTAATGAA GAAAAAAGA GGGATATTAT GGCACCTAAC TATAAACCAT	2400
TATGGATACA GTTAGCAAAA AAAGGACTAA AGAAAACAGA TGTAATAGCT ATGGCAGGAC	2460
TTACAACAAA TGTTATGGCA CAAATGGGAA AGGATAAACC AATTACATTT AAGAATTTAG	2520
AAAGAATATG TAAGGCTTTA TCTTGCACTC CTAATGATAT TATTAGTTTT GAAGATAATT	2580
TTAGTGACGA GGAATAGAAA ATGACTTTAA GGACAGAAGA TCAAGTTAGG GATTATGCAA	2640

1195

GAGAAGTATA GGCTTTAATG AAGTTGAAGA AAACATCAAT CAAGGTACTG GTCAAATAAC	2700
TACTTTTAAT CAATTAGGCT TCAAGGGATA TTCAAATAAG CCAGATGGTT GGTATTTACC	2760
TAAAAATATG AATGATGTAG CAATAATCCT TGAAACAAAA TCAGAAGAAA GAGATATTAG	2820
CAAACAAATT TTTATTGATG AGTTAATGAA AAATATAGAC ATAATTTAAC TAAAAATAAA	2880
AACTAGATCC TTTTTTGAAA AAATTATATT ATTAAATTTG TAACTGTATC TATTGACAAT	2940
GATAATTATT ATCGATACAA TAGACTTGAA ATATGTTTAA GGAGTTTTTA TGAAAaCAAA	3000
TTTTTTCTAA TmGCTATTTT AGCTATGTGT ATAGTTTTTA GCGCTTGTTT TTCTAATTCT	3060
GTAAAAATG AAGAAAATAC TTCTAAAGAG CATGCGCCTG ATAAAATAGT TTTAGATCAT	3120
GCTTTCGGTC AAACATATATT AGATAAAAAA CCTGAAAGAG TTGCAACTAT TGCTTGGGGA	3180
AATCATGATG TAGCATTAGC TTTAGGAATA GTTCCTGTTG GATTTTCAAA AGCAAATTAC	3240
GGTGTAAGTG CTGATAAAGG AGTTTTACCA TGGACAGAAG AAAAAATCAA AGAACTAAAT	3300
GGTAAAGCTA ACCTATTTGA CGATTTGGAT GGACTTAACT TTGAAGCAAT ATCAAATTCT	3360
AAACCAGATG TTATCTTAGC AGGTTATTCT GGTATAACTA AAGAAGATTA TGACACTCTA	3420
TCAAAAATTG CTCCTGTAGC AGCATACAAA TCTG	3454

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3752 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CGGGAGTATA CTTAATATAA TTATAGTCTA AAAATGACTA TCAGAAAAGA GGTAATTTA	60
GATGAATAAG AAAAAAATGA TTTTAACAAG TCTAGCCAGC GTCGCTATCT TAGGGGCTGG	120
TTTTGTTACG TCTCAGCCTA CTTTGTGAAG AGCAGAAGAA TCTCCAQAAG TTGTCGAAAA	180
ATCTTCATTA GAGAAGAAAT ATGAGGAAGC AAAAGCAAAA GCTGATACTG CCAAGAAAGA	240
TTACGAAACG GCTAAAAAGA AAGCAGAAGA CGCTCAGAAA AAGTATGAAG ATGATCAGAA	300
GAGAACTGAG GAGAAAGCTC GAAAAGAAGC AGAAGCATCT CAAAAATTGA ATGATGTGGC	360
GCTTGTTGTT CAAAATGCAT ATAAAGAGTA CCGAGAAGTT CAAAATCAAC GTAGTAAATA	420
TAAATCTGAC GCTGAATATC AGAAAAAATT AACAGAGGTC GACTCTAAAA TAGAGAAGGC	480
TAGGAAAGAG CAACAGGACT TGCAAAATAA ATTTAATGAA GTAAGAGCAG TTGTAGTTCC	540

1196

TGAACCAAAT GCGTTGGCTG AGACTAAGAA AAAAGCAGAA GAAGCTAAAG CAGAAGAAAA	600
AGTAGCTAAG AGAAAATATG ATTATGCAAC TCTAAAGGTA GCACTAGCGA AGAAAGAAGT	660
AGAGGCTAAG GAACTTGAAA TTGAAAAACT TCAATATGAA ATTTCTACTT TGGAACAAGA	720
AGTTGCTACT GCTCAACATC AAGTAGATAA TTTGAAAAAA CTTCTTGCTG GTGCGGATCC	780
TGATGATGGC ACAGAAGTTA TAGAAGCTAA ATTAAAAAAA GGAGAAGCTG AGCTAAACGC	840
TAAACAAGCT GAGTTAGCAA AAAAACAAAC AGAACTTGAA AAACCTTCTG ACAGCCTTGA	900
TCCTGAAGGT AAGACTCAGG ATGAATTAGA TAAAGAAGCA GAAGAAGCTG AGTTGGATAA	960
AAAAGCTGAT GAACTTCAAA ATAAAGTTGC TGATTTAGAA AAAGAAATTA GTAACCTTGA	1020
AATATTACTT GGAGGGGCTG ATCCTGAAGA TGATACTGCT GCTCTTCAAA ATAAATTAGC	1080
TGCTAAAAAA GCTGAGTTAG CAAAAAACA AACAGAACTT GAAAAACTTC TTGACAGCCT	1140
TGATCCTGAA GGTAAGACTC AGGATGAATT AGATAAGAA GCAGAAGAAG CTGAGTTGGA	1200
TAAAAAAGCT GATGAACTTC AAAATAAGT TGCTGATTTA GAAAAAGAAA TTAGTAACCT	1260
TGAAATATTA CTTGGAGGGG CTGATTCTGA AGATGATACT GCTGCTCTTC AAAATAAATT	1320
AGCTACTAAA AAAGCTGAAT TGGAAAAAC TCAAAAAGAA TTAGATGCAG CTCTTAATGA	1380
GTTAGGCCCT GATGGAGATG AAGAAGAAAC TCCAGCGCCG GCTCCTCAAC CAGAGCAACC	1440
AGCTCCTGCA CCAAAACCAG AGCAACCAGC TCCAGCTCCA AAACCAGAGC AACCAGCTCC	1500
TGCACCAAAA CCAGAGCAAC CAGCTCCAGC TCCAAAACCA GAGCAACCAG CTCCAGCTCC	1560
AAAACCAGAG CAACCAGCTA AGCCGGAGAA ACCAGCTGAA GAGCCTACTC AACCAGAAAA	1620
ACCAGCCACT CCAAAAACAG GCTGGAACA AGAAAACGGT ATGTGGTATT TCTACAATAC	1680
TGATGGTTCA ATGGCAATAG GTTGGCTCCA AAACAACGGT TCATGGTACT ACCTAAACGC	1740
TAACGGCGCT ATGGCAACAG GTTGGGTGAA AGATGGAGAT ACCTGGTACT ATCTTGAAGC	1800
ATCAGGTGCT ATGAAAGCAA GCCAATGGTT CAAAGTATCA GATAAATGGT ACTATGTCAA	1860
CAGCAATGGC GCTATGGCGA CAGGCTGGCT CCAATACAAT GGCTCATGGT ACTACCTCAA	1920
CGCTAATGGT GATATGGCGA CAGGATGGCT CCAATACAAC GTTCATGGT ATTACCTCAA	1980
CGCTAATGGT GATATGGCGA CAGGATGGGC TAAAGTCAAC GTTCATGGT ACTACCTAAA	2040
CGCTAACGGT GCTATGGCTA CAGGTTGGGC TAAAGTCAAC GTTCATGGT ACTACCTAAA	2100
CGCTAACGGT TCAATGGCAA CAGGTTGGGT GAAAGATGGA GATACCTGGT ACTATCTTGA	2160
AGCATCAGGT GCTATGAAAG CAAGCCAATG GTTCAAAGTA TCAGATAAAT GGTACTATGT	2220
CAATGGCTTA GGTGCCCTTG CAGTCAACAC AACTGTAGAT GGCTATAAAG TCAATGCCAA	2280
TGGTGAATGG GTTTAAGCCG ATTAAATTAA ATCATGTTAA GAACATTTGA CATTTTAATT	2340



1197

TTGAAACAAA GATAAGGTTT GATTGAATAG ATTTATGTTT GTATTCTTTA GGTACCTATC	2400
TTATGATTTT AGGAAATGTC ATTAAAAAAA CGACTCATTT TCTCTAACCT GAAAAATAGA	2460
TTAGAGAAAA TGGGTTGTTT TATCTATTAT AGTTATTTGA ATGAAGmTAA GAAGAAGGTA	2520
TACTCACATC ATTCACATAA TCTGTATATT GACTATAAGT TTTAAAAAAC AATTTTAAAG	2580
CTCTTCCTTG TCTTCTCTAA CCAAGCGTGT TATAATGAAT ACTGCTCAAG CGACCTTCAA	2640
TCGTGAAGCA CACACGACCT TCAATCGTGA ATAAACGAAT AGATGGGAGA CTTACCATGA	2700
GTGATAACTC TAAACACGT GTTGTCGTGG GGATGAGTGG TGGTGTGAT TCGTCGGTGA	2760
CGGCTCTTTT GCTCAAGGAG CAGGGCTACG ATGTGATCGG TATCTTCATG AAGAACTGGG	2820
ATGACACAGA TGAAACCGC GTCTGTACGG CGACCGAAGA TTACAAGGAT GTGGTTGCGG	2880
TGGCAGACCA GATTGGCATT CCTACTACT CTGTCAATTT TGAAAAAGAG TACTGGGACC	2940
GCGTTTTTGA GTATTCCTA GCGGAATACC GTGCAGGGCG CACGCCAAAT CCGGACGTTA	3000
TGTGCAACAA GGAAATCAAG TTCAAGGCCT TTTTGGACTA TGCCATAACC TTGGGGGCAG	3060
ACTATGTAGC GACTGGGCAT TATGCTCGAG TGGCGCGTGA TGAGGATGGT ACCGTTTACA	3120
TGCTTCGTGG CGTGGACAAT GGCAAGGATC AGACCTATTT CCTCAGCCAA CTTTCGCAAG	3180
AACAACTTCA AAAAACCATG TTCCCACTAG GACATTTGGA AAAGCCTGAA GTACGCAGAC	3240
TAGCAGAAGA AGCAGGCCTT TCGACTGCTA AGAAGAAAGA CTCGACAGGG ATTTGCTTTA	3300
TCGGAGAAAA GAACTTTAAA AACTTTCTCA GCAACTACCT GCCAGCTCAG CCTGGTCGCA	3360
TGATGACTGT GGATGGTCGC GATATGGGCG AGCATGCAGG TCTTATGTAC TATACAATCG	3420
GTCAGCGTGG CGGACTCGGT ATCGGTGGGC AACACGGCGG TGACAATGCC CCTTGGTTCC	3480
TTGTCGGAAG AGATCTAAGC AAGAATATTC TCTATGTAGG ACAAGGATTC TACCATGATT	3540
CGCTCATGTC AACTAGCCTA GAAGCCAGTC AAGTCCACTT TACTCGTGAA ATGCCAGAAG	3600
AGTTTACGCT AGAATGTACG GCTAAATTCC GTTACCGTCA GCCTGACTCT AAGGTGACCG	3660
TTCATGTCAA AGGAGAAAAG ACAGAGGTCA TCTTTGCGGA ACCACAACGC GCGATTACAC	3720
CAGGACAGGC AGTTGTCTTT TACGATGGCG GG	3752

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3580 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT TTTTATCTC TGGCATACTT TGATACCTTT TTAGACTTAA AGTCTTTAAT	60
AGTGCCTTTC CACCTCTTTT TATCTATAAA GATTCTCCTA CATCATAATT CATTTTTTTA	120
TTTAAACCTT TCTGTCTTAG TTTGTCTTTA TCTTCTTCAT ACCATTTTAA GATTGTCACA	180
TAGTGGTTTT GATAGGTCTT ACCACTGCTT TCCATGTATC TGGATAGTTT ATTTATCATT	240
ATATCTGTGT GTGAGTTTAA TTTTCTTTT AGATTTTTAT ATTCTTCTTT GCTTAACCTT	300
ACATTTTTGA ATTCTCCATA AAAAATGGGG GTGGACTTTT TATCTATCTC TCCCTCTCTC	360
TCTTTATCTA TCTCTATATC TTTCCATGTA ATTCCAATCT GGAGTACCTC TACTGTCTAT	420
CGGTAATTTA ATTTTGATAT CTGGCAATAC TGTGCTAGAT ATTTGATCTT TATATTCAGT	480
ATTTTTTAAA GCTTGCCTAA TAATTGAAAGT TAAATAGAAT GCTACTTCTT TATTCAATTC	540
TTTATTTTTT AATTTTAAAC AATGAATTTT CATATCTAGG CTTGCTTTAT ATTTATGATA	600
AAAGACTGCT CCTAAAAATG AACAGATAT AAAATTTTCA AAAACTCTAT AATTTTTATC	660
ATCTATATCT TCGTAGTAAC CTAAGATACC ATTGTCAATA TTTGTAGCAC TAATCTAGG	720
AGTTTTTCCA TCGAGTAAAT ATCTTTTGG AATAGATGAG CCTGTTGGTA CTTAACTCGA	780
TTTCCCCTTT TTTTCGGTAA TAAATATTTT TTTTATTTTT GTTGTCTGAT ATTTTTCCTA	840
CCTGTCCTTT GTAGGATGAG TATTTTCTAG ATTTTCYTGA ATAACTTTTT ACTTGAAGTT	900
TTAGCTTTTG AACTAGTCGT TGTACTTTCT TTTTGTTTAT TATCAGTCCT GATCTTTTTA	960
ATATTGCTGT TATTCTCTAT ATCCTATTTT TCATTCATGA TATTCTTTTA CTAATTTTAT	1020
CTTAAATTCT GTGCTGTATT TGCCATTAAA AAAGTACCT CTTTAGTTA GTTTTTTGGC	1080
CTAACTTTTG AGGGTCAGTT CAAAATTTGC GACTTTTAAA TGAATTCCAA TATTCAATTA	1140
TTAAGAGTTA ACATGGTGCT TGCCAATAGG AATCATTAGA GGCGAATTGG AAATAGGGTC	1200
ACGTATAATT TTTGCTTCAA GATTAAAGAT ATCTTTAACT AGTTTATCAT TTAGTATATC	1260
TTCAAGGCTT CCCTCTGCAA CAAGTTTACC TTCTTTAATT GCAAATAGGT AATCAGCGTA	1320
TCTTGCTGTT AGATTTATAT CGTGCAAAT CATGCAAATG GTTGTCTTAT ATTTTTGGTT	1380
TAGATCAGTC AAGAGGTCTA ATAGTTCTAT TTGATATGAG ATATCCAAGT AAGTAGTTGG	1440
CTCATCTAAA AGTAGGATAC TTGTATCTTG GGCTAGGGCT AGAGCTATCC ATACTCTTTG	1500
CCTTTGACCC CCAGAAAGTT CTTCAACTAG GTTATTTGCT AGATCTTCAA CATTTGGCCTT	1560
AACCATTGAT CTGTTTATTA TTTCAAGGTC ATCTTTTCCA AGACTCTTAA AAGGCTTTCT	1620
GTAGGGGAAA CGACCACGGC TTACAAGATC AGCTACTGTT ATTGATTCAG GGATTATTGG	1680
AGATTGAGGT AATATAGCTA TGTGTTTTGC TAAATCTTTT TCTTTATAAG AATTAATTGA	1740

1199

TTTATTATCA AGCAATACTT CTCCCTCTAA TGGCTTTATA AGTCGAGACA AGGTTTTAAT	1800
GAGTGTGAT TTCCCACAAC CATTGACCC AATAATAACT GATATTTTTT CTTCAGGTAT	1860
TTTTATATTT ATATTTTCCA AGATTATTTT TTCATCATAA CCGCAGGTAA GATTATTTGA	1920
CCACAGACCT TTCATTATAT ATTCTCTCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT	1980
GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA	2040
GAGAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTGGGCTT	2100
CTTTTCTTGC CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT	2160
CCTGTAATTG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTAA AACAAGCCTT	2220
GAAAGCTCGG GATTTGCTCC AAGTCCGATT GCTATTTCTT CACCAAGTTC AATAATTTCT	2280
AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA	2340
GGTATGTCAT CTAACTTTGT AAAAGATAAA GAGCCACTGA GCCATCTCAT AACTTCTTGT	2400
AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA	2460
AAACCAATAC CTAATATTAT CAGTCTTGCT GCTGAAAAAC CATCTTTTTT AGCTAGTAAA	2520
AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAATTCCAGT AGTTAAACTA	2580
TTTGTTTTTA ATACCAATAT GCAAAAGACC GCTGCAATAG ATGAAGAACT TGTGACACCG	2640
ATTATATCAG GACTTGCAAG AGGATTTCTT AACATAGTTT GAAAGATAAA TCCTGCCAAT	2700
CCAAAAGACC AGCCAGCTAT AATTCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC	2760
GAAAAACTAG CTCCAGGAAC AGTTTCACTA TTTAAGACTT TAATCAAAGT TGAAAAAGAA	2820
TAACTTTCAT CTCCGATAAG TAAAATGAAA AATGATAGAC TGATTATTAT TAATAAAAT	2880
AGTGAGGAAA ATAGTGTTAT TCTATTTTTT CTPTTTTGAA TACCTATAAT TAAATTTTGC	2940
ATTAGTTATT AACCCCTCTA TTTTTCATAG TTACATAAAT AAGTACTGGA CCCCCGATTA	3000
TTGCAGTAAT TATCCCTACT TCAATTTTAC CTGGTTTACC TAACATACGG CCGATTATAT	3060
CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCATT GTGCGTATAT	3120
CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTACGAAG CCAATAGGTC	3180
CACCAATTGC AGTAATACTT GAACATAAAA GCACACTTGC AATTATTGCA AGTGATCTTA	3240
TCCTATTAACTAATTAAC AGACCAACAG CCATTTTCATC ACCCATAGCT AAAGCGTTTA	3300
AATCTGATGA AATAAATATA GCTATCAAGT GACCTAAAAT TATAAAAGGT AGTAGTGTAG	3360
ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAAATCTA AATTTGTCTA	3420
AGACGTTATT ATTCGGTAAA ATTAAAAAAC TTACAAAACCT GCTTAAAGCC ATACTAACAC	3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG	3580

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGGCGTG ATATGTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCAGC TCCGTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC	240
TTTGCGTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCAGG	300
ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA	360
GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTAGAA CATCAGTGA AGGAATGGTT	480
GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA	540
ATTGTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTTAG AAAATGTCAA	600
TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAATC CCCAGTATGT GGTCTCAAT	720
CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTCAATGT	780
GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GGATTGATAT TCAAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAAGACG GTGAGATTGA TCGCTTGAT CTGAACTTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG	1080
CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTGTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCAATATGG CATGAAACTC AATGGTGTCT GGTTAGATTT GCATGCCAGT	1200
GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT	1260
ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT	1320

1201

TTGCTTTACA TAAGTTGGCA AACGTGCTAT ACTGATAGTA AGAATATGAA AAGTGAGGCG	1380
GGGAAATATC TTCGCCTCTT GCTTATGAGG AGGTGGACGC AATCGCAACA ATCGTAGAAT	1440
TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGCTCCTTT TGAACTCGTG GATATCGAGT	1500
ATGGAAAGAT TGGCAGTGAC ATGATTCTCA GTATTTTGT AGATAAACCC GAAGAATTAC	1560
CTTGAACGAC ACGGCAGACT TGACAGAAAT TATCAGTCCT GTCCTAGACA CCATCAAGCC	1620
AGATCCCTTC CCAGAACAAT ATTTCTTAGA AATTACCAGT CCAGGTTTGG AACGTCCTTT	1680
GAAAACCAAG GATGCCGTCG CTGGAGCGGT TGGAAAATAC ATCCATGTCG GGCTCTACCA	1740
AGCCATCGAT AAGCAAAAGG TCTTTGAAGG AACCTTGTTG GCCTTCGAAG AGGACGAGTT	1800
GACTATGGAA TATATGGACA AGACGCGTAA GAAAACCGTC CAAATTCAT ACAGTTTAGT	1860
ATCAAAAGCA CGTTTAGCAG TTAAATTATA GAAAAGAAA GGATAGCTTT TGAGGATTCA	1920
AAAGTGAAGA AAACATGAGT AAAGAAATGC TAGAGGCCTT CCGCATTTTG GAAGAAGACA	1980
AGGGAATCAA AAAAGAAGAT ATCATCGACG CAGTAGTAGA GTCGCTTCGT TCCGCTTATC	2040
GCAGACGCTA TGGTCAGTCA GACAGCGTAG CTATTGACTT CAACGAAAA ACAGGTGACT	2100
TTACAGTTTA TACTGTCCGT GAAGTTGTTG ATGAAGTATT TGATAGCCGT TTGGAAATCA	2160
GCTTGAAAGA TGCTCTTGCC ATTAATTCAG CTTATGAACT TGGAGACAAA ATCAAGTTTG	2220
AAGAAGCACC AGCTGAGTTT GGTCGTGTAG CAGCCCAATC TGCCAAACAA ACCATCATGG	2280
AAAAATGCG CAAGCAAACA CGTGCCATCA CTTACAATAC TTACAAAGAA CATGAGCAAG	2340
AAATCATGTC TGGTACAGTA GAACGCTTTG ACAACCGCTT TATCTATGTC AACCTTGGTA	2400
GCATCGAAGC CCAATTGTCA AAACAAGACC AAATTCCTGG AGAAGTTTTT GCTTCTCATG	2460
ATCGTATCGA AGTTTATGTT TACAAGGTTG AAGACAACCC TCGTGGTGTG AACGCTTTTG	2520
TTAGCCGTAG TCATCCAGAA ATGATCAAAC GTTTAATGGA GCAAGAAATT CCAGAAGTTT	2580
ATGATGGAAC TGTTGAAATC ATGAGCGTGG CTCGTGAAGC AGGTGACCGT ACGAAGGTTG	2640
CTGTTGCTAG CCACAATCCA AACGTGGATG CTATCGGTAC AATCGTTGGA CGTGGTGGTG	2700
CTAATATCAA GAAGATTACT AGCAAATTC ACCCAGCTCG TTACGATGCT AAAAATGACC	2760
GCATGGTACC AATCGAAGAA AATATCGATG TTATCGAGTG GGTAGCAGAT CCAGCTGAAT	2820
TTATCTACAA TGCCATCGCT CCTGCTGAGG TTGACCAAGT TATCTTTGAT GAAAACGACA	2880
GCAAACGTGC CTTGGTGGTT GTTCCAGATA ACAAGCTTTC TCTTGCCATT GGTCGTCTGTG	2940
GACAAAACGT GCGCTTGGCG GCTCACTTGA CTGGTTACCG TATCGATATC AAGTCTGCTA	3000
GCGAATTTGA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG	3060

1202

TAGAAGAATA	AAAGCTGCTA	GAGGAGGGAA	AGATGAAAAAC	AAGAAAAATC	CCTTTGCGCA	3120
AGTCTGTTGT	GTCTAACGAA	GTGATTGATA	AGCGTGATTT	GCTCCGCATT	GTCAAGAACA	3180
AGGAAGGACA	AGTCTTTATT	GATcCTACGG	GCAAGGCCAA	TGGCCGCGGC	GCTTATATCA	3240
AACTAGACAA	TGCAGAAGCC	CTAGAGGCCA	AAAAGAAGAA	GGTCTTTAAC	CGCAGCTTTA	3300
GCATGGAAGT	GGAAGAAAGC	TTTTATGACG	AGTTGATCGC	TTATGTGGAT	CACAAAGTGA	3360
AAAGAAGAGA	GTTGGGACTT	GAATAAGCAA	AAGATAAGTA	ATCTCTTGGG	GCTTGCTCAG	3420
CGAGCAGGGC	GCATCATATC	GGGTGAAGAA	TTGGTGGTCA	AGGCCATTCA	AGACGGCAAG	3480
GCCAAGTTGG	TCTTTCTAGC	TCATGATGCT	GGACCCAATC	TGACCAAGAA	GATTCAAGAT	3540
AAAAGTCATT	ATTATCAAGT	AGAAATTGTA	ACCGTGTTTT	CAACACTGGA	ATTAAGCATA	3600
GCAGTCGGGA	AATCGAGAAA	GGTTTTGGCT	GTAACAGATG	CTGGATTTAC	AAAGAAAATG	3660
AGGTCTCTTA	TGGAATAGAA	GAGGAGGACA	TGATTTGTCT	AAGAAAAGAT	TGTACGAAAT	3720
CGCAAAAGAA	CTTGGAAGAG	AAAGTAAAGA	AGTTGTAGCG	CGTGCAAAAG	AGTTGGGCTT	3780
GGATGTGAAA	AGCCACTCAT	CAAGTGTGGA	AGAAGCTGTC	GCTGCAAAAA	TTGCTGCCAG	3840
CTTTAAGCCT	GCAGCTGCTC	CGAAAGTAGA	AGCAAAACCT	GCAGCCCCAA	AAGTAAGTGC	3900
AGAAAAGAAA	GCCGAAAAAT	CTGAGCCAGC	TAAACCAGCT	GTAGCTAAGG	AAGAGGCAAA	3960
ACCTGCAGCC	CCAAAAGCAA	GTGCAGAAAA	GAAAGCCGAA	AAGTCTGAAC	CAGTAAAACC	4020
AGCTGTAGCC	AAGGAAGAGG	CAAAACCAGC	TGAGCCAGTC	ACTCCGAAAA	CAGAAAAAGT	4080
AGCGGCTAAA	CCGCAAAGTC	GTAATTTCAA	GGCTGAGCGT	GAAGCACGTG	CTAAAGAGCA	4140
GGCAGAGCGA	CGCAAGCAAA	ATAAGGGCAA	TAACCGTGAC	CAACAACAAA	ACGGAAACCG	4200
TCAGAAAAAC	GACGGCCGTA	ATGGTGGAAA	ACAAGGTCAA	AGCAACCGCG	ACAATCGTCG	4260
CTTTAATGAC	CAAGCTAAGA	AGCAGCAAGG	TCAGCAAAAA	CGTAGAAATG	AGCGCCGTCA	4320
GCAAGAGGAT	AAACGTTCAA	ATCAAGCGGC	TCCACGTATT	GACTTTAAAG	CCCGTGCAGC	4380
AGCCCTAAAA	GCAGAGCAAA	ATGCAGAGTA	CGCTCGTTCA	AGTGAGGAAC	GCTTCAAGCA	4440
GTATCAGGCT	GCTAAAGAAG	CCTTGGCTCA	AGCTAACAAA	CGCAAGGAAC	CAGAGGAAAT	4500
CTTTGAAGAA	GCGGCTAAGT	TAGCTGAACA	AGCACAGCAA	GTTCAAGCAG	TGGTTGAAGT	4560
CGTCCCTGAG	AAAAAAGAAC	CTGCAGTGA	TACACGTCGT	AAAAACAAG	CTCGACCAGA	4620
CAAAAATCGT	GACGATTATG	ATCATGAAGA	AGATGGTCCT	AGAAAAACAAC	AAAAGAATCG	4680
AAGTAGTCAA	AATCAAGTGA	GAAATCAAAA	GAATAGTAAC	TGGAATAACA	ACAAAAAGAA	4740
CAAAAAGGC	AATAACAAGA	ACAACCGTAA	TCAGACTCCA	AAACCTGTTA	CGGAGCGTAA	4800
ATTCCATGAA	TTGCCAACAG	AATTTGAATA	TACAGATGGT	ATGACCGTTG	CGGAAATCGC	4860

1203

AAAACGTATC AAACGTGAAC CAGCTGAAAT TGTTAAGAAA CTTTTCATGA TGGGTGTCAT	4920
GGCCACACAA AACCAATCCT TGGATGGGGA AACAAATTGAA CTCCTCATGG TGGATTACGG	4980
TATCGAAGCC AAACAAAAGG TTGAAGTGGG TAATGCTGAC ATCGAACGTT TCTTTGTCGA	5040
AGATGGTTAT CTCAATGAAG ATGAATTGGT TGAGCGTCCA CCAGTTGTTA CTATCATGGG	5100
ACACGTTGAC CACGGTAAAA CAACCCCTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC	5160
AGGTGAAGCA GGTGGTATTA CTCAGCATAT CGGTGCCTAC CAAATCGTGG AAAATGGTAA	5220
GAAGATTACC TTCCTTGATA CACCAGGACA CGCGGCCTTT ACATCAATGC GTGCGCGTGG	5280
TGCTTCTGTT ACCGATATTA CGATCTTGGT CGTAGCGGCA GATGACGGGG TTATGCCTCA	5340
GACTATTGAA GCCATCAACC ACTCAAAAGC AGCTAACGTT CCAATCATCG TAGCTATTAA	5400
CAAGATTGAT AAACCAGGTG CTAACCCAGA ACGCGTTATC GGTGAATTGG CAGAGCATGG	5460
TGTGATGTCA ACTGCTTGGG GTGGAGATTC TGAATTTGTT GAAATTCGG CTAAATTCAA	5520
CCAAAATATC GAAGAATTGT TGGAAACAGT CCTTCTTGTG GCTGAAATCC AAGAACTCAA	5580
AGCAGACCCA ACAGTTCGTG CGATCGGTAC GGTATCGAA GCGCGCTTGG ATAAAGGAAA	5640
AGGTGCGGTC GCAACCCCTC TTGTACAACA AGGTACCTTG AATGTTCAAG ACCCAATCGT	5700
TGTCGGAAAT ACCTTCGGTC GTGTCCGTGC TATGACCAAC GACCTTGGTC GTCGTGTTAA	5760
AGTTGCTGGA CCATCAACAC CAGTCTCTAT CACAGGTTTG AACGAAGCAC CGATGGCGGG	5820
TGACCACTTT GCCGTTTACG AGGATGAAAA ATCTGCGCGT GCAGCAGGTG AAGAGCGTGC	5880
CAAACGTGCC CTCATGAAAC AACGTCAAGC TACCCAACGT GTTAGCCTTG AAAACCTCTT	5940
TGATACCCTT AAAGCTGGGG AACTCAAATC TGTAAATGTT ATCATCAAGG CTGATGTACA	6000
AGGTTCTGTT GAAGCCCTTT CTGCCTCACT TCAAAGATT GACGTGGAAG GTGTCAAAGT	6060
GACTATCGTC CACTCAGCGG TCGGTGCTAT CAACGAATCA GACGTGACCC TTGCCGAAGC	6120
TTCAAATGCC TTTATCGTTG GTTTCAACGT ACGCCCTACA CCACAAGCTC GTCAACAAGC	6180
AGAAGCTGAC GATGTGGAAG TCCGTCTTCA CAGCATTATC TACAAGGTTA TCGAAGAGAT	6240
GGAAGAAGCT ATGAAAGGGA TGCTTGATCC AGAATTTGAA GAAAAAGTTA TTGGTGAAGC	6300
GGTTATCCGT GAAACCTTCA AGGTGTCTAA AGTGGGAACT ATCGGTGGAT TTATGGTTAT	6360
CAACGGTAAG GTTGCCCGTG ACTCTAAAGT CCGTGTTATC CGTGATGGTG TCGTTATCTA	6420
TGATGGTGAA CTCGCAAGCT TGAAACACTA TAAAGACGAC GTGAAAGAAG TGACAAACGG	6480
TCGTGAAGGT GGATTGATGA TCGACGGCTA CAATGATATT AAGATGGATG ATGTGATTGA	6540
GGCGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTTTG CTCCTTTCTT AGGTGGTGAG	6600

1204

GGACGCAAGC AAACCGATGG TTTCATTGCT TATTTTGTAG CCTAGGGTCT CAAAAATCCC	6660
CTGTGATGGG ACTGATAAAT CAGTTCCATC ACTTTCACCA CGGCGAAAGA AGCAGATGAC	6720
TTCAAATTGA ACTTCGTTTC AATTTAAACT GAAAATCAAG AAGTTTAAAA TAGCTAGGTC	6780
TGCTGGCCTA GCTTTTGGTT CAAAGTAGAG AAAGGAATAT CATGGCAAAT CATTTCGGTA	6840
CAGATCGTGT GGGCATGGAA ATCAAGCGTG AAGTCAATGA GATTTTGCAA AAGAAAGTCC	6900
GTGATCCACG TGTCCAAGGT GTGACCATCA TAGATGTTCA GATGCTGGGT GACTTGTCTG	6960
TTGCCAAGGT TTATTACACC ATTTTGAGTA ACCTTGCTTC GGATAACCAA AAAGCCCAAA	7020
TCGGGCTTGA AAAAGCAACT GGTACCATCA AACGTGAACT TGGTCGCAAT TTGAAATGT	7080
ACAAAATCCC AGATTTGACC TTCGTCAAAG ACGAGTCCAT CGAGTATGGA AACAAGATTG	7140
ACGAGATGCT ACGCAATCTG GATAAGAACT AAAGAAGAGG GGTGCCCCCT CTTTTTGGT	7200
GGAGGAAAAT AGGTTGAATT TGAAATGGAA AAATATTCTT TTATAATAGA TTGAACTAG	7260
AATAGTACGC CTCTACTTCT AAAATATTGT TAGAAATCGA TTTGACTGTC CTGATCGATT	7320
TGTCCTGTTT TGTTTTCATT TTAATATAAA AAAGGGATTG TGTATTTTTT AATGTTATCT	7380
AATTAGAAAA TGCTTTTTTT GTAGGAAATA TAATATGATA AGGTGCAAAA AAGAAATAAG	7440
GAGTTTGTAT ATGGCTGAAC AAGACTTAGC TATGCAAGTA TTGCAACAAG TGGTGAACT	7500
ACCTGTTGTT AAGGTTGATC GTTCGAAAT TTTAGTGGAT AAGTTTTCCA AAGAATTGGA	7560
TCCAAAAGAT ATTCCTACCT TATTGGAACA AGGTCCAACG ACTCTTCTAT CTCAAGAAAT	7620
ATTAGATCGT GTAGCTAATG CTTGTATTG GACAATGTA TTATTAGCGA GTGGGACTTC	7680
TGTTTTGGCA GGATTACCTG GAGGGCTTGC TATGGCAATT ACCATTCCAG CTGATGTGGC	7740
TCAATTTTAT GCTTCTCTC TGAAATTGGC TCAAGAATTA GGTATATTT ATGGTTATGA	7800
GGATCTTTGG GCTTCACGAG AGGAGTTGAG TGAAGATGCT CAAAATACCC TCTTGCTTTA	7860
TCTAGGCGTA ATGTTAGGGG TGAATGGAAC CGCTGCTTTG CTACGTGTTG GTAGTATAAC	7920
AATTGCCAAA CAGGTAATGA AAATAGTGCC TAATAAGCT TTAACAAAGA CGCTTTGGTA	7980
CCCTATTTTG AAAAAAGTCT TAAAAATATT TGGTGTGAAT CTTACCAAGG GAGGGTTGGC	8040
CAAAGGAATG GGGAAATTTA TTCCTATCTT GGGTGGTATC ATTCAGGTG GTTTAACCTT	8100
TGCAACTATG AAACCAATGG GGGAAAGCTT GCAGAAAGAA TTATCCAAGC TAGTCAACTA	8160
TAGTGAAGTT CAATATCAAG AAGATGTTGA AACAATCCGA AAAGAGGCTG AAATCATCAA	8220
AGGAGAGTAA TATGAATCCT ATCAAAGCTT TTGCTAAAAT TTATGGTAAT TACTTTTTGA	8280
CCGTGCAAGG TGTAAGAGTG ATGAAAACGA TAAAGAAAGC TGACCATGTC GTTGTGGTC	8340
TGGGGAACCT TTTTATTGCC GACAAGTTAA TGGATACGGC TCGGTGGCTC ATTAAGCCAG	8400



1205

AGGAGAGAGA ATGAAATTTT TTTGGTCTTC TTGCTATTCT TTTTATCAAA CCGATTATTG	8460
GGATTGTGAA ATTCTTTTGG ATGATCATCT CTTTTCAGT CCAATTGCTG TTTTACAAGA	8520
TAGTGTTTAA GATATTGGAT TGGCTCTTTA AACTTATCTA GATGGTAATC CAAGTTGCAG	8580
AGAACTAGCA GGAAGTCCAC TGCTAGTTTT TTATTCTCTT TCCATATGGT ATAATATAAG	8640
CAGTAAAATC ATTTTATACT CTTGAAAAT CTCTTCAAAC CACGTCAGCT TCACCTTGCA	8700
GTATATATGT TACTGACTTC GTCAGTTCTA TCCACAACCT CAAAACGGTG TTTTGAGCTG	8760
ACTTCGTCAG TTCTATCTAC AACCTCAAAA CACTGTTTTG AGCAACCTGC GGCTAGCTTC	8820
CTAGTTTGCT CTTTGATTTT CATTGAGTAT TAGAACATAC AATGGAGGTC GTCATGGACA	8880
ATATCATCGA TGTGTCAATT CCTGTTGCAG AAGTGGTGGA CAAGCATCCA GAAGTCTTGG	8940
AAATTCTAGT GGAGTTGGGT TTTAAACCCC TTGCCAATCC CTTAATGCGC AATACAGTTG	9000
GTCGTAAAGT ATCACTTAAA CAGGGTTCTA AGCTAGCAGG AACTCCTATG GACAAGATTG	9060
TACGCACACT GGAAGCGAAT GGCTACGAAG TGATTGGATT AGACTAATGA CAGATGAACG	9120
GATTCATATC CTACGGGATA TTTGTGTTAGA ATTGACAAAT GGCGCCCTCTC CTGAGTCGGT	9180
TCAAGATCGC TTTGATGCGA CCTTTACGGG CGTGTGAGCC ATCGAGATT TCCCTTATGGA	9240
GCACGAGCTG ATGAACTCGG ATTCGGGGCT CACTTTTGAA GATGTTATGG AACTCTGTGA	9300
TGTCCATGCC AATCTTTTTA AAAATGCTAT CAAAGGTGTC GAAGTTTCAG ATACTGAGCA	9360
TCCAGGTCAC CCAGTTCGTG TCTTCAAAGA AGAAAATCTG GCTCTCCGTG CGGCCTTGAT	9420
TCGCATTCTG AGATTGTTAG ATACCTATGA GTCTATGGAA GACGAGGAAA TGCTGGCGGA	9480
GATGCGTAAG GGTTTGGTGC GTCAGATGGG ACTTGTGGGT CAATTTGACA TCCATTACCA	9540
ACGTAAGGAA GAACTCTTCT TTCCTATCAT GGAGCGCTAT GGACACGATT CACCTCCCAA	9600
AGTTATGTGG GGAGTGGATG ATCAGATTAG GGAAGTCTTT CAAACAGCTC TAACGACAGC	9660
CAAGTCACTA CCAGAAGTGT CAATTAGCAG TGTAAGGAA GCTTTTGAAG CTTTTCGAC	9720
AGAGTTTGAA AGTATGATT TCAAGGAAGA GTCCATCCTC CTCATGATT TCCCTGAGTC	9780
TTTTACTCAG GATGACTGGC TTCAGATTGC GGAGGAGAGC GATGCCTATG GCTATGCCAT	9840
CATCCGTCCG TCAGAGAAAT GGGTGCCAGA ACGACAGAGC TTTATTGAGG AAAAGATTGC	9900
AGAGGAGCCT GTACAGCTAG ATACGGCAGA AGGTCAAGTT CAACAAGTCA TAGATACGCC	9960
AGAAGGCCAT TTTACCATTA CCTTTACCCC TAAGGAAAAG GAAGCTGTGC TGGACCGCCA	10020
TAGTCAACAG GCTTTTGGTA ATGGCTATCT TTCAGTCGAG CAGGCCAATC TCATCCTCAA	10080
TCATCTCCCT ATGGAGATTA CCTTTGTCAA TAAAGAAGAT ATTTTCCAGT ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GGCGCAATGT	10200
CGAACTCTGC CATCCGCCTA AGTACTTGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG	10260
TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTTCGAGTA	10380
TGTTTCAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC	10500
CCAAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAAGTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAAGATG CCATGATTCT CTACGAGAGT CGCTTGGATG CTTATCAGTT	10620
CTTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGGT GAGCGAAATT ATTAAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGATTT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGAAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTTCAAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTGCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT	11040
GGACTTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAACT GGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCCC AGCTACCATC	11160
AAGAAATTGA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCAATTTCCG	11220
AAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTTGA ATCCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAACTGGTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGTCT TTAAAGACGA GAGTTGCC	11378

## (2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGGCGAATTT GCTGCGGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTTA TGCCAAATGA AGGTCCTGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGGTTCTCCA TTAAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTMTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTG AAAAAATGCG TGAAGTGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGAAGTGGT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTGCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACCTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGGTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACTT GCTTCTGTCG CTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAAGTTG TTTGGTTCAT ACTGCAGATG	1380
CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCTGTCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAACTT CAATTAACCTA AATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGGTCT TGGAACCTTG AACGGATGCA	1920

1208

AAACTTGGGC	TGGGCTTATA	CACTCATTC	AGCTATCAAA	AAACTCTATA	CTAAAAAAGA	1980
AGATCAAATC	GCTGCTCTTG	AGCGTCACCT	TGAGTTCTTC	AACACTCATC	CATACGTAGC	2040
TGCTCCAGTC	ATGGGGGTTA	CTCTGCGCT	TGAAGAAGAA	CGTGCTAACG	GTGTGGAAAT	2100
CGATGACGCT	GCTATCCAAG	GGGTAAAAT	CGGTATGATG	GGACCTCTTG	CTGGTATCGG	2160
TGACCCAGTA	TTCTGGTTTA	CAGTACGCCC	AATCCTTGGA	TCTCTCGGTG	CTTCACTTGC	2220
CCTTACTGGC	AATATCTTGG	GGCCACTCCT	CTTCTTTGTT	GCATGGAACT	TGATTCTGAT	2280
GTCATTCTTG	TGGTATGTTT	AAGAGATTGG	ATACAAGGCT	GGATCAGAAA	TCACTAAAGA	2340
TATGTCTGGT	GGTATCCTTC	AAGATATCAC	TAAAGGAGCT	TCTATCCTTG	GGATGTTTAT	2400
TCTTGCTGTC	CTTGTTCAAC	GCTGGGTAAA	TATTAAATTT	GCTTTCGATG	TTTCTAAAGT	2460
TCAACTAGAT	GAAAAGGCTT	ATATCCATTG	GGATAAATTG	CCAGAAGGGT	CTAAAGGTAT	2520
CCAAGAAGCA	TTGCGACAAG	TAGGACAAGG	ATTGTCTCAA	ACTCCTGAAA	AAGTTACTAC	2580
TTTCCAACAA	AACTTGGATA	TGTTGATTCC	TGGATTATCA	GGACTACTCC	TTACTTTACT	2640
TTGCATGTAC	TTACTTAAGA	AAAAAGTATC	TCCAATCACT	ATTATCCTTG	CCCTCTTCGC	2700
AGTGGGTATT	GTGGCACATG	TTCTTCACAT	CATGTAATCA	AGCAACTAAA	AAGGAACCAG	2760
GTTCTAAAT	CTGATTCCTT	TTTTCTATGC	TTTTATTTCAG	CCAAGGCTCC	CATTGGATCC	2820
CATGGTGCAA	GTACGATTGG	TTCTGCTCCA	TAGGCAGCTT	GTTCTTCTGC	TGTCAGCAAT	2880
TCCTTACGAA	CAACGATTTG	GTATGTGTAT	TCGTCCATCC	AAGCGTCTGA	GGCAACAAAG	2940
TAACCATCTG	TACCGACCTT	GTCTCCCCAT	GAGTTTTCAA	CCTTCCACTT	GGTTGATTTA	3000
CCATTTTCGT	CCAAGTCAAC	ACCTGTCAAG	ACCATGGCGT	GGGTCAATCA	GCTTTCACTA	3060
TAGTCCAAAC	GTCCAGCCTT	GTCTTGAGTA	AGTTTAATGT	CCATGCTTGA	TTCAAAGTCA	3120
TAAACATCTG	TCGCAAGGAT	GCCAGCTTAC	GGTTGCTGAG	CTGGCCGACA	TCAGAACCAA	3180
ACCAAACAGT	CTCACCTGCT	TGCATTTGGG	CAATCGCCAA	TTCTTTCAAG	CGCTCCATTG	3240
GAACGTTGAT	GTAGCGAACT	GCACGGCTAC	CAACCACATT	CCCCAACATC	TCAACTGTGT	3300
AAGATTTTCC	GTAAGGTTTA	TCAGCAGTTG	GAGCATTGAT	AACAGAAACG	TAGTCTTCTA	3360
AAGGAAGATT	GACATATTTT	TTGTAAAAT	CTTGTGGTGT	GATTCCTTTT	TCACTTTTGT	3420
AGTTGTTATC	TTTATCGCGA	TAAGCAAAGT	CAAACTTGCG	TGGTGGAAGT	CCTAATGACA	3480
TAGCAAGAAA	GTAAAGATT	TCTTGCAAGA	GGTCTTCTTT	CTTAGCTTGA	ACAGTCGCTT	3540
GATCTGCACC	AGAAACAAGC	AAGTCACGCA	AGATTTGAGC	ATCTTGACGA	AGCAATTTAT	3600
TAAGGATCGC	ATTTAGCTCA	CGACTGCTGC	TAGATGAAAC	AGACTCAGGA	TAACTGACT	3660
TAGGCACGAC	ACCGTATTTT	TCAAAGAGGG	AAACGACCAT	ATCCCATTGA	CCGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACtT GCGGCTAGTC AATTCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTTCTGG TTAGTGACCT TGTCTTGGT	3960
TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATTCCG TTGTGGCTGG CAGCATTTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA	4140
GTCTACAGTG TATTGG	4156

## (2) INFORMATION FOR SEQ ID NO: 212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AAATAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA	60
TTTTTATTAA GTTATTATTT TGTGTTTCT AGTTTACTTT TTGATCGTTA AGAGTGGTGG	120
AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCGCAG GCTGTACTTG	180
AGTACGGCAA GGCGAAGCTG ACGTGGTTTG AATTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG	300
ACTTGAGAGA AGAAGTCATG GTTGGAAGTT CCTGTTGAAA TACCGTTCAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTTAT GAGAGCTTTA	420
TTGGCATTGT AGCGAAGGAA GGTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT	540
TTGAGTTTTT CTTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTT CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTT TGCAACGTTG	660
GCAAGTTTGT TGTTACCGAG ATAGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG	720
GTTTCGAGGA AGACGCTGGC AACTTTCTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTCC	780
TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTTCT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA	900

1210

GATTCCATAA ATTGGATGTT ATTGAAGACA GCTTCCTCAT GTGGTGTACG GATGTCTGCG	960
CGAAGGGCTT GAACCCAGT TTCAGATTGC ATAGTGTCAG GAAGGGTTAA ACCACCAAAA	1020
ACTTTTCCGA CCAAGTCTTT CTCTTTGTTA GATAGCTTTC TCCAGTCATC CAAGTCGTTT	1080
GATAAGGGAA TACGTGTATC GAGCCAAAAT TGCTCCGTCA GTTTTTCCCA AGTTGATTTG	1140
TCGATGACAT CTTGATGGC ATTCCAGTTA ATGGCTTTGT AGTAAGTTTC CATTTAAAAT	1200
CTCTTTCTGT GTTTAGTATT GCGAACTCAC AATTATTTCT ACTTTACCAT AATTCTATAG	1260
GAGTATCGCA CAAAAGTCG GAAGCCCGAC TTTTAAAATG TTACATAAAT TATGTTATGA	1320
CATAGTAGAT TTGATTTTAT CAGTGCTGCT TAGGGAAAAA TAGTGTTTCT ATGCTAGAAA	1380
CTAAATCACA CAGCTTTCAC ATTGGTTGGC GCCGACTTCT CCACCGTCAT CTGTAAAGGT	1440
ACGGACGTAG TAGATAGACT TGATTCCCTT GTTAAAGGCA TAGTTACGAA GGATGGACAA	1500
GTCACGTGTC GTTTGTTTAT TTTCCCTCTT CCATTGCTAA AGGCCTTTTG GAATGTCACT	1560
GCGCATGAAG AGGGTGAGTG AAAGTCCTTG ATCCACGTGT TCAGTCGCAG CAGCGTAAAC	1620
ATCGATGACT TTACGCATAT CCATATCGTA GGCAGAAGTG TAGTAAGGAA TGGTTTCTGT	1680
AGACAAGCCA GCAGCAGGT AATAGATTTT ACCAATTTTC TTCTCTTGGC GTTCTTCGAT	1740
ACGTTGCGTA ATCGGGTGGG TAGAAGCAGA AACGTCGTTG ATATAGCTGA TAGAACCATT	1800
TGGCGCTACA GCAAGGCGAT TTTGGTGGTA AAGACCATCT TCTTGAACCT TGTCGCGAAG	1860
TTGAGCCCAA TCAGCAACAC CAGGGATAAA GACATTTTTC AAGAGTTCTT TAACACGGTC	1920
TGATGTTGGA ACAAATTCAC CAGTTACATA CTTGTCAAAG TAACTTCCGT TAGCATAGTC	1980
TGATTTTTCA AAGTTGTGGA AGGTAATACC ACGTTCACGT GCAATATTGT TTGACTCTAC	2040
CAAGGTCCAG TAGTTCATAA GCATAAAGTA GATGCTTGTA AATTCAACAG ACTCAGGTGA	2100
ACCATATTCA ATGAGTTGTT GGGCAAGGTA GCTGTGCAGT CCCATGGCAC CGAGACCAAA	2160
GGTGTGGGCT TGGCTATTTT CATGGTCAAT CGTTGGTACA GCTACGATAT GTGAACTATC	2220
TGTAACGAAA GTAAGGGCAC GAACCATAGC ACGGATAGAA CGACCAAAAT CAGGTGAACT	2280
CATCATGTTA ACCACGTTGG TTGAACCCAG GTTACATGAA ACATCTGTTT CCATTGGAAG	2340
GAATCTTGA GCATCGTTGA TCAAGCTTGG TTCTTGAAC TGAAGAATCT CAGAACACAA	2400
GTTACTCATG ATAATCTTTC CATCAACAGG ATTTGCACGG TTAGCCGTAT CGATGTTGAC	2460
TACATAAGGA TAGCCAGACT CTTGTTGCAA TTTAGAGATT TCAGTTTCCA AATCCCGCGC	2520
CTTGATTTTT GTCTTGCGAA TATTTGGATT TGCGACCAAT TCATCGTATT TTTCAGTAAT	2580
GTCGATGTAA TTGAATGGCA CACCGTATTC TTTTCTACA GAGTAAGGGC TGAAGAGGTA	2640
CATTTCTTCA TTTTACGAG CCAATTCGTA GAATTTATCA GGTACTACAA CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT	2760
GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCAATTG	2820
GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC	2880
TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC	2940
ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT	3000
ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC	3060
ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTTCAT TGGCAATATC	3120
GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC	3180
CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT	3240
ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC	3300
TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTTCAAT	3360
GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC	3420
TTTAAAGAAA GCATCCAAGG CTTCTTGTC TTTATGAAGC ATGATTTGTC CATTAACAGG	3480
ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT	3540
AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC	3600
TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTTCAGTT TTCCTGGTTG GAAACCTGAA	3660
AAGACTTCAG TTGGTGTGTTG GATAACAGGA GCTGCGCTAA AACCGAGCTC TTAACTTGA	3720
TCGACGTACT CAGGTTGCTC ATCAAGATTG ATTCACGAT AAGAGACATT ATTACTGTCC	3780
AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTACCATT	3840
GTGTAACCTC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTCTG	3900
GG	3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTGTCAG TTAGTAGGCG GTGAGACTCA	60
CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT	120

1212

CAATTGAGGT TGTTCACATA AAACCTCTATA TCAGAGAAGC CTGATATAGA GTTTTTTCTT	180
GCTAGTTTTTA GGATTTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC	360
GGACAATTTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA	420
GCTGTGAAAA TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGTT TTTTGAAT	480
TTTCATGATA TAATAGTCCA TGTTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC	540
GGACTGTAAA TCCGCCCCCTT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTCATTA	600
ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGCTACCC CAGTTCCTTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAAGT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC	840
GAATTTGAAG ATTTGCTAAA TAGCGTTAGT CAAGTTGAGA CTGGTGATGT TGTTAGTGCT	900
GAAGTATTGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGTCTTGA CTCTTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTTCTTGTA CTTCTGCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTTGATC TAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAACTT	1140
GTTGGTCGCG AAGAAGAAGT TGTTACTGTT AAAGGAACGC GTGCCGTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATTT ATCCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAACG CTGAGCGTTT TGTAGGTCAA GAATTTGATA CTAAAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTTCACGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAAGTGG TAAAGTTGCT	1440
CGTATCACAA GCTTCGGCGC TTTCGTCGAC CTTGGTGGTG TTGACGGATT GGTTCACTTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CCAAATCAG TTGTAAGTGT TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA	1680
GAAGGAACAG TTAAACGTTT GACTGACTTC GGTGCATTTG TTGAAGTATT GCCAGGTATC	1740
GATGGACTTG TTCACGTATC ACAAATTTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT	1800
CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG AAAAAAGAA	1920



1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT	1980
CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA	2040
AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTCTGG CTCTTTGTCA	2100
ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTTT	2160
TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG	2220
CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT	2280
GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTA AAGACAGTCT	2340
GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT	2400
CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10974 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTACAA AAGTCCAATT ATATGCGGAT	60
CTATACCTCC ACAATGTCCA TTATTATACC TAACTATAAT ATGAGCCGAA AACACTATAT	120
CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATTGCA	180
TTGTAACCAT CTCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA	240
CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTC	300
GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT	360
TTTAGCACTG TATAAAAACG TTTCAATACA CTAACCTCAA GAAAACCTCC ACTATTAATT	420
GAAAAAATTG ATAGAGATAA ATTAATAATC TATATTGAAA CTCATCCCGA TGCTTATTTG	480
ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAATA TTCATTACGC TCTAAAGGCT	540
ATGGGATATA GTCTAAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT	600
CGGTTCCCTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA	660
GGGGTTGAGA CCTATTTTTA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT	720
CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT	780
ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTTCAATAT ACTATGGCTC CGATGACCTA	840

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TAAAGATACG ATGACGAGTG ACTTTTTTCGA AGCTTGCTTC CAAAAATTCT TACTACCTAC	900
TTTAGATACA CCATCCCTTA TCATTATGGA CAATGCAAGG TTTCACAGAA TGAACATGTG	960
TAAGGAGCAG GGCATAGACT GTTACCACTT CCTACCTATT CACCCGAGTA TAATCCCATT	1020
GAGAAAATAT GGGCTTACAT CAAAAACATC TCAGAATAAT ATTGTCAAAT TACGATGCTT	1080
TTCTTGAGGC ACTTTTGTCC TATTCTTGTT TCAGCCGACT ATACTCCGTT ATTGGGCAGC	1140
TACGGAACAG TCGATGGGAC GATGGGGGGA CATAAAAAAA TCCTCCAGTT TTGTTTTTTA	1200
TAACAGTATA CTGGAGAATT GACAATCTCG GTAGATACCT CGTTATAGCG CGGTTACTTA	1260
TTAGGCAGTT ACAAACAAC TGTGAACAGA AAACATTCCA GAGTCAGACA AGACTTTGGA	1320
ATGTTTTGGC TCTATAATTT CTGTAGTGGG TAATCCCACC CCAGGAATTA TAGGGTCGTT	1380
TCTTGTAGAA AAAAAGCCCC ATATGACCTA TAATGAAAAG CGTCTAACCA ACTCATTAGA	1440
AAGGGTTCAT ATGGAACAAC TTAAGAATAC CACAGATTTG CTCGGATTGG AAGACAAAAA	1500
TATCAAAATC TTGTCTGTTT TGAAATACCA AACCCATCTA GTCGTTGAGG CAAAGTTGGA	1560
TTCCCCGCT CCTCCTGTC CTCATTGTCA AGGGAAGATG ATCAAATACG ACTTCCAGAA	1620
AGCCTCTAAA ATTCCGCTTC TCGACTGTCA GGGTTTACCC ACGGTACTGC ATCTCAAAAA	1680
GCGCCGCTTT CAGTGCAAGA ATTGCCTTAA GGTGGTCGTT TCTCAAACAT CCATTGTCAA	1740
GAAAAATTGC CAGATTTCCA ACATGGTGAG ACAAAAAATC GCTCAGCTCC TCCTTGAAAA	1800
GCAGTCTATG ACTGAGATTG CCCACAGATT GGCGGTCTCA ACTTCCACCG TCATCCGAAA	1860
ACTGAGGGAA TTTAAGTTTG AAACCGATTG GACCAAGTTG CCAAAAGTTA TGAGTTGGGA	1920
TGAGTATAGC TTCAAAAAGA GCAAAATGAG CTTTATTGCC CAAGATTTTG AGTCCAAATC	1980
CATCCTCGCA ATTTTAGACG GGCGAACTCA TGCGGTGATT CGAAACCATT TCCAACGCTA	2040
TCAGAGAGAG GTTCGGGAGC TGGTCGAGGT CATCACCATG GACATGTACA GCCCTTATTA	2100
TCGGCTCGCT AAGCAACTCT TTCCAAAGGC GAAGATTGTT CTTGACCGCT TCCACATTGT	2160
CCAACATCTG AGCCGAGCTA TGAACCGAGT ACGAATCCAA ATCATGAACC AATTTGACCG	2220
AAAATCCTTG GAGTATCGGG CGCTCAAGCG CTTTTGGAAC CCTCGCTTTT TCGTTTCTAG	2280
GCTCGGGCTA AATCAGTCCA CTGGACTGAT TTA CTACACC AGTATAGCTT CAAGCTCTGT	2340
CAGAAACGAT TCTATCAGCC CACGTTTCGA ATGCACTTAA CCCATCGGGA AGTACGAGAT	2400
AAGCTGCTTT CTTACTCTGA GGGATTACAG GTTCACTACG AACTCTATCA ACTCCTGCTC	2460
TTTCATTTTC AAGAGAAGAA TGCCGACCAT TTCTTTGGAT TGATTGAGCA AGAACTGCCA	2520
ACGGTTCATC CGCTTTTCA AACGGTCTTT TGGACTTTTT TAAGGGATAG AGATAAGATT	2580
ATCAACGCAC TTAAGCTGCC TTATTCCAAC GCTAACTTG AAGCGACCAA TAATTTGATT	2640

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACTTTA ACAATTTTAA AAAACGGATT	2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTCG TACTCTCCAG ATTGCAGCTT	2760
TTCGCCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG	2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTCTT TTGTTCCACT CGCTGACGCT	2880
GGCATAGGCA ATCATACCTG CATTGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT	2940
GACATCTGTG ATTTCCGGCTG CTAGGCGTTC TCTGAGACCT TTATTGGCTG CCACACCACC	3000
TGCCACAACCT AGGATTTTAA CAGGATATTT CTCCAAAGCC TTCTTGGTTT TTGCCATGAG	3060
AATGTCCATA ACTGCTGCTT GGAAGGAAGC ACACAAATCT TCTGTAGACA GGCTTTCTCC	3120
CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA	3180
CTCCAGATTA TCTTCCTTAA TCATGGCAGC GGGGAAATCA TAAATATCCT GCCCCTGATG	3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT	3300
ATCATAAGCC TCACCAACCG CATCATCAGC GGTTCCTCCA ACAATCTTAT AATCTCCTGC	3360
CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGCTGACC AAGAGGGCTA GCAAGGGAAA	3420
CTCCAAAGGC TCCACACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT	3480
CAGTGGAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC	3540
TCCGACCAAG CCTGGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC	3600
TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAATGACC TCGACATGGT GACGACTGGC	3660
TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT	3720
GGACAAGAGC TCATCGTCGT TTTTCAAGAC GGCAGACTG GTCTCATCAC AGGATGTCTC	3780
AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA	3840
CTGGGTCATG GTAGTAGGCC TTTGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAG	3900
ATGCTTGCGC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCTTGT TCTGTGGCA	3960
ATTGAGCAAA CAAGGCTGAC GCAATCCCCT GACCCTGATA AGCTCCTTTG ACAGCGATT	4020
GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC	4080
CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA	4140
GAGTCCAAGG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT	4200
CAGGCTGTTG TTGAATTCGC TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA	4260
CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC	4320
AAAATCATGC AAGGAGTCTG CTTCTTGTG CCAGGCCAAA AGAGCTAGAT TAGCTGCATT	4380

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GGGCAATGTT	TCTTTGTAAT	CAGTCCTTGG	CAAGTGTTTT	TGAATCTGCT	CAACAAAGGG	4440
GCCAACTTCT	CCGACAAAGG	TTACCTGACT	AGTACCCTTG	ACTTTTTCTA	GCACCTCTTC	4500
AAAAGATAGG	TGCGCTTCTG	CCATGACAGG	TTTGGCATT	TCATAAAATC	CTGCATAAAC	4560
ATTATTGCGA	CGCGCATCCA	TCAAGGGGAC	AAACAAACCT	TCTTGTGAT	GGGGCACCAG	4620
AGCCAAGAGA	CTCGACATAC	CAACCAACTC	GATGTTTCAGG	GTGTGAGCTA	AGGTCTTAGC	4680
AGTTGCTACC	GCAATTCGCA	AGCCTGTATA	GCTACCCGGC	CCTTCAGCTA	CCACGATTCG	4740
GTCCAAATCC	TTGGGTGTCC	AATCCAAACT	TGCCATCAAA	AAATCGATGG	CAGGCATAAG	4800
AGTAATACTG	TGATTTTCT	TAATATTAAT	CGTCGTCTCG	GCAAGAACCT	GCTTATCCTC	4860
TAAATAGCC	AGAGAAAGAG	CCTTGCTGGA	CGTATCAAAA	GCTAATACTT	TCATAACACA	4920
TTCTATCTT	TTTGTCTGCT	TACTATTATA	CTACAAAAGC	TGGCACATGG	GAATTTTCTT	4980
TGCCCCCAGA	CAAGAGTGCC	CTCACTTAAC	TAAAAATAAT	TTAAAAAAT	GCTCACTTTT	5040
CCTTTTCTTT	TCCGAATATA	AAAGTGAACA	AGAAAAAGG	AGGAAAGTTC	AATGACAAAT	5100
TTTGACATTC	TTGACAATCA	ATTTTATCC	TTATCTGAAA	ATGAATTATC	AGATATTGAT	5160
GGCGGTCTCG	CTCCCTTGGT	TATCTTTGGA	GTAGCAGTAT	CTTGGAAGGC	TATTGCAGGT	5220
GGAACAGCAC	TTATAGGTTT	TGGTTTGGCA	GCTGGTTATT	TTTTAGGAGG	AGATTAATAT	5280
GATGAAAGAT	TTGAACAATT	ATCGTGAAAT	TTCTAATAAG	GAATTGCAAG	AAATCAAGGG	5340
TGGCTTTGGT	GTCGGTGTG	GTATCGCTTT	ATTTATGGCA	GGTTATACCA	TTGGAAAAGA	5400
CCTTCGTAAA	AAGTTTGGTA	AGTCATGCTA	GATAAGAAAC	ACATTTTATAG	AAGGATAAAT	5460
TTTATTGTCT	TCATCTCTTA	CAGTTTGCTC	AGCATTCTCA	ATGATTTGAA	CATTACTACC	5520
ATCCCTTTAC	CATTGATTTT	ATCTGTTTGT	ATTGTTTTAT	TTTTATGCTT	CAACTCTATT	5580
TTTGATCAGA	ACAATGACTC	CCATAAAAAT	AATAAGCTTT	GAAAATTCCA	TTGTCATGTC	5640
ATGTTAGAAA	AATGCAAAGA	CCACCTCATC	TTGATAGATG	GGGTGGAATT	TTCGTGTCGT	5700
AAATCTACTA	TCTCTACATT	CCCAAACAAA	AAACCCAGC	ATAAGCAGGG	CATCTAAGCA	5760
TTTAATTCAA	AGTAAAATAC	AAACCAAACG	ACATAGGTCA	CGAGGAGGAG	AAAAAGCGAG	5820
TAGAGAGTCA	CAAAGGTCAT	TTCCACAAG	AACTTGGTTT	GTCGTGCTTC	CAGTTTGGCA	5880
AATAGAAGAT	TCCCCGCATA	AACGCAAGCA	ACAAAAACAA	TAAAAGCTAC	CAAGCGAGCT	5940
CCGATAGCAA	AAGCAAATAA	GTTATACATA	GGGCAACCTC	CTTGACTTAA	AATCTATATG	6000
GAATTATGAC	AAGCAATAAA	TTTCACTTCC	GTTATCAACA	TAATACATTT	TCTTTATTTT	6060
TGAAAACGCT	TACCAAAGAA	ATCGTCCCCT	AACTTTCTCG	TTCCGTCTT	TTACTAATTT	6120
TTCATTTTGT	GGTATAATTG	AAATAATTGT	AACGAATCAA	GGTCAATCTA	GACACAAAAT	6180

1217

GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTGTGAATA AGCTGACCTG TAAATAGAAA	6240
GGAAGTATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG	6300
AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA	6360
CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT	6420
TGTCTGACAA ATTGCTCGAT TACGAAAAAG AAAGTGGCGC CTTCGAAATT ACGGAGTTCT	6480
AATATGGCCT AACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA	6540
GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT	6600
GGGATTAAAT TCCCAGAAGA TGAAGTGGCTT GGTATCGACT ATGTCATTCC TGAAGTACTCT	6660
TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTTAA TCACACACGG ACACGAGGAC	6720
CACATTGGTG GGATTCCGTT CCTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG	6780
CTTGCCCTGG CTTTGATCCG TGGGAAACTC GAAGAACACG GCCTCTTGGC CAACGCCAAA	6840
CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTTCTTT	6900
AGAAGGACTC ACTCTATTCC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGAAA	6960
ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCGGACTTG	7020
CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT	7080
GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTTG GTCAGTCCAT TATGAAGATT	7140
ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC	7200
CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCGTTCT	7260
ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC	7320
TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA	7380
GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA	7440
GTACAATTAC AACCAGGTGA TACCGTTATC TTCTCTTCTA GTCCCATCCC TGGAAACACT	7500
ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTGGAAGT TATCCACGGT	7560
AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC	7620
TGCTTGATTA AGCCAAAATA CTTTATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC	7680
CACGCTGGAC TAGCAGTGGT TACTGGTGTG GAGAAGGACA ATATCTTTAT CATGAGCAAT	7740
GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA	7800
GATATCTATG TCGATGGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCCT CAAAGATCGT	7860
CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG	7920

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ATGATTCTAT CTGGTCCAGA CATCCTCAGC CGAGGCTTTG TCTACATGAG AGAGTCTGGC	7980
GACTTGATTG GCCAAAGCCA GCGTATCCTC TTCAATGCCA TTCGTATCGC ACTGAAAAAT	8040
AAGGATGCTA GCGTGCAATC TGTCAATGGT GCCATTGTCA ACGCTATTTCG CCCCTTCCTC	8100
TATGAAAATA CCGAACGTGA ACCGATCATC ATCCCGATGA TCCTCACACC AGATGAAGAA	8160
TAAAGCAAGA AAACAGCCCC GTCTCCGGAG CTGTTTTTCT CTATGCTTTC TTTTGAGATT	8220
AAAATCATA CTCAATGAAA ATCAAAGAGC AAAGTAGGAA GCTAGCCGTA GGTGCTCAA	8280
AGCACTGCTT TGAGGTTGTA GATAGAACTG ACGAAGTCAG TAGCCATACC TACGGCAAGG	8340
CGACGTTGAC GCGGTTTGAA GAGATTTTCG AAGAGTATCA ATAAAAATCG AAATCAGACT	8400
AGAAGGCTAA GCGAAAGCAT AACTTGAGTT AGCTCCCATG GTTCGGGAAA CTATGGGAGG	8460
CTGGAGATGA ATCAAAGCCA AGCTTTGAAC TCATTTCGTAA GAAGCCGACG ACGTATCATT	8520
TTGATTTTTG AAGAGTTTTA GAAATACTAC GATTTTTACC TTCCAGATAC ACCATCAAAA	8580
TAGAAATATC TGCTGGGTTT ACTCCCGAAA TACGGCTGGC TTGGCCGATG GTTTCTGGAT	8640
TGATGAGTTT GAACCTTCTGA CGGGCTTCGG TTGCGATAGA ATCAATGTCA TCCCAGTCGA	8700
TATTGGCCCG AATGCGTTTT TCTTCCATGC GTTTCATCTT GGCAACCTGG TCCATGGCTT	8760
TGGAAATATA GCCTTCATAC TTGATTTCTG TTTCAATCAA TTCGATAATC TTGTCATCCA	8820
AGTCTTCTGC AGCTGGTCCG ATGAAGGCCA CCACATCTTG GTAAGAAACT TCTGGACGGC	8880
GAAGGAATTC CTTGGCTGTC ACTGCATCGG TCAAGGGTTT GAAGCCCATC TCCTCAACCT	8940
TGGCATTGGT TTCCTTGACT GGCTTGAGTT TGATACTGTC TAGGCGCTTC ATCTCATTAT	9000
CAAATTGATT TTTCTTGATT TCAAAACGAG CCCAGCGTTC ATCGTCCACA AGGCCAATCT	9060
CGCGTCCCAT CTCAGTCAAG CGCATATCAG CATTGTCTAG ACGAAGAATG AGACGGTATT	9120
CAGCACGACT GGTCAAGAGA CGGTAGGGTT CAATGGTTCC CTTGGTCACC AAGTCGTGCA	9180
TCATCACCCC GATATAACCA TCACTGCGCT TCAAAATCAA TTCAGGCTTG CCTTGATT	9240
TCAGAGCCGC ATTGATACCC GCGATAATCC CTTGGCCTGC TGCTCTTCG TAACCTGATG	9300
TTCCATTTGT CTGAACAGCA GTGAAGAGAC CTGAGATTTT CTTGGTTTCC AAAGTCGCAC	9360
GCAACTGATG AGGCAAGACC ATATCATACT CAATAGCATA ACCTGTCCGC ATCATCTCTG	9420
CATTTTCCAA ACCTTTGATG GAATGCACCA AGTCACGCTG GACATCCTCA GGCAGACTGG	9480
TTGAAAGTCC TTGCACATAG ACTTCTCAG TATTGCGCCC TTCTGGCTCA AGGAAGAGTT	9540
GGTGACGTTT CTTGTCCGCA AAGCGCACAA TCTTGTCTTC AATCGACGGA CAGTAACGAG	9600
GCCCCACTCC CTTGACCACA CCTGTAAACA TAGGCGCACC GTGGAGGTTG TTTTGGATAA	9660
TCTCATGACT GGTACCATTG GTATAGGTCA ACCAGCATGG TACTTGGTCC TTGACATAAT	9720

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CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG	9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC	9840
CGATTTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT	9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTC CCCACGGAGA GCAGTCCCTG	9960
TCGTCACAAT AACAGCCTTA GCAGCATATT CTTGATGGGT GGCTGTACGC ACACCGACAA	10020
CCTTGCCATC TTCCACCAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT	10080
GGTTTTCAAC CGTCTTGGC ATCTCCTTAG AGTAAAGTTC CTTGTCAGCC TGCGCACGAA	10140
GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT	10200
CAATGGTTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG	10260
CAGAACCAACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG	10320
CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGTG	10380
CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT	10440
ATTCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTAAAA	10500
AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC	10560
TTTTCTCATC TTCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA	10620
ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA	10680
GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCTTCAC TTCACGGACT ACCGCGTCTT	10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA ATACTTGCCC TTGTCTTTGG	10800
TAACTAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT	10860
TGTCTACTTT TGTCCGAAAG TCTTGTGAG TCATTCTTGT CTTTCCCTT AAACGACACA	10920
AAAACAGTCA AAACACAAA GAAGTGCAGG ACAAAAAAGC CTGCAACATC CAGG	10974

## (2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 987 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCGTTATGA TTATGGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTTATCT	60
ATATAATAAG TGAAAATATA ATAAGTGTCA AGTAACTGAA GTGAATTTTA TAAAAAATT	120

1220

ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTTGTC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAACATATCAA	240
CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAAT	300
CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTTCAAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATTCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTCGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCCTCTT	780
ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TGCGCTATTT CAACCAATTT	840
TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC	960
ATAAGATTCT ACTGCCCAA CTTAAG	987

## (2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTTCGAG TGAGCCCAT AGCTTTGAGC	60
GCATAGTGGG TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTTCAGT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTAAAGT CTATCTCTAT CAACTTTTCT TGGTTTTGTT	180
CCTTTTACTT GGTGGTTTAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACAA	300
TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAATT	420
CAAAGCACTA TAAAGTAAAT TGAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACCAACGTT	540



1221

CCTCTTTTTT	ATTACTAAAA	TTCAAAGAAT	TCCAATGCTT	TTTTCAAGAG	CAAATCCGTA	600
TATTCTGGAT	CTTCTTGGGC	TACTTCTATT	TCCCGCTGAA	CTTTTCCAA	ATCATCTGTA	660
ATCACTCCAT	CTACTCCTAA	GTGAAGAGAT	TTGCTGATAG	CTTCTGAATC	ATTGACAGTC	720
CAGACATAAA	GTTTCTGATC	CGTTGTCCAT	AGTTTGCTTA	CAAAATATTC	ATCCAAGGTT	780
GAGTACTCCA	TAGTATATCC	TGTCGCTCTT	GTTTTAGGAA	AGACAGAATT	GTAGGGCATG	840
ATGAAATAAA	CTGGTAGTTC	GGCATCATAC	TGCTTACTTT	TTTCGACAAC	ATGGTAGTCT	900
AAAGACTGGA	TTTGATGTCC	ATAAATCTTG	AGCTTTGCAG	CATAACGGGC	TAAAAAGCGG	960
TTCATCATGT	CTGGACTATC	TTTTTTACTG	GTTTTAATTT	CAATTAGTAA	TTTTTGACCA	1020
AGTTCGTTGG	CTCGACTGAG	ATAATCTTCA	AAGCTTGAAA	TTTTAGTCTG	GTAGCCATTT	1080
TCAAAAATAT	CAATCCCTTT	AAGCTCCTCC	AAGTTTAAGT	CTTGAGGACT	TTTATTGATA	1140
CCTGCTAGAT	TTTTCAAGTT	AGCATCATGC	ATCATGACAA	ACTGCCCATC	TTTTGTTTCC	1200
TGCACGTCCG	TCTCCACCAA	GTCTGGTTTG	AGTTGTGCTG	TAGTTTCCAA	GGACTCTACT	1260
GTATTTTGAA	TCCCATTTGC	ATTGGAAACC	CCTCGGTGAG	AAATAAGTTG	AGGTAGATGA	1320
ACCATGGGAG	CCTCCAGATA	AATATAACCT	TCTAAGGCAA	AGAAAAGACT	GGCACAAGTC	1380
ATGACACCCC	ATCGCACGAT	GTGATCTTTT	TCTCTCCTAG	GAAGCATATC	CAGCTCCTTT	1440
CCTGTCAAAA	ATGAAACAAA	TTTAACCAAA	AAATAAGTCA	GAGCCATATA	ATAGAGATTT	1500
TTAATCACGA	CAAATTTCAA	AATACCAAGA	ATCAGAGACT	CTCTCTGAGT	GATATCATCT	1560
ACCAAAGTTT	GAGCCAATAA	TAAAGGAATC	AAAGGAAGAT	AAATAATAAA	ATGTGCTTTG	1620
AGCAAGATGT	AAAATAAATT	CCAAGCATAA	AAAGTAACTC	TCTTCTTGGT	TTTCTCCAAG	1680
CTAAACATCA	CTGCTTCTCG	AACAGTCAGC	TGATCATATA	CAATCTTCGG	AAGGGCAAAC	1740
ATCAATCTGA	CAGAGACATA	GAGAAAGATA	AGAGATAGAA	GTAGGATGCT	CAGCCACCAC	1800
ATCCAATATC	TATCTTCTAA	ATAAGCTTGG	ATAAACTCTG	GAATGACGAT	TTTATTAAGA	1860
TAATAAATCT	TCAGCATTTT	CCGTATAAAA	GGAAACAGCA	TAGCTATATA	GAAAAAGATA	1920
AACAAGGCTT	TAGCGCAAGT	TAGCTTTTTT	ATAAATCCAA	AACTTTTCATG	GAAAACCTTG	1980
CGGATATACT	CAATTAGCCT	TCGCTTTTCA	TTATAGAGGA	GATGACGAGC	ACCAATAAAG	2040
AGGAGTCCTA	TTTGAAAATA	AGCAACCAGA	AGGTTAATTA	CAATCAAGGC	TAAAAAAGCT	2100
AGACTAATCA	ATGGAGAATG	AGTAAGGATG	GCTAAGACAT	TGTTATAGGA	AATAAAAAGA	2160
TAACCTGTCT	GATCTAATAA	GAAGCTAGCC	AACCATGAAT	TGAATGGTAC	CCACAAATAC	2220
TCCACTATCA	TAAAAATCAA	GAAAAATAGA	AAGAGGATTT	TATCAAGATC	GAGGTAAATC	2280

1222

TGTTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTCATAG GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTTCTGTC TCTAACAATT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA CCTTGAAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAAA AGCTTCATCA TACAAATCCA	2580
CCTTGACTTG TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG	2640
CAGCATTGTA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5638 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG	60
AAAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGA CTACATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG	240
AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTGC TGAACCAGTT GGTGTTGTTT	420
GTGGTATTAC TCCAACAACA AACC CAACAT CAACAGCAAT CTTCAAATCA TTGATTTTCA	480
TGAAGACACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCCT TATGAACCAC GAAGGTGTTG	660
CGACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC	720
CAGCTCTTGG GGTAGGTGCC GGAAACGTTT CAGCTTATGT TGAAAAATCA GCAAACATTC	780
GTCAAGCAGC ACACGATATC GTCATGTCTA AATCATTTGA TAACGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTACTTTGTA AACAAAAAAG AAAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
GCGTCAAAGC AAACAGCAAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGGCGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC	1140
CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA	1260
CTAAAGAATT TGGTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACTCA CCTTCTACTT	1320
TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC	1620
GTGCAATAA GGTGTGTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA	1680
CTGTAAACCG TGGTACTGAG ATTATGCGTG CTTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG	1800
TGGACTTCCG TGACCTTGTC CAAAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTTCCAG	2040
GATTTGTTGC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAATCTCGA AAGCTCAGTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG	2220
CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG	2280
CCCATAAGAT TGGTGCGCAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GGTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGCAGATGAA AAATACCAAG ATATCGCACG CATGCTTGGA CTTCCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT	2580
CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTT ACCAGCTAAC CCACGTCTTC	2640
CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC	2700
CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG AAAAAACTC AATTTGAGGG	2760

1224

AAAGATCCAG TAATTTTCT ATGATAAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT	2820
AGGATGCCTT TTTATGATAT TGAGGCCTTT TTGCCCTTT TGAAAACTA GAATAGAAAC	2880
AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTTCTAAAAC ATTGTTAGAA	2940
TTGATTGA CTGTCCTGAT CGATTGTCC TGTCTTATT TCATTTGAT ATATAAAAA	3000
TATAGTATAG TAGACTGAAT CTAAATAGT ACGAAACAAT TGCTAAAACA TTTATAGAAA	3060
TTAATTTTAC TTTTCTGATA GAGTTGTCA CATCTTATT CAATTCATA TAGTTAATT	3120
TAAGAGTAGT ATTTACTAAG GCCCAATTAA AATCAAAGAG CAACTAGAA AACGAGTGCC	3180
ATTCAGCTCA AAACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT	3240
TACGATAAAA CGATGACAAG GTGTGTTGCT TTTTGATTTC TAAAGAGTAT AATGATAGAT	3300
CTCTATAAAA TAAGTGCAG GGAATGAGC TTTTATAGTC CTTTCGTTTT AAAATACTAT	3360
CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCCTCATCAT ACATATTAAA	3420
TAAATAGTGG CTCATTCAAT TTTCACTAG AATAATAAGC TAGTATAGTA AACTGAAATA	3480
AGATATAAAC AAATAAATG GAGCTTAACA TCCATTTCCA GCAATTTTTT AGAACTACA	3540
GTGGACTATT CTAGATTCAA CATATTATAA AAACAGAGT AAAAGAAAAG GATTGGATCT	3600
TGTGTAATGC AGGATCCAAT CCTTCAATC ATTTTGTCCA ACTTTTGAG GTTCCTACAA	3660
TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTTAT TTTGATAGAG	3720
ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCCATTT GGTCTTCTGC	3780
ATGCATAAAT AGCAAGGAGA ATCCTATTTT TTCTCCAGTA GCTTCTTTTT GTATGAGATT	3840
AGAGTGAATC TTGTGCGCTT CTAATAAGGA GTCTTCCGCT TCTTCAACTT TAATTTTCGC	3900
TTCTTTTAAA TTTCTGCCT TAGCTAGTTG GATGGCTTCA ATAAAGGATG ATTTGGCTGC	3960
TCCACTATTG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTTCT	4020
CCTATCCATG CAAGTGCTTG TTCCAGAACT TTTGCTCCAT TCATCATTCG GTAATCCCGC	4080
ATATCAATGG TATCTACAGG GATATTTCTT GCAATTTCTT TCACAGCAAG TAACTCATAA	4140
CGAATTTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATTCTTTTT AGCTTCTGTC	4200
ATTGATTTTG CTTGGATAGA GATTTCAATC CCACGTTTCA TCGCACTTTG TTGCATTTTT	4260
TTAACAAGCA TACTTGTCGA CATTCCCGCA TTACATACTA ATAAAATTG TTTCATAATC	4320
TTAACCTTCC ATTTCTTGTT CAACAACTTT GTCATTAACT TTGATAAATG GAATGTATAG	4380
AAGAACTCCA AGTGCAAAGA TGATGAATTG AACTAGAACT GCTCTCACGT CCCCTGCTGT	4440
TGCTAACCAT GCATTTAAGA ATACTGGTGT AGTCCAAGGA ACTTGATATAA ATGCAGGACT	4500
CATGAATTCT GTAAGTGTG CTAAGTAGCT GATTAAAATA CCAAGGACTG GAACTGTGAT	4560

1225

AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTATAGAGA CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTTCT AGGATGGCAC TGTAATAAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTTCTTAAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTTCATT TGTAAGCTT TAACGTTTGA TAATTCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCAGCGAA CATTGCGCCT GTACCTGTGT TGTTGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAACACAG AACTGTATT TGGCATCATC	5280
ACAATTAAAG AACTAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATAC CTGAAATACT TAAAGTACCG	5400
TTTGCAATTG TTATTCCTCA ATATTGGAAT CTGTGTAATG TATCCCCTTG GAAAATCCAC	5460
TTAAATACCG TGTGTTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTMTTAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCCTTTT AAAAAAAA	5638

## (2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4745 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTTACCGTA TGTTCAAAGA ACATGGTGTA	300

1226

GCTGTGCCTA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTCAGA TACCCTTCTT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTG CTCCTGAATT GGCTGAATTG	420
GCTGGTGTGA ACTTGGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT	480
AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTGAACCT CAACGGAAAT	540
AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTGGGA ACGCCAAGCA	600
GAAATTGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAACTCA GAAATCTTGG CTCCTGGTGC CAATATGGAC	720
AAGGTCGAAG CGGCTTTCAA CTTCAAACCTT GAAAACAATC ATGCCCTCCT TGCTGGTGCC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT	840
GGGTGTCAGC TCAAAATCGG AAAGTCTAGT TTGCCCTATA TCGCAAGGAG TTTCGGCTCC	900
TTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTG ATTTTGTGA GAGATGGGTC	960
AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAACAT AGCCATGTTG CCATTTATTT	1020
GGATGGGATG ATTTATCATG CTAGTGGACA GGCTGGTGT GTCTGTCAAG AACCGGCAGA	1080
CTTCTTTGAG TCCAATCATT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTAC AATGCTTCTT TCTATCCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAAACTAT	1260
TCCTATGAAA TTTGGAGWTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCCTGTTT CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC	1380
ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTCTACGG GAAATTAAGG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA	1560
GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC	1620
GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGTTGG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAAAGA CGGACTTTGC GCGCATTAAT ATGACCCTGT CCAATTATTT	1800
TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT	1980
AGCCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA	2040
GAGGTTAACT TTCTACTTAG CGTGATTCTT TGTTCCTGAG TACATTGTTT GACTTTCCTT	2100

1227

AGTATTCGGT ATAACTATA TGTAACCGGT AACACATATC GGAATAAACT AAAGGAGACA	2160
ATCATATGTC ACTTGAAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAAA GAAGGTTTTG	2220
GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTGAAAAA ACAGTTGCTA	2280
AGGCAAAAGA CGTTGTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCCGTT GAAGGTTTGA	2340
AAAACGTTTT TACTAAAGAA TAGGAAAAA TCAAGGGTTT CATTTTCCCT TGATTTTTTC	2400
TATTCCTATA AATAATTTTC TGCGACGGCT GTATCTCCTG GGTAGGATTC TTTCTTGCCC	2460
TGGATGATTT GGTAACAATC GGCTCCCTTA CCCGCAATAA TAACTGCATC TAATTCGTGA	2520
TTTGTGATAG CCATTGCCGC CTTGATGGCT TCTTGCGGAT CCGCAATCTT TTCAACAGGA	2580
TGATTGATGT AGCTACTAAT TTCATCTGCA ATGGCCATTG GGTCTTCATA GTTAGGGTCA	2640
TCAGCAGTCA GAAAGACTTG AATCTCAGGG TGTGATTGA GGAGGAGGCC AAAGTCCTTA	2700
CGACGACTTT CTCCCTTGTT TCCTGTTGAT CCCAGAACCA GAGCAATCTT TCCGGTTTGA	2760
TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTGTGGGC ATAGTCGATC	2820
AAGACCTTGG CTCCATTTTT CTGAGTGAGG ACTTCCATAC GACCAGGAAC GCGGGTTGCA	2880
GCGATGCCTT TTTTGATGTC CTCAAGACTT GCTCCGAGAC GGAGACAAGC AAGTCCAGCA	2940
GCAACTGCAT TTTCTTGGTT GAAGTTGCCA ATGAGTTGAA TATCATAATC TCCAGCGAGT	3000
TTACCCGTAG CTGAAAAGCT AAAGGCTTTC GAATTCTCGA TTTGGTTATC AAATTGGCTA	3060
CCATAGAAAT CATGGTCTTG ATCTTCAACC TGTTCTTTCA AGACTGAGAA GTGGTCCATC	3120
TCACTGTTAA TGATGACTGC TCGGCTCTTT TCCATCAAGA GACGCTTGTG GTAGAAATAG	3180
TCTTCAAAGC TAGGGTGTTT AATCGGGCCG ATATGGTCTG GGCTGATATT TAGGAAAAC	3240
CCCACATCAA AGGTTAGACC ATAGACACGT TTGACCAGAT AGGCTTGACT GGAGACTTCC	3300
ATGATGAGGT GGGTACGGTC ATTTTGCAAC GCCTGATTCA TCATGTCAA GAGGTCAATA	3360
CTCTCAGGGG TTGTCAACGC TGACTTAAAG AAAGTCTCGC CATCAAGAGT TGTGTTTCATG	3420
GTCGACAACA TAGCAGGTCT ATGCCCTTGA GATAAGATGT TATAGGCGAA ATAGGCTGCT	3480
GTTGTCTTAC CCTTAGTACC AGTAAAGGCA AGGAGTTTGA GTTTTTCTTG TGGATTACCA	3540
TAGAACTCCA TGGCAATCAA ACTCATGGCT TTCTTTATAT CGTTCACAAT GATGACAGGG	3600
ATACCGACTT CGTAGTCCTT TTCAGCTACA TACCAAGCTA ATCCTTGTGT TATAGCAGAA	3660
AGAAGGTATT CTTTTTTAAA GGCAGCGCCT TTTGCGAAAA AAAGAGTGTC TTCTGTTACT	3720
TTTCGGCTGT CGTAGCTGAT GCTATCAAAA ATAACCTTGC TGTAGTTGTA GTGGTAATGA	3780
CCTTGGTCAA TAATTCGCG AAAAAGGCCA TCTTCTTTTA AAATATCTAA TACGGTTTCA	3840

1228

ATCTTAATCA TACTTTCTAT TGTAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCGA TGTTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACTTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCTG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCT	4440
ATGCCATGAG CCAAATGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGTA GCCAGTTTTG CAGTCTTGAT TTATTTCTCT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGGTTG	4680
ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

## (2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1900 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAACCATC ACACCAGTTA TACCATTTTG CTTCATACCC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAACAGAG TAAATCTTTC TTTCCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTCTCTCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTTAAATCGC	480



1229

CATTGGAAGC GGAgCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA	540
CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAAGTCCCA GATAGACTCT TGATACCAGC	600
ACACTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA	660
ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC	720
CCACTTGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC	780
TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG	840
AAGAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA	900
GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAAT AGTCAAATAA	960
TCTGGTAAGT CTCCTCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA	1020
GGGTAAATT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC	1080
ATTAAAAATG TTTGTTTATC TCTCATAATG TTTTAAGGTT GGTTTCAAGA GAACATACAA	1140
CAACCAGAAT GAAACGGAAA AGATAACACC TTCAATCAAG TTAAAAGGTA ATACCATGGT	1200
CATTAGGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA	1260
CAAAGGAACA GCATAAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC	1320
AGCTAGAGAG CCTAGTAGGA AACGAAGGT TGTCCGTTCC TTTTCCAAA TCAAAGCAAA	1380
TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTAC	1440
TCCTTGGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsc	1500
AGGCAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAATT CGATCTTGAG	1560
GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAAATG AGATGGCTGA	1620
TAGAATTGCA ATGGTCGAAA GTCGACGTGT GTTTGTCATA ACAGGTTCTT CCAATTTTCT	1680
ATAAAATCAG AAGAAGTTGG AAAGGATTCC TCTATCTATT CTCACTTTTT ATATCCCAA	1740
AGTCCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC	1800
TATCAAAACA GACAAGGCTA TTCTTTCGTC TTCTCCCATC CAGACTATAC TGTCGGTTGT	1860
GGAATCTCAC CACATCACGT TCGCTCACG GACTTCTTTA	1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4692 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA AAAAAATAA TCCTCCTCTC	300
TCTTTTATTG AAACCGCTTT CTTATGTGAT AAGAATAACT TTTTATLAT TTGTTGTCAA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTTAACT	540
AAAAAGCAAT TCAAACTATT GTAAAATTCC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATTGC TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA	720
GATAGAACCA ATAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTCTGG TGTCGCAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTTCT CTCTTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTTGTT	900
AGCTTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTCC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTTCTTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCCT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCAGGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTTCCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

1231

ACCAGCAAAT GGTGAGTTGT TGACCAAGAA AGTCATTTGA AGAGTTGGCT CATCGATGTG	1800
TAGGATTGGA AGAGCTTCTA CTGCATCTGT CGGAGTGATG GTTTCACCGA CAAAGATGTC	1860
TTCCATACCT GAAACGGCAA TCAAGTCACC CGCTTTGGCT TCTTGGATTT CACGACGTTT	1920
CAAACCAAAG AAACCGAAGA GTTTTGTAAC ACGGAAGTTT TTAGTTGTAC CGTCAAGTTT	1980
AGAAAGGGTA ACTTGGTCCC CAACCTTAAC TGTACCACGG AAGACACGAC CGATACCGAT	2040
ACGTCCAACG AAGTCATTGT AGTCCAAAAG TGACACTTGG AACTGCAAAG GCTCATCTGA	2100
GTTATCTACT GGAGCTGGGA TATGGTCGAT AATCGTGTC AAGATTGGTG CCATAGTCGC	2160
TTCTTGGTCA GCTGGATCAT CTGACAATGA AGAAGTTCCG TTGATCGCTG AAGCATAAAC	2220
CACTGGGAAA TCAAGCTGGT CGTCATCTGC ACCAAGCTCG ATGAAAAGTT CCAAGACTTC	2280
ATCCACTACT TCTGCTGGAC GAGCTGATGG CTTATCGATT TTGTTAACAA CCACGATTGG	2340
GACAAGGTCT TGTTCCAAGG CTTTTTTCAA TACGAAACGA GTTTGTGGCA TGGTTCCTTC	2400
ATAGGCATCT ACGACCAAGA CAACACCGTC AACCATTTTC ATGATACGCT CAACTTCTCC	2460
ACCAAAGTCC GCGTGTCTG GTGTGTCCAT AATGTTGATA CGAGTTCCGT TGTAAGCAAC	2520
GGCAGTATTT TTAGCAAGGA TGGTAATTCC ACGCTCTTTT TCGATATCGT TTGAGTCCAT	2580
AGCACGCTCT GCCAATTCAG TCCGTGCATC AAGCGTTTCT GATTGTTTCA ATAATTCGTC	2640
AACCAGGGTT GTTTTACCGT GGTCAACGTG GCGGATAATC GCAATGTTAC GGATATCTTC	2700
TCTTAATTTT GTCATGATTT CCTCTATAAT ATTCAAAATT TATTTTCTAA CTGAACGATT	2760
ATACCATAAT TTCAAATAAA TAACATAACT CAAGCAAGTG TAAATGTTTT CACTCTGCTT	2820
TTCTTTTCAC GTCAAGCCTT TTCAAAGCGA GCGACTTATG ATAAGATAGG CACAGTATGC	2880
GTTTAGATAA TTTATTAGCT CAAGAAAAA TCAGCCGAAA GGCCATGAAG CAAGCACTCC	2940
TCAGAGGGGA AATTCTAGTC GATGGTTGCC CAGCCCGCTC CCTAGCTCAA AATATCGATA	3000
CAGGACTACA AGAACTCCTT TTTCAGGATC GAATCATTTCA AGGCTATGAA CACACCTATC	3060
TTATGCTTCA TAAACCTGCT GGTGCCGTTA CAGCCAACAA AGACAAGGAA CTTCCGACCG	3120
TCATGGACCT GCTTCCATCT AACATCCAGT CTGACAAGCT CTATGCCGTT GGCCGACTGG	3180
ACCGAGATAC AACGGGACTC CTCCTCTTGA CCGATAACGG TCCCTTGGGC TTTCAGCTCC	3240
TCCATCCCCA ATATCATGTC GATAAGACTT ACCAAGTTGA GGTAAATGGA CTTCTAACAC	3300
CTGACCATAT CCAAACCTTT CAAAAGGAA TTGTCTTTTT AGATGACACT GTCTGTAAAC	3360
CCGCAAACT AGAGATTCTA TCTGCAAGTC SCTCCCTCAG TCAAGCCTCT ATCACCATT	3420
CAGAAGGAAA ATTTTCATCA ATCAAGAAAA TGTTCCTCTC GGTGTTGTT AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTGAACCC AGATTTAGCA GAAGGTAAC	3540
ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAAA CTATTTAGAG ATGAGTCGAT	3600
AAAACAAAAA AAGCTTTAAA ACTAAAGCTT TTTCTTTTA TTTACGAAA AATTAAGGCG	3660
ATTGCTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAATTGTGA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCAAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA	3840
AAAAGTGGAT TTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT	3900
TAATTATACT ATAAACAAT AGCTTCATCC TATCATTCGA CTAATTGGA AATAAGGTTA	3960
GCTAGTCTTC ACTTCCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AATCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAC	4080
CGTTGCGCAC GTTGGTTTTC	4140
GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTCA ACTGACTTGA	4200
AGGAATATTG CGTGCACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGGT CGCGCAAATC	4260
AATCAATTGA CCCGTACGAA TCAAGGCTTC AAACCTCTCA TTGTCCACAA TTTTAGCCGC	4320
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA	4380
CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTCT CAATATAATC CAATTCTACC	4440
TTGTGCTCTC TGCGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCCT	4500
GCATCGTAAA TCCGAGATAG TTCCAACCTC ATCAGTTCAA TATCATATAA GCGTTTCCC	4560
ATGTAAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4620
AGACTCATTC TAGCAAAATT TTGTGTTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA	4680
TTTTCCTATC TTCTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC	4692
AACAATTACA TT	

## (2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA	120
AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAA GCCTCCTCCA	180

1233

AAACTACCA AAGTCTTTCG TAAATCCCAG ATTTTATCCA ACTGCTTGAC GAGGGAAGTC	240
GTCTGACGAA CGCCTACAAT AGTTGCTAAC ATACTTCCTA AAAAGAATGG ATAGACATGA	300
GTTAAACTCG AGAAATAAAC AGAGGAATAA GAGGTCCTA GAAACTACC AATAAACATG	360
GAGAAGAAAC TGATCAAGAA GGCAACAGCA GATAAGAGAA AGACCATCCC CTTCAACTGA	420
CCATTGATT TAGCTTGTTC GGATAAGAAC CAACTGCCA ATCCCCAAG AATATAGTAG	480
TGAACCTCAA CTGCCAACT CCAATTATGA ACAAACAAAT GAGGAATGAA CTGAGATTCA	540
TAACTCCAC CTGTTAGGAG TTCATAGAAG TTGGTCATAA AGCCTAAGAC GCCCGCAATC	600
TGGCCACCAA TTCCAGCAAC ATAGTCTTGG CGAACCAAGA AAGTAAAAGG CATGGTCACC	660
AAGACCATCA AAACCACAGG TGGCACAATC TCGATAAAAG CGTCTT	706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTCAATT AACTTTTGAG CAATTTTTTG	60
GTTGATGATA CGAGGGATTT GGTGATTTTT CTTACCAGG GGAGTCTCAG CAACCATCAT	120
TTTTGAACAG TGATAGCACT TGAAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC	180
AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTGAAAG TCATATTTCT TCATTAGACT	240
TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTGTGGGT	300
ATCCATATTG ATGATATCTA GAATCTTGAT GTTTGGGTCT TTAATATCGA GCAGTTTGT	360
GATAAAATGT AATTGTTCCA TATGATTCTT TCTAATGAGT TGTTTGTGCG CTTTTCATTA	420
TAGGTCATAT GGGACTTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT	480
TACCCACTAC AAATATTATA GAGCCCGAAA ATATGGGAAA ACTGATCCTT GTTCTGCTT	540
TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAATT CTCCGATATT CTCTAAAGTT	600
TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTTGCCATAG AAATATAAAG	660
CGTTTTATA TATAATATAA TTATCAAAG ACAAAGGAG TTCACCTCAT GGTAGAATTG	720
AATCTTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCAGT TGAAGATTTC	780
AACTTGAACA TCAAAGATAA AGAATTTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA	840

1234

TCAACTACAC	TCCGTATGAT	TGCTGGTCTT	GAAGACATTA	CAGAAGGTAC	TGCATCTATC	900
GATGGCGTAG	TTGTCAACGA	CGTAGCTCCA	AAAGACCGTG	ATATCGCCAT	GGTATTCCAA	960
AACTACGCTC	TTTACCCACA	CATGACTGTT	TATGACAACA	TGGCTTTCGG	TTTGAAATTG	1020
CGTAAATACA	GCAAAGAAGA	CATTAACAAA	CGTGTTCAAG	AAGCAGCTGA	AATACTTGGA	1080
TTGAAAGAAT	TCTTGGAACG	TAAACCAGCT	GACCTTTCAG	GTGGTCAACG	TCAACGTGTT	1140
GCCATGGGGC	GTGCGATTGT	CCGTGATGCG	AAAGTATTCT	TGATGGACGA	ACCTTTGTCA	1200
AACTTGGAATG	CCAAACTTCG	TGTATCAATG	CGTGCTGAAA	TCGCTAAAAT	TCACCGTCGT	1260
ATCGGAGCTA	CAACTATCTA	TGTAACCTCAC	GACCAAACAG	AAGCGATGAC	ACTTGCAGAC	1320
CGTATCGTTA	TTATGTCAGC	TACTAAGAAC	CCTGCTGGTA	CAGGTACTAT	CGGACGTGTA	1380
GAACAAATCG	GTA CTCTCA	AGAAGTTTAC	AAAAATCCAG	TTAACAAATT	CGTTGCAGGA	1440
TTTCATCGGAA	GCCCAGCTAT	GAACCTCATC	ACCGTGAAAT	TGGTTGGTAG	CGAAATTGTT	1500
TCTGACGGTT	TCCGTTTGAA	AGTGCCAGAA	GGAGCATTGA	AAGTTCTTCG	TGAAAAAGGC	1560
TACGAAGGAA	AAGAATTGAT	CTTTGGTATC	CGTCCAGAAG	ACGTGAATGC	AGAACCTGCT	1620
TTCTTTGAAA	CATTCCCAGA	CTGTGTTGTA	AAAGCGACTA	TCTCTGTATC	AGAACTGCTT	1680
GGTTCAGAAT	CTCACCTTTA	CTGTCAAGTT	GGTAAAGACG	AGTTTGTGTC	AAAAGTTGAT	1740
GCTCGTGACT	ACTTGCAAAC	AGGTGCAACA	GTTGAGCTTG	GATTTGACTT	GAACAAAGCA	1800
CACCTTCTCG	ATGTAGAAAC	TGAAAAAACA	ATCTACTAAA	ATAAATAAAA	TTCAAAGCAC	1860
TACAAGAAAA	GATATCTCTT	TATCAATTGT	AGTGGAGAGA	TATCAGTTAA	TCTAGGGAGA	1920
GAAACAAAAT	GCTTCTCTCC	TTTTTGCTAG	AGAAGTCATA	TTATGCATCT	ATATTGTGAT	1980
GCTCTTTAAT	ACTCTTCGAA	AATCTCTTCA	AACCACGTCA	ACGTGCGCCTT	GCCGTACGTA	2040
TGATTACTGA	TTTCGTCAGT	TTTATCTGCA	ACCTCAAAGA	TGTACTTTGA	GCAGCTTACG	2100
GCTAGTTTCC	TAGTTTGCTC	TTTGATTTC	ATTGAGTATT	ATTTGTGGGT	ACCATCTACA	2160
AGTGAAGCTA	TATGCGTAAA	CTACGTGAGC	AATTGAATTC	GAAGTAGAGA	GGTAATAATA	2220
AATTTATGCT	ATAGTTATGG	TGACTTGTAT	GCTTTTGATT	CTAGTTTATC	AAATAATAGA	2280
TTAGAATTGT	CAGATAATAT	CATTTTGTGT	TATAATGAAG	AAAAACAGA	GGTGTTCAAA	2340
TGTCAGAAGC	AGGTCATAAG	TTTTTAGCAA	AATTGGGGAA	AAAACGCTTA	CGTCCAGGTG	2400
GAAAGCGTGC	CACAGATTGG	TTAATTGCAG	AAGGAGGATT	TTCAAAGAA	AAGAGAATAC	2460
TAGAGGTTGC	GTGTAATAGG	GGAACCTACAG	CAATTGAGTT	GGCACAGCGT	TTTGGTTGCA	2520
AGATAACTGC	TGTTGATATG	GATGCTCAAG	CTTTAGAAGT	GGCTAAAAAA	TCTGCTGGAA	2580
CGGCAGGTGT	TGCTCATTTA	ATCAGTTTGT	AAAGAGCAAA	TGCAATGAAA	CTTCCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG	2700
CTAAGAAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA	2760
CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA	2820
TTCATGTAAA TGTAGGTCCT TTAAGTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG	2880
GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA	2940
TTTATGACGA AGGTTTGCTA GGAAGTTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA	3000
ATAGAAAGCA GTTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAAACAG AAATTGGGCT	3060
TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTT	3120
CCTTTTTTCT TTCTTAAAAA ATATGCTATA ATAGAGAGTA AAAAAGTTTG AAAGAAAGAA	3180
AAAGATGAAT TTAAAAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2885 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG	60
CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT	120
TGTAAGTTAA TTCATTGTCA CATATTACTC TTAACTGAT TGAGTGAGTA CCGCTTATAT	180
TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC	240
CGCTCATTGT AAAGTATCTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT	300
TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA	360
ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA	420
GTAGCTTCAA ACTCTGTAAG TGTGACACCT TTACCATAAT TCCACCCCTC TTTAATTTGT	480
TTGATCATTT CGGTTAGGCT TACAAAAAGC AACTCTTAG GTTCTCCTTT TGTCTTATAC	540
CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAGTG TTTTCCAAT CCCTGTACCT	600
CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA	660
AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTAA AATCATCAAA AGTTTATAGTT	720
TTAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT	780

1236

AGTTTAGCAT TCAAATTATC AGCAATCGCA TCTTCTTCAT CTTGCTTTTT CTGTTCTTCT	840
TGGCATTGTT CACAATAGGG TGGGATACAG CGAACTTCTT TTATTGCCTC TCCGTTCTCA	900
TTCCACCCCA CTA CTACTACATG TCTTCTCCT TTGATTTGTG TTAGCTGTAT TTCATGCTTA	960
GGACACAATT CGTCTAGTTT AAATGTCTCA ATATTTCTTA AACTAGATTG TAATGATTTT	1020
ATTTTCTGAC CTCCTAAAAT GGTTTTTCTT GTGTTGGTAT CCAATCTTCA TAGCTGGTAG	1080
GCTCTAGTTG ATTGGTTTGC TGTTTTTTAG CCTCACGCGC TGCCCTGCTA TTTCTAACAA	1140
GTTCCACCGT CAATAAATTG TCCTGTTTCC AACGGTTAAG GATTACCTTG ATGTATGCAA	1200
AGTTTGCTTT ACCCTGACTG ACAGCCTCTT TTAACGCCTC ATGGATAAGC TCTGGGCTAA	1260
AATCTTCTAG CATATACTGC AATCTTTGAA TCTGTAACGG TGACAATGCT TTACCTGTCT	1320
CAGCTCGCTT CATATTCAAC AAGTCGTCTA TTTCCACACT GGTTACTTTT TTATTACAA	1380
AATCAGAAAT CAGTTGAAAA ATGTTTGGAC TTTGTAGCTG GATTTAGCC ATTACCTCAT	1440
CAAATTCTGC TTGTGTCATG TTGTCTAAAT CTAGTGTCTAT TGCATTGCCT CCTCAAACCT	1500
CTCTATAAGA CAACTTTTAT TTGCTTTCTG AGTTCCATTT TTAGAGTTAA AAAGAATATC	1560
TTTAAGGTT ACAGTAGCCT CTAAATACTC CTTTTCAGCA TGCTCTATAT ACGCCTGTTG	1620
CTCTGCTTCG TTCTCAAAAA AGTGCTTAGC TTGGCGTTTA AAGAAATGCTT TTCGCATAGC	1680
GTCCATTCA AAAATACCAG GGGCGAAAAA CATTCCCGTA GTGCTTTTAG AGACCGCTTC	1740
GATTTTATGG CTTTCATTCA ATTCAGGAAG TTCAATCCAA AGTAAACGGG ACAACTCATC	1800
TTTGATGGAT TTTGTCTGAC TTTCCAATAA AGAAAGGATT CTTAGGCCAT TTTCTTCGCT	1860
AATTTCTCGC ATTTCTGCGC TAATTCTGTC TATACGTCTA GTTAAATTCT CATATGTTGT	1920
TTCTGTCATG TTTTACCTC TGTTCCTTTG TTGGTGTGAT TTTTACCTT ATTTTCTTAC	1980
TTCTAAACAT CATGTCTTA ATTTCTGAT AACTCATTTT CAATTCAATC ATAGCTATTG	2040
CCATATCCTC AAATGCCTGG TACTGCTCCA ACTCCTCACT AGTCAAGCTA TCGATACCGT	2100
TATAGCCCCC ACGCTCTTCT CTTAACTGCT TAGCGTTCAT GTCTGTACT GCCTTTAGTA	2160
GCAAGTTGTT CATGGTGCTA TGCGCGTGCT TTGGTGCATT AGGCCATGTT TCTATACTGT	2220
CATGCAAGGT TTTTCTTTT CTTTCTTCTA GCGCCCTCTG CAGACGAATT TCAGAAAGTT	2280
CCTCACGCAT TTCAAAGAAT GCTTTGACTA GGTTTAGTTT GAATTGCCGT ACTGTTTCGG	2340
TATTCTTTAA ATAAGTGATC AGAAAAGTAG CCTGTTGCTC GTTCAGAATA TAGGATTTTT	2400
TAGGTTGTCC TCTAGTATCT AATTTATGGA TTTTAAATCC AAGTATTCCC AACTCTTCAA	2460
AGTCAGCCTT ATTTTCTCTT ATTAAGCGCG TGATAGTGTG GTGTTGTACT TCAGCACATT	2520
CAGCGATGAT CTCGCTTGTG GTGTACGGCT CTTTCTTACC GTCCATGTAA ACTAGTTCCA	2580



1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATTGCC TCCTCTAGCC	2640
TCTTTTTTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGACTAATTT	60
ATGTATTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTGGAC	120
TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGGTA GCTGTTTCAGT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATCG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC	720
GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGTATTTTAT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACGTA AGAGTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAY ATGTCTATGA TTGACCACAT TCCAGATATG ATTGAAAATG	1020

1238

GTGTGGACAG TCTAAAAATC GAAGGACGTA TGAGTCTAT TCACTAYGTA TCAACAGTAA	1080
CCAACTGCTA CAAGGCGGCT GTGGATGCCT ATCTTGAAAG TCCTGAAAAG TTTGAAGCTA	1140
TCAAACAAGA CTTGGTGGAC GAGATGTGGA AGGTGCCCCA ACGTGAAGTG GCTACAGGAT	1200
TTTACTATGG TACACCATCT GAAAATGAGC AGTTGTTTGG TGCTCGTCGT AAAATCCCTG	1260
AGTACAAGTT TGTCGCTGAA GTGGTTTCTT ATGATGATGC GGCACAAACA GCAACTATTC	1320
GTCAACGAAA CGTCATTAAAC GAAGGGGACC AAGTTGAGTT TTATGGTCCA GGTTCCTGTC	1380
ATTTTGAAAC CTATATTGAA GATTTGCATG ATGCTAAAGG CAATAAAATC GACCGCGCTC	1440
CAAATCCAAT GGAAGTATTG ACTATTAAAG TCCCACAACC TGTTCAATCA GGAGACATGG	1500
TTGAGCTCT TAAAGAGGGG CTTATCAATC TTTATAAGGA AGATGGAACC AGCGTCACAG	1560
TTGCTGCTTA ATGTAGTTGT TTAGTTTTAA AAACTATGC AAAGCTCCAT ATACAACACT	1620
TAAACGAGAT TAAAGAATGG CGAAATCCCT TGATGCGCAA GAGATTAGCT GTCTTTTTTA	1680
TTTTTTAAGT GATAAAGTCG GAGTTTAGGC ATCAAAGCCT ATCAAATTAA ACAAAGAAGC	1740
GATGTCTTAG ATATTTTGAA AAAAATTAAT AAGCAGAAAA CTCTCTATTA TTTTGTGTGA	1800
GAGAGTTTTT TGTTAATAAA ATTTACAAA ATGACATTTA TATATTGCAT TAAGTTAGAT	1860
ATATGATATA ATATTGTTAA AAAGAGGCGC AACTTTTTAA AATTAATGAG AATCAAAGAG	1920
AAAACCAATA ATATTAATGG AGGAATAAAA AATGTAAGTA AGCATTATGG TCATTCAATC	1980
ATTCTCAAAG ATATAAATTT TGCACCTAAC AAGGGTGAAA TTGTTGGTCT AGCAGGGAGA	2040
AATGGAGTTG GTAAGAGTAC GTTGATGAAA ATTCTGTGTC AGAATAATCA ACCGACTTCA	2100
GGTAATATTA TAAGCAGTGA TAATGTTGGG TATTTAATCG AAGAACCAAA ATTATTTTTA	2160
TCTAAACAG GTTTAGAGAA TTTAAAATAT TTGTCAAAT TATATGGTGT TGAACAAT	2220
CAAGAAAGAT TTAGATGTTT GATCCAAGAG TTAGATTTGA CTCAGTCTAT TAATAAAAAA	2280
GTAAAGACCT ATTCTTTGGG TACAAAACAA AAATTAGCTT TGCTTCTAAC TCTCGTTACG	2340
GAACCTGATA TATTGATTTT AGATGAACCG ACTAATGGTT TAGATATTGA ATCATCACAA	2400
ATAGTTTTAG CGGTTCTAAA AAAATTAGCT TTACATGAAA ATGTGGGAAT TTTAATATCG	2460
AGTCATAAAT TAGAAGACAT TGAAGAAAT TGTGAGAGAG TTCTTTTCTT GGAGAACGGG	2520
CTTTTGACAT TTCAAAAAGT AGGAAAAGAT AGTCATAATT TCTTGTTTGA GATAGCTTTT	2580
TCATCAGCTA CAGATAGAGA CATTTTCATT ACCAAACAAG AATTTTGGGA TATTGTTTAG	2640
GAAGAGGGAT TGAGAATTAC TATGTCTGGG AATATTCAAA ATAGTGAGCT TTTTAAATTT	2700
TTTAACGAAA ACTCTATTAA AGTAGTTGAT TTTGAACTA AAAAAGAGAC GCTTAAAGAT	2760
ATTTACCTAA ATCGTTCAAA ATAAAGGAAG GTTATAATCA TGAAATTAAA TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCTT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATW TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTCCGG AAATCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACCGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TCGCTTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAACTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA TCATGTAGCC CAGCATTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA	1080
AATCAGTCTT TGCCCAGCAG GTTGGACTCA AGGAAGTCGC AAATTATCTG GGTGAGATTT	1140
TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTTGTCATGG	1200
CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC CACTATGACA	1260
CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC KTTTACGCTT TCGGTCCGCA	1320
ATGGCTTCAT GTATGGGCGT GGGGTTGATG ACGACAAGGG TCATATCACA GCTCGCTTGA	1380
GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCAATATC AGCTTTATCA	1440
TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA AAGCATGCAG	1500
ACAAACTCCG TGGGGCGGAT TTGTTGGTCT GGGAAACAAGG GACCAAAAAT GCCTTGGAAC	1560
AGCTGGAAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG	1620
CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTTGTGGA ATCAGCTCCT TGGTATCTCC	1680
TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTTGGTTGAA GGCTTGACG	1740
AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAACTTAT GGTCAACGAA	1800
ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG GAGGAGCGGA	1860
TGGCCTTTCT AAAACGTTTC TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG	1920
GTTATCAAGG TCAGGGTGTT AAGACTATTT TACCTGCAGA AGCCAGTGCC AAGCTAGAGG	1980
TTCGTCTGGT TCCGGGCCTA GAACCGCATG ATGTTCTGGA AAAAATTCGG AAACAGCTAG	2040
ACAAAAATGG CTTTGATAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA	2100
GCGATATGAG CGCACCAGCC ATTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC	2160
AGGGCGTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG	2220
CCCTAGAGGT ACCAATGGTT GCATTCCGTC TAGGAAATGC CAATAGCCGA GACCACGGTG	2280
GAGATGAAAA TGTGCGAATC GCTGATTATT ACACCCATAT CGAATTAGTA GAGGAGCTGA	2340
TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCA	2400
AAGAAGAGAA CCATCACAGC GGTTAAGGAT GTGACCATTG ACATCCAAGA AGGGGATATC	2460
TACGGAATCG TTGGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAATCTC	2520
TTGCAAAAAC CATCTGCAGG GAAAATTACC ATTGACGACG ATGTGATTTT TGACGGCAAG	2580
GTGACCTTGA CGGCAGAGCA GTTGCCTCGT AAACGTCAAG ATATCGGAAT GATTTTCCAG	2640
CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC	2700
TCTGAACTCA CCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTTGGA CTTGGTTGGT	2760
TTGGCAGATC GTGCTGAAAA CTACCCTTCA CAACTATCTG GAGGGCAAAA ACAGCGTGTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT	2880
GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA	2940
TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTTCAG TTATGCAGGA TGGGCATTTG ATTGAAGAGG GTAGTGTGCT TGAAATCTTC	3060
TCAAACCTA AACAACCTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG	3180
GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGGAAATATCG AAATTCTCGA TGGTACTCCT	3300
GTTGGAGAAT TGGTGGTGGT TTTGTCAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGGAGAA	3600
TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACCTTC TCACTTGATT GTTAAAACAA GTATCGGGCC	3720
AAATGCAGCC CTTGTCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTGCTC GGGACAGGAG CTGTTGTTTT	60
TGGAATGGT CTGATGGCC TTGGTCACCT TGGAATCGCC TTGCTTTTG GTTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAACTGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC	180
GATTGCTATG TTTGTAAACA AACGTTTGTC ATCTTCAGAA CTTGTAAACT ACATCCTTGG	240
TCAGGTGTT GGAGCTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAATCAGG	300
TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGTCACTG TCTTGGTGG	360
TTCTTGTGTT GAAGTCATCG CAACTTTCTT GTTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG GGCAATGGCG CGATTGCTGG TTTGGTAATC GGTTCGTCAT TGATGGCGAT	480
GATTCTTGTC GGATTGAAGA TTAGTGACT TTCAGTAAAC CCAGCTCGTA GCTTGGCACC	540
AGCTGTCTTG GTAGGCGGCG CAGCCTTCAA CAAGTTTGA TTTTCATCCT TGCACCAATC	600
GCTGGTGGAG TTCTTGACGC CCTTGTTGCA AAAAATTTCC TTGGAACAGA AGAATAATTG	660
AAACTCAAAA AGCCTTGCTC CTCATCTTGA GGAACAGGGC TTTTTCGTAT GATACTCTTC	720
GAAAATCTCT TCAAACCACG TCAGCTTCAT CTGCGGTAG TATGGTTACT GACTTCGTCA	780
GTTCTATCCA CAACCTCAA ACAGTGTTC GATCTGACTT CGTCAGTTCT ATCTGCAACC	840
TCAAACAGT GTTTTAAGCT GACTTCGTCA GTTCTATCTG CAACCTCAA ACAGTGTTC	900
AAGCTGACTT CGTCAGTTCT ATCTGCAACC TCAAACAGT GTTTTAAGCT GACTTCGTCA	960
GTTCTATCTG CAACCTCAA ACAGTGTTC AAGCTGACTT CGTCAGTTCT ATCCACAACC	1020
TCAAACAGT GTTTTGATCT GACTTCGTCA GTTCTATCCA CAACCTCAA ACAGTGTTC	1080
GATCTGACTT CGTCAGTTCT ATCCACAACC TCAAACAGT GCTTTGAGCA ACCTGCGGCT	1140
AACTTCCTAG TTTGCTCTTT GATTTTCATT GAGTATGACT TTAGCGGTTG TCAATTTCT	1200
CTGGATAAAG GTCGTGTTGG AAGAGGCGTT GTTCTGCCAA GCCCTCATA TTAGTTCCTT	1260
GCTTACCGTA GTTGTAGTAG GGGTCGATTG AAATGCCACC GCGCGGAGTG AATTTTCCCC	1320
AGACTTCTAA ATAGCGAGGG TCTAGCAAGT TGACCAAGTC TTTCCCGATG GTGTTGATAC	1380
AGTTTTCGTG GAAATCTCCG TGGTTTCGGT AGCTAAATAG ATATAGTTTG AGGGATTTTG	1440
ACTCGACACA GAGCTTGTC GGAATGTAGG AAATATGAAT CGTCGCAAAG TCTGGCTGAG	1500
CAGTGATTTG TCCCAGCAGA GACATATCGA GGATATGGTG ACGAATGCCC GTTTCCTTAG	1560
CGATTTCTCT AGTAATTTGA ATTTTCGAGG GATGACGTTG GCCGTAGGCA AAGGTGACAG	1620
CTTCGACTGT TTCATAGTGT TGCATGACCC AGAAAAGGCA GGTGTTGAA TCTTGACCAC	1680
CACTAAAGAC GACCAAGGCT AATTGACGTT TCATAGTACT CCTTCCAAAA TGGGAAATGT	1740
TCAGAGCACG CAAAAAGCTC CCATTAGGGA GCTAAAAAT ACCAAATCGA GGTTTTTTTA	1800
GCGATGGCAT ATCCCAAACA TCGTAATATT CTACTTATAT AGTAAATGA AATAAGAACA	1860
GGACAAATCG ATCAGGACAG TCAAATCGAT TTCTAACAAT GTTTTAGAAG TAGAGGTGTA	1920
CTATTCTAGT TTCAATCTAC TATAGTCTAG CATATTTTTT GAAAAATGGC AAAGGGCAAG	1980
AAAAAGAGA CCAAAGAAAG TACTTGGTCT CTCGTTTGAT TAGCTCAATT CAGCAATGAT	2040
GGCCTTGATT TGTTCGCTG TGTGAACACC TGCAACTTGT TTGACAACTT GGCCGTCTTT	2100
TTTGAAGAGA AGAGTTGGAA TAGACATGAT TCCAAAAGCA CGAGCTGTGT TTGGATTTTC	2160
ATCAACGTCC ATTTTAACGA TTTTCAAGAC ATCTTCTGAA AGTTCTTCAG ACAATTTGTC	2220

1243

CAAGATTGGA CCTTGCATAC GACATGGACC ACACCAAGTT GCCCAGAAAGT CTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CTTGTAAAGT TAATTTTTGG ACAGGGTAGT	2460
AKKCTGCGAC GCCGATAAGG CAAGCTTGTT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGTTTT CAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTCGAAA ATTATAATGT TTTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CACCCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTTTATCT	240
ATTGGTAATT TAAAACAAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAACTAAA	300
TTGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAACTTGG	360
TATTACGTCC CCTCCAAGA CTTTACGGTC AATTCGGACA TTGATTGGAC ACAATCAGTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATGCGCTTT	480
ATTGAGAATC ATGTAAGGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATTG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCCTAAA GAAATTCATC CTAAAATCTA	720
TGCCTACACC ACACCGACAG TAACCAGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTT CACCATTTC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAACTC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTTCAAG	1020
TGATTTGTCT GGTTATCAGC CTGAAAAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGGCA AGTTTCTCTG	1140
GAATGCCAAG CCACGCTTTG GTAAAACCTT GTCTACCTAT GACCTAGCTC GACGGATGGA	1200
AGCTGTCAAT GTCCTAATTG TAACAAACCG CCCTGCCATT GCTAACTCAT GGTATGATGA	1260
TTTTGAAACA TTCATAGCAG GTCAAACGAC TTACAAGTTT GTTTCTGAAT CAGATAGCCT	1320
TAAGAGTCGT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG	1380
ACAACTTGCT TTTATCAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA	1440
CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA	1500
TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTCGAC GAAATTTTAC	1560
TCTGCATTTG TCAGGTACAT CATTTAAAGC ATTGGCTAAA GGAGATTTTA CAGAGGAACA	1620
AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCGTGGT CTCTTGAGCA	1680
AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTTACCT ATCAAATGTC	1740
TCAGATGATT GCGGAAAAGT TAGAAAAAGG CGCTCAGATC GATGGTGAAA ATATTGACTA	1800
TGTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GGGAAATTTA TTCATGAGCA	1860
TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTTCAACCAA	1920
AGAACTCCGT AATGAACTCA AGCATACTTT TTGGCTTTTA GAACGTGTGG CTTCGGCCAA	1980
AGCATTAATA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGAGA TCGTTCTAGC	2040
TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AAACCTCAAAT CCTTGGACTT	2100
GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC	2160
GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAATT TGAAATCACC	2220
AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAATCCT TACTCATGGA GCGATAACAA	2280
AGGAAATCAC TTTGCAAAG AAAGAGCCTA TGTATTTGAC TTTGCGCCGG AAAGAACCTT	2340
GATTCTCTTT GATGAGTTTG CCAACAACCT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC	2400
TTGAGCTACA CGCGAAGAAA ATATTAGAGA ATTATTAAAC TTCTTTCCAA TTATTGCCAA	2460
AGACCGTGCT GGTAAGATGG TTGAAATTGA TGCAAAGGCA GTTCTAACCA CTCCTCGCCA	2520
GATAAAAGCT AGAGAAGTTC TTAAACGAGG TTTTATGTCC AATCTCTTAT TTGATAATAT	2580
TAGTGGTATT TTCCAAGCAA GTCAAACAGT TTTAGATATT TTAAATGAGC TGCCAGTTGA	2640
AAAGGAAGGG AAGGTACAAG ATAGTTCTGA TTTATTAGAT TTTTCAGATG TTACAGTCGA	2700
TGATGAGGGA AATGCAGTAG TAGACCATGA AATTGTAGTT AATCAGCAAA TGCGACTTTT	2760
TGGTGAAAAA GTTTATGGAC TTGGTGAATC TGTTCCTGAG TTAGTCACAA AAGATGAGGA	2820
ACGAACTCAA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTTCTTCAG TGATTGTAGA	2880



1245

GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAAACT GAGCAAATTA AGAAACAAAT	2940
TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC	3000
TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA	3060
TAAGATTCAA GAAGATTTGG AAAAACGTTT AGAAGAAAAAT AAACTCATTC ATAAAGAAAA	3120
ACTAGAACAA ACACTCAAAA AAGAAGTGGA AAAAATGCCT GAGAAATTTA TCGAACAGGT	3180
TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATT	3240
ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AAACCTAAC	3300
ACTTGATAAT TTTGATGCCT TTGTTCTGA ACATGTTTTT TATGAAGTAA CAGGGATTAC	3360
GATTGATCAG TTTAGATATT TGCGAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA	3420
TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAG AGTTGGCGGA	3480
TTATTTTAAA GATCAAAAAG AAGACATTTT TGAATATATT CCACCGCAGA AGACCAACCA	3540
AATTTTCACT CCTAAACGAG TGGTGAAAAG GATGGTAGAT GATTGGGAAA AGGAAAATCC	3600
AGGGATTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA	3660
TATTGCAGAA CTTGTGAAGC GGTATATATA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA	3720
TCCTGAAGAA CGCTTAAAC ATATTTTGGG AAAGCAAGT TATGGATTG CTCCGTCTGA	3780
GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG	3840
GAAGAATTTT GTTTTAGCAG ATACCATTCC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT	3900
GGTGTATTCC TATTTTGAAA ATAATTAAAA AGAAGGCCGA GTCAAAATTC TTTGAAATCA	3960
GAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCC AAAAGTTAGA CAGAAAAAAT	4020
CTAACTTTTG GGGGGCAGTT CAGACAATCC TTGGTATTAT GCGTTTTATT GTGGGAAGAT	4080
GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTTAAAGC ATTTTATAAC	4140
AACGTTTTAG AGTAATGGGG GGCTATTTCA ACTTCAACCT ACTATAATAC AGAAAAAAC	4200
AACTCCCTGA TAATTCAAGG AGTTGTCTAT AGTTAAATTA GTTTTATAGAA GCTTCTTGGA	4260
ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTA TTTCTTAGCA GATGCTTGCA	4320
TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC	4380
CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGAATA	4440
CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG	4500
CTACTGCGAT ACCGTAGTAT GTTGACCTT TTTTGTGAT GATTGTGTAG GCTGCATCAC	4560
GAACACCTTC GAACAATTCA ATCAATTCAG CTTCTTGAAC ATTTTGAGTG TCTTTAAGGA	4620

1246

ATTCTTCAAG GTTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCAACC CATGATGTAG GCGTGCACTG AACGAGCATC CACATCCAAT TTTTCAGCAA	4740
GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTTCTTTAG	4800
GGAAACCAGA GAATTTCCAA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA	4860
GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTG TTGATAGCAA	4920
GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA	4980
TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTtagGTG	5040
AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTTT GATAATTCCA AGCTCTGTG CAATTCCTTG GTTAACAAGT GCAAAAGCGT	5160
AAGATGAACC TACAGCACCA TCACCGACAA GGATAACTTT TTTGTGTTGT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAT TTAAAGGAGA ATCTAGCAAA TGGATTTCAC ATGGGCACTG	60
AAGTATGCCA CTGAATTTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCAGTT	120
GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT	180
GGTTATGGTA TGGGGGTTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATTCTACTT GAAAACTGAA AACCCAAATA ACATCTTGGG AACTTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGGT	480
TTGATTAATG AGTTTGTTGG TTCATTTGTT TTGTTCTTTG CAGCTCTTGG TTTGACTAAA	540
AACTTCTTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA	660
CTTTCTGTGG CTCACTTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCACTTGGA	720
GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT	900
TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGGk TCTCTCTTTT kGATTTTtaG GGAAATGAAA GAaCTCTAAA CAAACTCCTC	1020
TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCTCC	1140
AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTTCT	1260
CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCAATT	1320
TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTGTT ATCGTTTAT CTGCAATTTT AACTCAATG AAAATCAAAG GGCAAACATA	1440
GAAGCTAGCC GCAGGTTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TTGTTTCATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGGATGG ATAATGCTGA AAACCTCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTACCAA GAATAATTCA CAAAACGTT GTAAACACT TGCAATTTAG	1740
CTGAAATTG ATAAATAGT AAGGAAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTACTCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC	1920
TATCACAACT GTTTTGGCAC G	1941

## (2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGAAGTTTT	60
ACTTGGAAC TGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTCAGT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTTGGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTTGAA GTTTGTTCAT TTAATAACAT CAAGCTTTTT CAATTTTCATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TGATTGCGGA CTGAGCGACT AGAGTATGTT TTAATAACC CCTCTTTTAT TTATTAAAGG	420
TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTAGTAGG	600
GAAGAAATAT TTTTAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT	660
ATAAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

## (2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGAATTG ATTTTCCAAA AAGAATACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG	120
CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGCACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CATCTCTATT TATTGTGGAG TTTGGGGATG TGAAGGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGACT	360
AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTTC AAGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG	540
ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCAGAG GAAATGGATC GATTGCGCGT	600
GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATTCTCGTC AGTGACTTC TTTGTAGCC TTTCGTTTGA GTAATGTCAA TGGTTTTGAA	720
ATTCCGGCAG CTTATGAAA TCGGAATGAA TGGGACATC GTGCTCGTCG GGAAGGTTAT	780
CGTGTAGATA ATACACCGAC GATTGGTTCC ATTACTTGGT CTACTGCAGG AACTTATGGT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTTATT	960
CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAATCATT ATTTAAGAC CAAGTCTGCT ATTAAACTG AACCTCTAGC TAGCGGAACT	1080
GTGATTGATT ACTATTATCC TGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC	1140
GGCTATAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAACTCT GTTCTTTCTT CAACAGGTGG AACTCATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAACTGAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT	1440
TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1027 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT	60
GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGAA AACACTGTTG	120
TCGGAACTCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTTGAAAAA CAAGGAAAAC	180
AAAAGAAAGT GGTACTTAC AAGTACAAAC CTAAAAAAGG TAGCCACCGT AAACAAGGTC	240
ACCGTCAACC ATATACAAAA GTTGTCATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC	300
ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA	360
CTGGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTTTCTT AGGTATGGCA AACTTATCGG	600
AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AAATAACAC GGAGGAAAAC	660
ATTATGTTAA AAATGACTCT TAACAACTTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT	720

1250

TCTACATCAA	ACGGACGTGA	TTCACAAGCA	AAACGTCTTG	GAGCTAAAGC	AGCTGACGGA	780
CAAACGTGTA	CAGGTGGATC	AATCCTTTAC	CGTCAACGTG	GTACACACAT	CTATCCAGGT	840
GTAAACGTTG	GTCGTGGTGG	AGATGATACT	TTGTTGCTA	AAGTTGAAGG	CGTAGTACGC	900
TTTGAACGTA	AAGGACGCGA	TAAAAAACAA	GTGTCTGTTT	ACCCAATCGC	TAAATAAAAA	960
GGTCCATTGA	ACCTTTTATC	CCGAACCTTG	AAATGTAGAG	GTGAGGAAGC	TAGAAACAGC	1020
TTAAAAAT						1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT	GGTGCAGGTA	AATCTACGTT	AATTAATTCT	ATTGTAGGTT	TTCAAGAGAT	60
TTATTTAGGA	GAAATAGAGT	ATTGTGATAA	AGATTTGATA	GTTAGTTCTC	AACCTTTTGC	120
TCATTTAGGC	TTACTCCTC	AAACCACAGT	AATTGATTTT	TATACTACTG	TGAAGGACAA	180
TGTAATATTG	GGGCTGAACC	TTGCTGGAAA	GTTTGGGAAA	AATGCTGAGA	AGTTGTGTCA	240
AATAGCCTTA	GAAATTGTTG	GGTAGCTGA	TAAAAAAAT	AATTTGGTAG	AAACATTGTC	300
AGGTGGACAA	CTGCAACGCG	TCCAGATTGC	TAGAGCAATA	GCTCATAATC	CAGATTTTTA	360
TATTTTAGAT	GAACCTACCG	TTGGTTTAGA	TACTGAATCT	GCCGAAAAAT	TTTAAATGTA	420
TTTAAAAGAT	AAGAGTTTGG	AAGGAAAAAC	TATTATCATA	TCTTCACATG	ACATAAAATCT	480
ACTCGAAAAG	TTTGTAAAA	AAATACTTTT	TTTACAAAAT	GGCTCCATAT	CATTTTTTGG	540
TGATATGCGT	GACTTTGTAG	ATAATTCAAC	TATCAAATTA	AATTTTTCAT	TGCAGAATAG	600
AATTTCTAGA	TATCAAATTG	AATTTTTAGA	AAATTTTAGA	TTTAAAGTTC	ACATCGAAGA	660
TAATGATAGT	TTTACAATAG	AAGTCCCTAT	AGAAGAAAAG	ATCTTAGATG	TTATCAATGA	720
GGTAGGAAAA	GCATGTGAAA	TTAAAACTT	TTCAACAAGT	AAATTAACCT	TACAAGAAAG	780
TTATTTGCAA	AGAATAGGAG	GAGAAAAATG	AAGGCTGATC	AATTAAGGCA	CAAATCGGAC	840
TTAGGTTTAA	GAGGTCTAGC	GATTATTGCT	AAAAATGAGA	TTATTGCTTT	TTTTAGAAGT	900
AAAGGTTTAA	TTATTTCTCA	GTTTCTACAA	CCAATCTTAT	ATGTTGTTTT	TATAATAATA	960
GGATTAAATT	CTTCGATAAA	GAACATTGAG	TTTAATGATA	TAAAAACCTC	TTATGCAGAA	1020
TATACAATCA	TTGGTGTTAT	AGCTTTATTG	ATAATCGGGC	AGATGACTCA	AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTA TTATTTGGG ACTCCCTTGC AATTTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG	1380
CTTGTTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAAGTATTT TGAGAACTT TTATTTTAAA	1500
AATTCAACAA CTTTGGAATT AGTTTTCTTA TTGTAAACAT CATTACTTGT CCTTATATCT	1560
GTATCTTTTA TTATACCAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAGAAC CTCCTAAAAT GATAAGATAG AAGTGGTTTC TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTGC ACCCAAATAT CGTCGTCAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAT	1920
AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

## (2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAAGTATATT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAAAATTG CATATTTAAC AAGTAAAGAC GCAGGTAATA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTTG TTTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252

TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCAATTTTA AGTACTCCAA ACTCCACAAA	480
TGGTCGTAAA CACGGACAAA TTTGGATTGG TCTAATTAAT GATGATAATA CAATTGATTG	540
GCGTTATCAT CACGACGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA	600
GTTACCAAAT CATGAAATTG GATTGATGTT TGAAAAATTT GATTCATGGT CTCGTAATGA	660
ACTTCATATG AAAAATGTTG TACCATATAT AACATTTAAG ATTGAAGATC TGAAAAAGAA	720
TTAAAGCTGA AATTTGAAAA TATATAAAAA GAGGATAAAA ATTATGGTAA ATTACGGTAT	780
TGTTGGAGCT GGATATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC	840
AAAAGTGGTT GCGGTATTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC	900
AGATGTTTGT GCAAGTTTAG ATGAACTTGT AGCACGTGAA GATATTGATT GTGTGATCGT	960
AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTTGTGAAA GCTGCTCAAC ATGGCAAACA	1020
CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTATGAAGAT TGTAAGCCA TGGTTGACGC	1080
ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACTTCT TTAACGGTGT	1140
ACACCATGCT AAAGAATTGA TTAATCAAGG TAAATCGGT AAAGTTCTTT ATTGCCATGC	1200
TGCTCGTACA GGTTGGGAAG AACAACAACC AACTGTATCA TGGAAGAAAC TTCGTTCTCA	1260
ATCTGGAGGA CATTTGTACC ACCATATTCA TGAATTAGAT TGCATTCACT TTATCATGGG	1320
AGGACTTCCT GAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATAAAG GTGAAAACCT	1380
TGGTGATGAA GATGATATGC TCATTGTAAA CTTAGAATAC TCTGATGATC GTTATGCTGT	1440
TTTGGAATAT GGTAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATTC AAGGAACTGA	1500
AGGAGCTATC AAACCTGACT TGTTCATAC TGGCGGTACT CTTGCTGTTA AAGGTGAAGG	1560
AGAATCACAC TTCTTAGTTC ATGAAACTCA AGAGGAAGAT GATGATCGTA CAGCTATCTA	1620
TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCAT	1680
ATGGTTGCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAAGGTGG	1740
AGAAATTACA GAAGAATTTG AAAAATCTCT CAATGGTGTA GCTGCTTTAG AATCAATCUC	1800
TACCGCTGAT GCATGTACTT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT	1860
CACAAATGCT TAACTTTTGT AAAACAGAAT AGTAAATCTT TGTCAATATA TAATTTCTAA	1920
AGTTCTGTGA TACAACTCAT TGAATAAAGA AATAGAGATG GGAATGGGAT AATGCCCAGT	1980
CCCATTTTPT ATCAAAAAGT AATGAGATCA AAAATGTGGG AGTGTGAAA TGAAGATTAT	2040
AGGTATCGAT ATTGGCGGAA CAACAATTAA GGCAGATTTA TACGATGAGT TTGGAACGAG	2100
TTTGAATCAT TTCAAAGAGA TAGAAACAAT TATTGACTAT GATTTGGGAA CGAATCAGAT	2160
ATTAAATCAG GTCTGTGATT TAATTGGTGA GTATACTTTA AATCATTCAA TTGATGGTGT	2220



1253

TGGGATTTCC ACTGCTGGAG TTGTTAATGC TAATACTGGA GAAATCATCT ATGCAGGCTA	2280
TACAATACCA GGTATATCG GAGTAACTT TACTGCCGAA ATAGAAAAAC GTTTTGGGTT	2340
GTATACTTTT GTTGAAAATG ATGTTAATTG TGCTGCATTA GGTGAATTGT GGAAGGGACA	2400
AGCCAAAGAT AAGAAAAATG TAGTAATCGT TACTATTGGA ACAGGTATAG GAGGCAGTAT	2460
TATTGTCAAC GGACAAATTG TTAACGGATT TAACTATACT GCTGGTGAAG TAGGTTATAT	2520
TCCTGTAGGT AATTCGGATT GGCAAAGTAA AGCCTCAACA ACCGCATTGA TTCATTTATA	2580
TCAAAAAAAG AGCTTGAAAA CTAATCAAAC TGGACGTA CTCTTCACTG ATTTAAGATC	2640
TGGAGATAAA GTTGCTGAAG AAACTTTGA AATTTTGTGTA GAAAATCTAA CAAAAGGTTT	2700
ATTAACGATT TCTTATCTAC TTAATCCAGA AATTCCTATA TTAGGAGGTG GGATTCTGGA	2760
TAGTAAGGAT ATTTTGTTAC CTGAAATTCA AAGTTCTTTA GCTAAAAATG CAATGGATAA	2820
TAGGTTTTTA CCTAAAAATC TTGTGGCAGC TACATTAGGA AATGAAGCTG GTCGTATAGG	2880
AGCTGTAAAA AATTTCTTAG ATAGAATTTT TAATAAATAG TATGTAAGAT AAGGAGGTGT	2940
CACAATGACT AACTCTGTAT TTTCGACAAT GCAAGATATT GAGAATGTTG CAACCGATAT	3000
TATAAAATCA TATGATAATG AGATTTATAC TTATAAAGCT GTTTCCCAAG AAGAATTGGA	3060
AAAAC TAGAA AAAAGTTATG ATGAAAAAAG TCACGAAGAA TTAGTTTCAA TAGAAAGCAA	3120
TTTAGAAATG AAACAACAGA ACCTTATTGA TGAGGTTAAT AAAACAATCA AGGAAAATGA	3180
TGCAAATATT CAGTATATTT CATCAAGTAG GAGAGGAGAA TTTGTAGAAA AAATTATTGG	3240
TAGGGTGGTA GAAAAATATG GCCATTAGTC AGATGAAAAG AATCTCTCTA CTATTTTCTA	3300
AAAGTAGTCT TGATGATGTT TTAAAACTA TTCAAGAACT AGAGTCAGTG CAGTCCCGTG	3360
ATTTAAAGGT TCAGGATAAC TGGTCAGAAG CTCTAGAAAA AGATGAAGTT GTATTTCCAA	3420
CTATTCAAAT TTTTCATACT TCTAATTCCA ATCATGGGGT TATTGAGGGA AATGATGCCT	3480
TGACTTATTT GATGAATCAA CAACAACATT TAGAAGCAAC TGTAGAGAAA TTACAAGAAT	3540
ACCTACCGAA AGAAAACACG TTAAATTAT TGCAGCAACC TCCGATAACT ACCTCTTATG	3600
AAGAATTAGA GAAATTTGGT AAAGCTAATG TTGCTGAGGG TGTCTTAAA AAAGTGAATC	3660
ATCAAATTAA CAGAGTTCAT GAATTAGAAA GACACATTCA AAGTAATAAT GAGGAAATAG	3720
AGCGATTAAT AAAGTGGGAA AAATTAGAAA TTGTTCTGTC GAATTTAGAA CAATTTTCTT	3780
TCTGTAAAGG AAAAGTCGGA ACAATTCCAA GGACTGAAGA TAATCGCTTA TACAATAGTC	3840
TTTAGAAAA CAATATTGAA GTTCAAGAAA TATTTTCTAA TGATAGAGAG TACGGTGTG	3900
TTGTTTTCTA TCAGTCTAGT TACTCTATAG ATTTTGATGA ATACTTATTT GAACCATTG	3960

1254

ATTATTCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCAAT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGCACCA TTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTTAG	4440
GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTAA AAATCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTCAT GACTATATTA GTAGTGTGAG TTGTGTTTGG GTTTATTACA GTATTTGCAG	4680
GTTTGTAGC TTCAGGACTA CAAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTTGC GTGGTGTGTT ATTCTG	4766

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTTGAA GATAGAGCCT ACCAAGGCGC ACTTGTCATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAG	360
aGATGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCCCTCT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGGG	TGAAAATGGT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAAGTCCA	TCCTATCAAT	GAAATTGCCA	AGGAGCATGA	TGGTGGAGGC	CACCCTCTAG	840
CAAGTGGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAGG	AAATATTGCA	AAATGAAAAr	1020
AGATATCCAT	CCAGAATATC	GCCCAGTTGT	CTTCATGGAC	ACAACTACTG	GTTACCArTT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTCGAAGGCG	AACTTACCC	1140
ATTGATCCGT	GTGGAAATTT	CATCAGACTC	ACACCCATTC	TACACTGGAC	GTCAAAAGTT	1200
CACTCAAGCA	GATGGACGCG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AATAATGATA	1260
AGAGAACAGT	TTGGCTGTT	CTTTTTTGT	TCTTGAAATC	AACTGCTGTT	TTCATGTTCC	1320
AGACTCATCT	GTAGGTTCGA	TTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCATAA	TGAGCTATAC	TATTGTCACG	AACCACACTT	TCATTGATGG	TCCAAGTGGG	1440
ATTCATTTTC	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCAA	TGGCCTGCTC	1500
TAAGGTTTCA	AAACGAGGAC	TTATACTCAT	CTGCTTTCAA	AAAGCATTCCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCCTT	GTATGACATC	TTGAAGTTGA	1620
TTCATGACAT	CTTCCAAAGT	TCgAAAGGCT	TTATTCTTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAATGGG	TTCATCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAATCAA	1740
TATTAGTCGG	AATATTTAAG	GTACTTGATT	TATGCCATAT	AGCATTGTCC	ATAACGAGTA	1800
AAAGGATAAG	CTTGTGAAAG	CTCTTCTAAA	AAGGCGTTCA	TCCACACTCC	TTTTTATAAA	1860
CCTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAGGC	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAGGAG	AGAGTCGAGT	CCGAACTCCT	CATATTTTTT	TACGTTTCGC	CAAATCGTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCCTGTTCT	TGTTTCATTT	TACTATAGAA	CGATTTGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTAAAAGT	GTTTTGATGG	TTTGGATTTT	TTCTTTAGTT	GATTTTCATAT	2280
TACTATTATA	TAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTGCTTTC	CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATAC TTAAAGATTT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAAA CGTTCGTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTG TATCAAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTGTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAATACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTAAATGTT CTACTATCCA AATAGAACTC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATTGTATAA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTCG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTTAGTA TTCTAACAGA TATTGCAAAT	660
AAAAAACAG GGGTAAATC AAAATGACAG TATTAAGG AGATAACTTA GAAATATTAA	720
AACTATTGA ATCCTCAAGT ATTGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTGGAAGAT ACGTGGACTT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATTGTG ATAAATTGC AAATCATCAT ATTAGATTAA	960
TTTAGATAA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGGAACGA AAACGAGATG GAACTCTAA AACTATATAT AAGGTTGATA	1200
ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTTCA GATGTTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AAATGATATA GTTTTAGACC	1380
CGTTCTGTGG AAGTGGAAGT ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGA AATGTTATAA	1500
AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG	1560
AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTCA AAGAAATAAA GGAATTGATG	1620
GTTCCTTACC TAAACATTTT CAAAAAAGC CGATACCTAT AAAAATTCAA AAAAATAATG	1680
AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AAAGTCCAAA AAAGTTGATT	1740
TTGGAGTAGT TATAAAAGT CATTCC	1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 748 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
GCGCGGAGAA TTTCTAATTC TTCCTTGCTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC	180
TCATCTAATA CTAAAGTTCC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTGG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAAG	360
TCTTTGAGAG GAATACCCTC AGCAAATGTC TCCACATCTT CTTGGGTCAT GATTCCCTTG	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAAGACCA TGCCTGTCAA TATCCAAGCG TCCTACTGGG	540
AAAGTTTCTT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTTCT GTGCTTGGGA	600
TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTATCA TGTAGTAGAC AAAGTCTTCA	660
TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTTATCAAT CTGCAATTTA	720
GCTGATTTTT CTTTTTGACC ATTTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1449 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT	60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA	120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG	180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGCGCCT GTTCGTAAGC CAGGTAAATT	240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT	300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTTCCTATT GTAGATGACC TTTTGGCGAC	360
AGGTGGAAGT GTTAAGGCAA CTATCGAGAT GATTGAAAAA CTTGGTGGTG TTATGGCAGG	420
TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA	480
CTACAAAGTT CTTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA	540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAACTAT AATTGAAAAC TATATCTTCT	600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTTGTCTT CAAACATATG CAATTATTCC	660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCTGAAT TGATAAAAAA TTGCCAGCTG	720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG	780
ATATCCGTCC TTTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA	840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAACCT GGATATTGAT TTTCTCTATA	900
TGGAGAGCCA CCGTCTTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT	960
TTCTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC	1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA	1080
AGACTCATGT CTATTCGACC CTTTATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC	1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA	1200
CCCTAAAAGA GGTTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT	1260
CACGGCACAC GGAGATTTCT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT	1320
CAGAAGGACC TCAGGTTGGG GTTTCTATTW TGGCCAGTCG TGATTTACGA GAAATTTATA	1380
GTTTGGTCA TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG	1440
ATGCAGGTT	1449

1259

## (2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 904 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TACCCGCTTC TTCAAGAGT TGGAGCAGGG CTTGTTTGGC ATCTTTTGTC ATAGTTCTTC	60
CTTTTAACGG CGTTTTCGAA GCACTTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT	120
ACTATGGATA ATTGTACCAA ATCCAAC TAG TACAAATAGA ACATAAAACA TATTTTCTAC	180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGCATGAAC	240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA	300
TTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC	360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAACTA GAGGCTAGGA TGACAAAAAC	420
TGCCATCAAG GCGACAAGA ACATGGCTAT AAAATAGCG ATGTGGCTCC CCAAAGTATA	480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC	540
CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGATTCA CAAGAATCTC	600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAACCA GACAATAAAG CAAGAATTTA	660
CTTGGGTTTA TAGATCATT TTTAGTTAAA AGTTATAGTA GATTGAACT AGAATAGTCC	720
ACCTCTACTT CTAAACATT GTTAGAAATC GATTGGCTG TCCTGATCGA TTTGTCCTGT	780
TCTTATTTTCG TTTTACTATA GTAAAGATT CATTA AAAAG AAAGTGTATA GAGCAAAATC	840
TCCACCTTCA GGT TTGGAAA GCGGAGATTG TTTTATT TTTCCAGGGT TTGTAGTCGT	900
GGA	904

## (2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 946 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

CACTCAAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT	60
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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACtTCGTGT ATACGGTGGA ACTTTCTTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTcAGC CTTACAAGGA CTTCTGTGA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTt AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTTGCTA AAGGTGCTTA TGTTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GGCGAAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATTCT TCCAAATGCA	660
GTCCGCCGTC GTGTTGCAGT CGAAATGGGT GCAAGTCAAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAAGT TGTTCGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	946

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTTCTTAG GGAGCTATTT TTGTTTTTTC AAGAAGTTAT CTTCTTGTAT	60
TTTATACTCA ATGAAAATCA AAGAGCAAGC TAGGAAACTA GCCGTAssTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTAAct GGTGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGTCTAGG CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT	540



1261

TGGGTCAC TA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACTG	600
GGAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG	660
TTCAAGTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA	720
CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAAC AGTAGGAGAT ATCGAGTCCT	780
TGCCATTCCCT AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCGGAT AATGTCATGT	840
ATATCCATAC AACCTTGCTT CTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA	900
CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTC	960
GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCCAAGTTC TGTGATGTGG	1020
CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT	1080
TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG	1140
CGGATATGAC AGAATGCTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA	1200
AGATTTCCCT TGTGGTAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG	1260
CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA	1320
ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTTGTCTGA TGCGGACGGG ATCATCGTAC	1380
CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAATCCA AGCCATCCGC TATGCCCGTG	1440
AAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG	1500
CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGACCA GAAACAAAAT	1560
ACCCATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCCCTC	1620
GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA	1680
ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTTATGA GTTTAATAAT GCCTTCCGTG	1740
AGCAGTTTGA GGCAGCAGGT TTTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG	1800
AAATCGTGGA AATTCCTGAA AATAAATTCT TTGTAGCTTG TCAGTATCAC CCTGAACTGT	1860
CAAGCCGTCC AAACCGACCA GAAGAACTCT ACACTGCCTT TGTTACTGCA GCAGTTGAGA	1920
ACAGCAATTA GCAAAATCAG AACCTTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG	1980
ATATTGCAGT ATATCTGAGG TAGGGGTCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT	2040
AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTTATC AGTATATTGA AATGAAATAA	2100
AATTTGAACA AATTAATTCG GAAAGCCAAA TCAATTTCTA GCAAAGTTTT AGGAACTGGA	2160
TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT	2220
AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTTAAT	2280

1262

TTAATCCACT ATAGTAAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG	2340
ATTTCTAACA ATGTTTTAGA AATAGAGGTG TACTATTCTA GTTTCATAT ACTATCCCAA	2400
ATCATTGATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTT CAGTATCGTT TTTCTCGCT	2520
AGATTTCTTC AAAAGGGCAG ACTCCTCCCT TGGTGCGTCA CACGATTTTT TCATCTCGAC	2580
TGTTCTTTAA TGCATCATT ACGACGCTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG	2640
ATTCAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAATTCGG AATAGGCATA	2700
GAGACTAGAC AATTGAGGA GCTGCTGCG TCCTGTTGCA ACACATTTTC CCACCACGTG	2760
AAGA	2764

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATTGTTTCT TACTACAAC TACGTTGTAG CGCCCTGCAC ATTGGTTCGT	60
CTTGTTTCTG TTTCAAAGGT CTTTGTCTCT TGCTTCTCTC AAGCGACAAC TATATTAGTA	120
TATCACAAC TCTTTCTGCT GTCAACACTT TTTGAAGAT TTTTAAGTTT TTTTAACTT	180
TTTTTCATCA AGTGGTCTCT ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTTATTTTC	300
AACTCTTACT ATTATACAGT CTTTTCAAAC TTTGTCAACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAATCACG AGCCAAGGTC GAAACATTAC	480
AAGAAATATA AACCATTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT	540
CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTGTACC	600
AACGAGGAAT AATCTCTTCT GCCGTTCAG CTTTATAATG AGTATTGTCA AATCCCATTC	660
TTTTAGCATT TCGCTTGGCA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAGTGCTTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC	900

1263

CTTCTTGAAT ACTCTCTTGC CCCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG	960
TTTGTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACCTC TGGGAAATCT TTAACCAACT	1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTGTGTAAC AATAATAATC TGAACCTGTC	1080
CGGTCTTTCT CGCGCTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG	1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT	1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTAATAATA GTGAGAGTTT TGTGCATATA	1260
AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACCTA GCTCTGTAAT	1320
ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTTTATA ATTTTCATAT CCTGCAGGAG	1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTTGAA CTCCAGCTGC TTATCATAAT	1440
GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC	1500
GAAATTTAGA CTTCTTGTTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG	1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT	1620
TTTGGTAAAA GCCGATTCCC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT	1680
TT	1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG TCAATTCCTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC	60
CCTTTATTGC TAAAATCACC AATTCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT	120
TTCAAATTTT CAAAATATCT TGATTGCAA ATACCATCTG CTAACAATTT ATTTTCTTGC	180
ACAATCGTTG CATTATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC	240
AGTGATTCA CATGGTATTT AGCGTGATG TGAAGTAGGAC CACCTGCTAG AGGATAGAAG	300
TGAACATTC GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC	360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT	420
TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT	480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATTGGTATCA	540

1264

AAATTCTCTA TTTCAATTTT AACAAATTCCT ACATTCCTTG CTTCTGTAA CATTCTACTA	600
ATAGAGGTTT TATAAATTC TAATTTTGCT GCTATTTGTG ACTGATTTAA GTTTTCAATA	660
TAATACAGAT AAGCAATTTT AGAAAGCAGT TTATTCCTAT CTTGATTCAT AACTTAAACC	720
TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA	780
GAAAGTTTTT CGTCTGTTAT TACTTCATAG ACTTGACTTA AAGCAAATCT TCTTACTGTA	840
CCTCTTTTAT CAAATTTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA	900
ATATATTGAA CTACCTCACT GCGCATTAAT TCTTTTCCGG TAAAGCCCAT CTCTTTATCG	960
TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAAG TCTGTATCAT TTCTTTTAAT	1020
AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAAGAAC AATAACACGA	1080
CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAAACG AATTTGTTAC AATCGTAACA	1140
TTTCTTTTTT GCTTGCAAAT TTCCTCAGCA AGTAAAGCAC AGGTCGATCC AGATTCTATC	1200
ATTATTGTTT CATTATCTGA CACCAATTTT ACTGCTTCCT GAACAATTTT TCTCTTAGTT	1260
TCATAATTAA TTGACAAACG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA	1320
TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTTATCTA AATCTTTTCT AATCGTTACT	1380
TTCGATACAT TTAATTTTTT CGATAATGTA TTAACGTCGA TCTTTTCATA TTCTGATACT	1440
AATTTAATAA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATTCT ACCAAAATAA	1500
AAAGCAAAAA ACAACAAAT AACCTTTTCGT TCGTAATTGT TTTTCTTTCT TTTTGTGAT	1560
AGGATAGACT TATGAAGAGG AGGAACTCTT ATGGAAATAT CTAAAGGAAT TATTTTAAAT	1620
ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTCTGA CAACTGTTTT TTTAAAAGGA	1680
TGTCCTCTGC GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAATGAA ACCTGAAAAA	1740
ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAAGAC TGTAAGAGAA	1800
ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTGG AGGTTAACT	1860
TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCCATCTT AAAATCAGCT	1920
AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAAAAATTT	1980
ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAAACATTA TAATCTATA	2040
AAACATAAAA AAGTGACTGG GGTTTTAAAT CAAATGATTA TTAACAAAT TCATTATGCT	2100
TTTTCACAAA ATAAAACTAT CGTTTAAAGA ATCCCAGTTA TTCCTAATTT TAACAATAGT	2160
TTAGAGGATG CAGAAAAATT CGCTACTCTA TTTAACTCAT TAAATATCGA CCAAGTTCAA	2220
CTACTCCCTT TTCATCAATT TGGTGAAAAC AAATATCGTT TATTAAATCG GAAATATGAA	2280
ATGGATGGAA TCAACGCACT TCATCCWGA GATCTTATTG ATTATCAAAA GGTATTTCTG	2340

1265

AACCACCATA TTAATTGTTA TTTCTAGTTT ATTTCTTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAACT TTTCAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2359 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTGTTG CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTT	120
GGATGATTCA GTCAAGTAGT GGTATTCACCT CCTTTGAACC TTCGGCAAAT GATATCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGGAACG TGTCCCTGGA CTAGAGGATG TGAAGCAGG GGATGGAGTT GATGAAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCCG	480
AAGCCTTTAT CAAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAAATCAAC AGGTGTGGGT CTAAAACTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTTT CCTATGAGCT TGGACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAGG CAGAAACTT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GGTTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTT AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACCGCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACTTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAAGTGGCCA AGCAGGAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTACTTGATA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGGAAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGGAAG ATATTCTTG	2359

## (2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTAAAA	60
TTTGGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTAAAA CATCGTCAAA	120
AGCGATTCAG AGCGTCGTTT TGTAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCCGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTCACG CCTTGGCCAC TCTTCCTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTC TTCCTGGTTT CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACTTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTG CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCCTGCC	840
TACCGTGGAA AAATTCCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 855 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAGGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAAGC TGAAAAAGAA AAACCTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AAACCTGAGT ATTTCTGCGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAAGAAAT TGATGTTTCCT TATGATATTC	540
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAATAAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA	660
ACTACAAAAA TCTACAATAT CTTTCACCTG AACAAAGCGCC TTCCCGTGCT AGAAAATTAG	720
TTTCGCAGAA TAGTGTCTTA TTTTCAACAG TTAGACCATA TCTAAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAAGTCTCT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAAAATGGT GAGATAATTT TTGATTTGCC GAAAATTTTA	180
CAGGAAATTA CTTTAGAGGA TGTCCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCCGTAGA	600
GTTCAAGTAA GAAAAAGAAG AAAAAACAT CATTTTACC TTTATTTTAT TTTATCCTGG	660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1805 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:



1269

CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTTCAAGTAT AGCATATCTC CTATTTTCTT	60
ACAAGTAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCAAAA	120
AGCATGCTGA GGTAaaaaaac GCTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA	180
TAGAAAATCG TCAAATAGGC TGAAAAGACA ACGCCAAGGA CAAAACTACT AAGCAGGCTA	240
ACAAATATGA ATCCTTCACG CAAAAAAGGA GTGTGCTTGG TTCGGAAATA ATCTCCAAAA	300
GCCAGCATGG TCCGTTTGAT ATTCCCTGTC ATAAAAGCGT TATTATAGGC AATACCCGAC	360
ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG	420
ATATTATCCA CAGTTTGCGG CACAAAAGCA ATAATGATTG ATAAGATTGC CAAGGGAATC	480
AAGGACAGAA TAGGTTTTTT CACAATTCTC AATTTTTCTT TATAAATCGT TAATAAAAAG	540
ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCT TAACATCCGA AACATTATTT	600
TTAATTAATT CTACTGAAAG AAAGACAACA TTTCCAGTTT GTCCAGCTAC AAGGGTATTC	660
CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT	720
AACCTTTTAG ACTGACGTGA TATTTTCTT ATAGGTAATA ACCTCATTTT ACCTCCCATT	780
GTATTTTCTC TTAGAAATAT TGTACCATT TCTTTCTAAA AAATCGTAGG CTACCATTTA	840
GATTTTACTA TTAGCATAAA AATAATAATA GACAACTATT TATCCAAAA TAGATAGATG	900
TAACATGTTT GCAAACAAAG CATACGAACC TTTAGTAAAA TCATTTCAT GAAACTAGAA	960
TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTT TAATCACTCC TTGACATAAA	1020
TAACTCTCAC CAATAAAAGA CTATGTCTTA AAAAAATGGT ATAATAAAAT CAATACTTGG	1080
GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACTT GTTAACAACA	1140
AGGATTATCC CCTTGAGATG AAAGGAACTT TAGAAATCTT ATGATGAACA TGCAAAACAT	1200
GATGCGTCAA GCACAAAAAC TTCAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC	1260
TATGCAATTT GTTGGCAAAT CTGCTCAAGA TCTTGTCCTA GCGACCTTAA CTGGCGATAA	1320
GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCGTTGAC CCAGAGGACC TTGAGACTCT	1380
TTCTGATATG ACCGTTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AAACTACCAA	1440
GAAAAAACTG GGTGCTTTTC CTGGGAAATT ACCTTTCTAA AAACAAGGAG CTAGAACAAT	1500
GCTTGTCGAT AACAAAGGCT AAGAAAGGTG CAAAAATGAC TCTATAATAT TTGTAGTGGG	1560
TAAATCCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT	1620
ATAATGAAAA GCGACAAAAC AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT	1680
CACAAAATTA CTAGACATTA AAGACCCTAA TATCCAGATT TTAGACATCG TCAATAAGGA	1740

1270  
TACACACAAG GWAATCATCG CCAAACCTGGT CTATGAAGCT CCATCTTGTC CTGAGTGCGG 1800  
AAGTC 1805

## (2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2516 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTTAA 60  
CGTCGCCGCG TTGGGGTTTC GATACAATA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG 120  
GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG 180  
CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA 240  
TGTAATAATA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC 300  
CACAATTTCG AAATCATGTA AGAATTCATA CTTCAGGTTT TTGGAATCCA GATTCTTATT 360  
AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTGATTGT GGGTGTAGCA TGAAAAAGA 420  
ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTTGTAATCT 480  
TGTAAGAGTC GTTCAATCAC CTCGATTTTA TATGCTTTTA TTTTGACCC TTCTTTGCAT 540  
GAGTTTAGGA AATTCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGT TATCGATTTT 600  
TTTTGCCGCT TCTTCTATTC GAGGATTTT ACCGATTAGC CTAGTAGCTG CACTTATCTG 660  
TAACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA 720  
ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTT 780  
TTCTTTTCTA GTCTTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC 840  
TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAAAGAAT TATTTGATTC 900  
CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT 960  
CTCTATTTTT GGAAGTACTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT 1020  
CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT 1080  
AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG 1140  
TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CATTTTCTCT 1200  
ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTTCTTA 1260  
GCAGTATGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA 1320

1271

TTGCGCtGTC GCCAATATTC AATCCATCCA AATGTATTAG AATGGATCTT AGTTTTACTT	1380
CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT	1440
TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTGCGATTG GTCTGAAATC AATTAAGCAC	1500
TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTGAC GCGACTTTA	1560
TTTTTATTGA TTTTCTAAT TGCATTTAGT AATGGTTTTA GCTTCTCTTT GGAGATAAAG	1620
GAGGTTGATT TTTTAAGAGA ATTTTATGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT	1680
ATAGGATTTT TTTTCTCTTA TATAGCATACT TATTCTTTTT TATCCTTACT TACTATTAGC	1740
AGTTTTTCTT GGTTTAAAAA ATCAAACATG AGCTTAGTAT TTCTGTTTAC TTTTTTATTT	1800
GTAGAATCCT TATTCTGGAT TTATCAGTTG GACAATGGGA TAATTGGATT ATTGCCAATT	1860
TTTCAGTATA TGGTAAATTC CAATCCGTAT GCATTGATTT ATTGGCTTAC ATTACTATCT	1920
ATCATAATTC CATTGACTGT ATTTTCTGTT CATAGAAACT GGAGGAGAGT GTAAAAGTTG	1980
GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTTGAATC AGATAATCTA TACCAAGTAC	2040
TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTATGGTA TTGGTTAGAA	2100
GGAAATGATA GACTTGTTAT AGAAATTTTA AAAGGGCCTA ATCTGAGTCA AACTCTTTT	2160
TTAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTTT TCTAGCAGTT	2220
GTATATCGTA GAAGAGCATC CGATTCTTTT ATGGAAGTGA TTCGATTTTC TTCTATTAAG	2280
CTCTGGATTA GGTATCAGAT TTGGACCTGT TTTCTTTATG GACTCATTTT AATCATGGTA	2340
AAAGTTCTAG TGATTCAATT TATGTTACAG TTACCAAACCT GGGATATAGG AGTTTGTGTT	2400
ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA	2460
GGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT TTGTAAATTT TCTAGCACTT GTATGGTAAA ATAGATACAG GTGTTTATTA	60
AACTAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC	120
AAATCCAAGA AACCATTCAA AACGAGACTT ACGCTGTCGG AGATTTCCTT CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTTCCCAG AGTTTCGGAT GGTTCGGAAG GTGGTCCGCC AGCGTGTTGGT	480
GGATGATCTG GTATCCGTTT TGGATACGGA CTATCTGGAT ATGGAAGTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACCTCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT	660
CATGGACATT GGCAAAGACC CTTATGTCGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCCATTA TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AAAGTCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACTGGT ATGCCTACTA GAATTCTCCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAAATG ATGGTCGCTG AAAGTTCTAT CGTCAAGAAG AATCATCAAA	1260
TTCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

## (2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1227 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTTCCATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACCGC AAGGTTCTGGT TTTCTTTCTC TTTTGTCTA TAATTTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCCTC AAGACACTAG 300  
AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTTT AACATGATTG 360  
GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTTATCTA 420  
TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTGGT GGAGCGAGAC CGTAAGCTCA 480  
GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTC AACTCCTCAA 540  
GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA 600  
CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT 660  
TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACCGATAAA GCCGTTGAAC TTCCAGAAGA 720  
AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTATGGA ATTAGTAAGG TGACAGTCTA 780  
TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG 840  
ATATCATTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTTTAATC 900  
CCCACAAACA AGGATTTCTC CCTCTTGAAA ATCGTAAACG GGGGTTAGAA AAGGCTGTGA 960  
AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA 1020  
AAAGACTGGG GGCTACTTGC CTAGTGGAG GTTTGAGAAA TGGCTCGGAT TTGCAATATG 1080  
AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC 1140  
ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG 1200  
GTCAGGATAT TGCCTGCTAT GTTCCCG 1227

(2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTITAGGA GTGGTAACGT 60  
ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA 120  
ACAGAAATTG GCTTTTCAAC ATAAGCTTGT AAGCTTTCTT TCATCTCTTT TGCCCAATCA 180  
TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC 240  
AACTCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT 300  
TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT 360

1274

ACACGGCTAA TTCGTCCACC TTTGACAAGA TTTTCCAAAG TTGAAACACC AATATAAAGC	420
TCTGTATGGT TTTTAACCTC TTCTACATGA GATAAAATTG CCTCCATATC TTTACCTTCT	480
TGAGCTAACT TCGCAGCCTC AACAACTTGG AATTTTCAGGG CTTGGTCAGT GAAGGAACTA	540
TCAACAACAG TCACATCTGC AGTAGATAGG CTAGCACCTT GCGGTGCTGC TTCTACCGTA	600
CCCGAAAGAG CATGGGACAT ATGAATAGCA AGAATCTGGC CACCATCTTT GCATAGGTCT	660
TCAAAAATCT CAGCAAAGAC ACCTACAGGT GGCTGACTTG TTTTCGGAAG ATTCTTACTT	720
TCTTGCATCA ACTGAAGAAA TTTACCTTCT TCTTTCAAAT CCGCATCAGA ATAAACAACA	780
TTATCAATCA TTACAGATAA TGGAACAATT GTAATATCTA ATTGCTTTAC TAGTTCAGGT	840
TCAATAGTAA CAGATGAATC GGTTACAATC TTAATTTTGG TCATAGTATC AATCTTTCTA	900
TTTTAGGATT CAGATTGGTT TCCTTACTTC TAATTATATC AAAAAAAGA TTAATAATCC	960
TAATGGAGTC AATCAAATTT TCCGTAAAAT TTGATATAAT CAACTTATAA GAAAAGAGGT	1020
GTCCTATGAT TAAAAAATT TACCCCATTT TTACCATTTT ACTAGGTGCT GCTATTTATG	1080
CTTTTGGACT GACTTATTTT GTAGTTCCCC ATCATCTCTT TGAAGGAGGG GCGACAGGCA	1140
TTACCCTCAT CACCTTTTAT CTTTTTAAAA TCCCTGTTTC CCTCATGAAC CTGCTGATTA	1200
ATATTCCCCT TTTCATCCTA GCTTGAAGA TTTTGGAGC CAAATCCCTC TATTCTAGTT	1260
TACTAGGAAC CTTAGCTTTG TCCGGCTGGT TAGCTTTTTT TGAGCATATT CCCCTTCATA	1320
TTGATCTTCA AGGTGATTTA CTAATCACAG CCCTTATAGC GGAATCCTA TTGGGAATTG	1380
GCCTTGGAAT TATTTTAAAT GCTGGAGGTA CAACTGGCGG AACTGATATT CTAGCTCGTA	1440
TTCTCAACAA ATACACTCAT ATATCCATAG GAAACTGCT CTTTATCTTA GATTTTGTGTA	1500
TTCTCATGTT GATTCTCCTA ATCTTCAAGG ATTTGAGATT GGTTCCTAC ACGCTTTTGT	1560
TTGATTTTAT TGTTCCTCGT GTTATTGATT TGATTGGTGA AGGAGGATAT GCCGGCAAAG	1620
GCTTTATGAT TATCACAATA CGTCCTGACC AACTTGCTAA GGCGATTAAT GATGACCTCG	1680
GAAGAGGTGT TACTTTTATT TCTGGTCAAG GCTACTATAG TAAAGAAAAT TTGAAAATCA	1740
TCTACTGTAT TGTCGGAAGA AATGAAATTG TGAAAACGAA GGAAATGATT CATCGAATCG	1800
ATCCTCAAGC CTTTATAACT ATTACAGAAG CCCATGAAAT CCTAGGAGAA GGCTTCACCT	1860
TTGAAAAAGA ATAAAAAGAG GTAATGTCGT GACCTCAAAA GTTAGACTAA ATCATCTATC	1920
TTTTGGGTTA CAGACAACCT CTTTTTTATT TTATTTACTC AAGCTCTTAA GACCAATTCC	1980
GAGTTACTTC TTCATCAGCC TTAACTGAT CCACTAATTG GTCAACTGAG TCAAATTTGG	2040
TCATATCTCG AATGCGATCA AGCCAATAAA CCATGACGGT TTCCCCATAA ATATCTTGAT	2100
TAAATCAAAA AATATTGACT TCAAAACGTG CTTCTTCTCC ATCAAAGGTC ACATTTTTC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAGCGGT GCCCCCAAAA	2340
GTTTTCTGCTG TTTCTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCTCTT CTCTCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTTCTACACC TTCGCGCTTT AATTTCTTTT	2640
CACGTCAGC AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTTGT	2940
TTTTTTCACA TGAAGTGAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACTTTGC AATATTCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAACTC CTGAGAACTT TAAATTACTA ATTGGTCCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAAAC GTGTTCTATT CCAGATTCAT ACTCAATGAW	3600
AATTAAAGTG CAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 743 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1276

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTTGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAAATGGAA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTTAT CTCAAATTG ATGGGAAAAT GGCTGAAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGGTACTACT TCAAATCCGG TGGTTACATG ACAGCCAATG AATGGATTG	300
GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGA AGCGATGGTA AATGGCTTGG	600
AGGAAAACT ACAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAA AGCTTTCCTA TATATCGCAA AGTAGTGTCG TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

## (2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTGGTTGA TGATACGAGG GATTTGGTGA TTCTTCTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCAGTCG TTTCAAGATA AGGAATTTTA GAAGGTTTTT GAAAGTCATA TTTCTTCAAT	180
TGGTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAGTCCA GTTTGGCGAT GATTTCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAATC TCGATATTAG GGTCTTTAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTTCTAA TGAGTTGTTT TGTGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540



1277

TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA	600
TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA	660
TTGGCAAGCT TGAAGTAAGT TTTTTTCAAT CTCTCAATCT CGAAATGGTA GAACAGCTTT	720
TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA	780
TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCATTGG CTTATCTGGT TAAAACCCAG	840
TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC	900
TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC	960
GGAAACTGA CTTGGCCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA	1020
GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT	1080
TTCTATTGAA ATGAGGACTT TCTTTT TAGT TATAATAAAG TTAGGAAATA AGGAGAGGAA	1140
GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAATTGA TAGTCTCACC	1200
AATGAACTTG CCCTTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAAGCT CTATGGAAAA	1260
TCCTCTGAGA AAAGTGT TTG CCCATCTGGA CAACTCAGTC TTTTGAAGA GGAACAAAAT	1320
ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA	1380
AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA	1440
AGTAGAAGAG AGCATTG GCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCCT	1500
TCAACGACAA GAATTAGTCT TTATTCTGTC GCAATTAAAA CGAATAGATC ATATCCAACA	1560
CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC	1620
TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT	1680
CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCCCCAA GAAGAAGATT GGGCTAAGAT	1740
GGGTTTACCA ATCACACGTA AGGAAATTGC TAATTGGCAT ATCAAGGCGA GTCAATACTA	1800
TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC	1860
GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT	1920
TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG	1980
TGGTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCTGGC TATGTTTCATT GTGACATGTT	2040
GCGGCAGTAA CTTAGGACTT TAGTCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT	2100
TAGGAGTAAG GCGACGCTAA GCTTGGTAAA CTGCGAACAG CTAGAAGCTT ATCGTCAACT	2160
GGAAGAAGCT GCACTTGTTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC	2220
CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT	2280

1278

ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA	2340
AGAACATCTC CAGCCCCTAA TGGAAGACTT CTTTGCTTGG TGCCGCCGTC AGTCAGTTTT	2400
AGCAGGTTCA AAACCTAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA	2460
GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT CTAGCTGAAC GCGCCATTAA	2520
ATCATTGGTT ATGGGACGGA GTAAAAGAGT CCAGTGGACT CTTTGTAGCCT GAGCTCAGTT	2580
TAAAAAAGCG AGGGTGGTTA TTTTCTCAA GTTTTGAAGG AGCTAAAGCA AGAGCTATTG	2640
TTATGAGCTT GTTGGAACA GCTAAACGTC ATCAATTATA GTGCGTTGAA TCTATAACAG	2700
TACGCATCGA CTGCTAAAC ATTTCTATA ATCAATTTTC CTTTCCTAAT CGATTTGTTC	2760
ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCCTATCTT CTAGAATGTC	2820
TTCCAAACGA GGAACTCTC GTAAACAAAG AGGTTTTAGA GGCCTATTTA CCGTGGACTA	2880
AAGTTGTACA AGAAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACTATC CGTGAGTTCT	2940
CTAGTCTGGA GATTTTTCAA TAGACTTCGT TATTGGACGG TTACAATTTA TTATATGAAA	3000
ATCCCATATT ATTCTCCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACTACCTA	3060
ATTATAGCAT ATAACGCAGA TTCCTTTCAA TCGTATGATT TACTGCATTA AATTAAGTAA	3120
AAAAATAAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTATGGTAA	3180
GTAAATAAAT AATTTCCCTA AAGATATGGA AATTATTAAT ACTATAAATA CATATTATAA	3240
AGTTTATAAA TACTGTAAAA ATCCTGAAGT TAATTTTCTA ATAAATATCA ATATGTGTTA	3300
GTATCTTTTA AATTTTGA CAATTTACTA GTTCTATAGA CATGTTTAAC AGACTCTATT	3360
TTACAATTCA AAAATTTTCA CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAAT	3420
AAAAATTATT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT	3480
GGAATAATCC ATACCACTTG AAGGTTCTGC AAAAAAGACA AATGGAGAAT TCTTGACAT	3540
AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCCTCCTGAT AAACTCATCG GATGCCTTTC	3600
AATAAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCAACTAGA	3660
TGTAACCTAC AAAACCCCTG ACCTCATGAG CCACTTTCTT CCTCCTCATG AGGTCAGTTT	3720
TACTTTCTGC TGTTCAGTA TCGTTTTTCC TCGCTAGATT TCCTCAAAG GGCAGACTCC	3780
TCCCTTGGTT CGTCACACGA TTTTTCATC TCGACTGTTT TTTAATGCAT CATTAACGAC	3840
GCTTTTCTTC TAGGTGGTTC ATAAGGAACA GGAAGATTCA GGTGACTTT TCTAATCCTA	3900
GAATAAAGTG CTGAAAACAA TTCGGAATAG GCATAGAGAC TAGACAATTT GAGGAGCTGC	3960
TTGCGTCCTG TTCGAACACA TTTTCCCACC ACGTGAAGAA AAAGATGGCG	4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2789 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTCCTAA TTTAAAACAG AAAAACCAG	60
GAAAATGACA TAAAAATATC ATTCCTAGGC CTATTTATGC TATTTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCAATGA	180
TTGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT	240
CTCGATTCAT CTCTAAGAGA AACTTCAAGA CCAAATCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTAA GATGGCTCTA GCAACTGCAA	360
TTGTTGTTG TCGCCCCCA GACAACTCGG AGACCTTTG ATGCAAAGTA GCTGATAAAC	420
CTACTCTCTC TAAATCTCT TCCACCTTTT TGAGCTTGTC TTTCTTAGGC AATTCACAT	480
ATTCAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTGCGAC TTAGCAGAAT TAACCGCTAG	600
ATTGTCTGA CAAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCTATAA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT	780
TTTCAACTCA ATCATAAGAT GCCCCCTTC AATAACTCTA CTAGACTTCT TTTCTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAACCTGC AAACAGTAGA	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AACTTCTTG	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTACTA GTAAGAAGTA GGAAATCATC	1080
ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTAAAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTTGTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAATTTCT CAACTAACTC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA	1260
ATCGGATTAT TTAAGCCAGT TGTGACAGG GAGGCTTTCT CATCCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTCGT	1440

1280

TTTTGCTGCT CTTCACTACTT CATCGAATGA AAGGCAATTA ACTTCCCCAA GAGCTGATTT	1500
TTATCTTCTT CACCTTTCGT ACTTGCTGGC ATCAAAATAA CTTTTTTAAT ACCGGTATTT	1560
GGTAGCTTGA ATCCCTTGCT CTTTAGAAAA TTGCGATTGG CATAGTAAAC ATCCACCGTA	1620
TCTGTAACT GATATTGCTG AATCTGTTCT GATTGGACAA AATTTTTTAC AGGAAGACTG	1680
CTACTCTGCA CATAGCCCCG CTGCGTTTTT TCTACCAAAT CCTGATAAAA TCGATAGAAA	1740
TAATCTGTAG ATTTCCCTGA CCCTGCTAGC TCTTCTTGCC ACAGATTATC ATTGAGTTTG	1800
AAGGTTTCTA AGGTCAGGTA ATTACCTTGA CTTACCCACT GTTGCTGATA AGCAAGTTCT	1860
TTGTTTCTT GTTCTAACT TCTGCCCCACC CCAATCAGTA AGGCCGTCAG TAAAATAGTT	1920
GTCCCTATTT TCATCACATA ATTGAAGATA AGACCAAATT TGAAAGATGA AAAACCTTTC	1980
AGCAGAGAGC TGATTGTCAT TTTTGGATT AAGAGGTAAG TCAACCAACT GATAAAGAGA	2040
TAAAGCTGCA ACAGCAAAAA ATGAGACAAC CACAGCATAG GAAACAAATC TTTTGGCTTA	2100
TAATCAAGCA AGAAAAACAC GCCTAGATTG ATCACAAGAG CCCCACCTAG GAGGAGGTAA	2160
AGGTTGCCTT TTACAACATC AGCTAAAACA GCCCTATCTT GAAAACCAAG TAATTTTGT	2220
ACCCCAACTC TTTTCATCTC CATCATCGGT TGATACTCTG TCACTAACAC AAGAAGCAAA	2280
ATAGCCAAGA CAAAAACAAT GGCAGATAAA AGCAAATCTC GATTATGAC TTCCACTGCA	2340
CTTTTGTAGG TCGGCTCTAG CAAGGTAGCC TGGTCTATCT TGAAAAAATC GCTCCATTTT	2400
TGTACAATCC TATCCTTGTC CATCTCTTGT GTAGAAGTTA TCGTATAGCG ACCATTTAAA	2460
CTACGAGATG TATCCTTGAT ATAGGTTTGA AAAGTCATAA GCTGAATAGG TTTGGCTTTT	2520
AGAAAGGTCG GAATCGTACC AAGTTTATTG GAAATTTCTT TATTACTATA GACTCCTTCA	2580
CCATCTGTGG TAAAATCAAG AGAAGAAATC CCAAATCTT GGTAGGGGAA GGTATCTTTA	2640
TCAAAAACAC CAGACTTGAC CACCTCATCA CCACTGTCTG TTTTGATGAT GGAGACTTTA	2700
TACTCCTTTG ATACATCCTC AAAAAATCGA AGAACAGACG CTGCAGGTTT GTTAATATCT	2760
TTCAAATACA AATCCAAAGA ATCTACAGG	2789

## (2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT TATTAAAGAT AATGTGTTAA TTACAGCGGC TCACAACTAC TACAGACATG 60

1281

ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGGC TGTTAGTCCA AGTCAAGAAC	120
CATTTGGAAA GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAATT	180
CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAATTCT AGAAGAGCCC ATTGGTGCAA	240
AATTAGGGAC TTTGGGTCTT CCTACTAGTC AAAAAAATTT GACAGGAATA ACTGTGACTA	300
TCACAGGCTA TCCATCATAT AATTTTAAAA TTCATCAAAT GTATACAGAT AAGAAACAAG	360
TTTTAAGTGA TGATGGCATG TTCTTGGAAT ACCAAGTTGA TACTTTAGAG GGGTCTAGTG	420
GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG	480
CTAATCAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAWTCGG	540
TTCTTAAAGG TTA CTCTCTT GAAGGATGGA AGAAAATAAA TGGTAGTTGG TACCATTATA	600
GACAACATGA TAAACAAACG GGTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA	660
GTTCCGGTAA GATGCTTACA GATTGGCAA AAGTCCATGG AAAATGGTAT TATCTCAATT	720
CAAATGGAGC AATGGTTACA GGTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT	780
CATCTGGTGA GTGGATTAA TGTGGAGGA TATATAAAAT GAAGCTTTTG AAAAAATGA	840
TGCAAATCGC ACTAGCCACA TTTTCTTCG GTTGTAGC GACAAATACA GTATTTGCAG	900
ATGATTCTGA AGGATGGCAG TTTGTCCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG	960
ATCTAAAAGA AACCTACTGG AGAGTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT	1020
CCGGAGAGAT GGTGTGCGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG	1080
GTCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTTATTTT GGTCAAGATG	1140
GTGTATTACA AGAATTTGTT GGCAAGCAAG TTTTAGAAGC AAAAAGTCT ACGAATACCA	1200
ACAAACATCA TGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGTCTAT TATTTTGAAG	1260
ATCAGCGTAG TTATCATACT TTAAAACTG GTTGGAATTA TGAAGAGGGT CATTTGGTATT	1320
ATTTACAGAA GGATGGTGGC TTTGATTCCG GCATCAACAG ATTGACGGTT GGAGAGCTAG	1380
CACGTGGTTG GGTAAAGGAT TACCCTCTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC	1440
CATGGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAAC AGGTTGGCAA TATCTAGGTA	1500
ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT	1560
CAACTTGGTA CTATCTAGAT GCTGAAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG	1620
GGAACAAATG GTACTATCTC CGTTCATCAG GAGCTATGGC AACTGGTTGG TATCAGGAAA	1680
GTTCGACTTG GTACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAAG	1740
TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTTAAT ACCACAGTAG	1800

1282

GTGGTTACTA CTTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAACT	1860
GTGATGGATA CTTAACTTTG TATAATAGGT GGATAAAAGT CTTCAACATC AAAAAACGCA	1920
TAGTATCAAG GTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAATAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAGCGACT GAAACGACTT	2100
CTCATAACCG TAAAACATTT CCGATTTTCAG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTGTGACT TGTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGGCGATAA TTTCGCTATT AAAGCCATCT AAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTTGAATGAG ATTTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 870 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTTCGC AGTTCTTTTA	60
GCAAGTCATC CACAAAAATA GTTTCAGGTA CAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCCTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCTTCA TCCCCATCAT AAACCGGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTC	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTCATCAC	420
GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAAGCCAA ACAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTTC GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT 780  
TAGGATTTTC TAGTACCTTC AGCAGCGGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT 840  
GTTCAACTCG GGCACGATTA AGAGAAACGG 870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCCAGA AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTGGGCC CTTTCTCCAA 60  
AATCCAATC AGCCTATGTA GCTATGGATA AGGCACTTGC TGACCTCAAA ACATCAGGGC 120  
ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCACACAG TGAAGCAAG GAACTGGGGA 180  
ATGCCCAAGA CTATCTCTAT CCACACAAC ATCCTGGAAA TTGGGTCAAG CAAGACTATC 240  
TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC 300  
GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGCG AAAAATCTGA AATCCTTTTC 360  
AAAAAATTGC ACTTTCCTCT TGATTTTTTT TGAAAAAGTG GTATCATATA AATATAGAAA 420  
CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTTTGTA TTATTAGGGA 480  
AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AAACAGCTTC AGTTAGAGCG 540  
AGTTGCCCAC CTGCTTAATT GCGCGGCTTC AATACAAACC GTGAAGTTTC GGCACCAATA 600  
CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG 660  
TCACAGGTTT GATCCCTGTA GGGGGCATAT AAATACAACA GGAAAAGCCT TATAATATAG 720  
GGCTTTTTTT GCTTTCCTTT TAAAAATTGT CGTGCAATTT GCCGTGTTTT TACAACAAAC 780  
TTTTACAGC CATAAACTCC TCACTAATTT TTTCTCCAA GGTATGCCCA TAAACGTCAA 840  
TCAACATGGA GATATCTTTA TGTCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTTGA 900  
AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTTCT TTTTGTATAT TCAGAGCGAT 960  
AAAAATCCGT TTTTGAAGT TTTCAAAGTT CCGAAAACCA AAGGCATTGC GCTTGATAAG 1020  
TTTGATGAGA TTATTGGTCG CTTCCAATTT GCGGTTAGAA TAGTGTAGTT GAAGGGCGTT 1080  
GACGATTTTC TCTTTGTCCT TTAGAAAGGT TTAAAGACA GTCTGAAAAA GAGGAGGAAC 1140  
CTGCTTTAGA TTGTCCTCAA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG 1200

1284  
AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG

1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1684 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAAGAT AGTTTGTCTG	60
AAGCTGAGAG AGCGGCACCC AGGCTTATGC TAAAGAGAAA GGTTCGACCC CTCCTTCGAC	120
AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTTGA	300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCG CATTCAGATA ATGGTTTTGG	420
TAACGCTAGC GACCATGTTT AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA	480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC	600
AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAAAGGTT GAAGAAAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG	900
TTCTCATTTT TTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAACTAGA ATAGTATACC	960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTCTTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTGTA AATAAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA	1200
GGATTACTCT TTAGTCTAT TTTAGAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAAGTATT AGTAAAGTAG	1320
CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380



1285

TTGAACAAGT AGATAGGGTT GTTCCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTGTG	1440
ACCTAGGTTT TGCTAAAATG AACTTAAAAA TGGTGAAGTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

## (2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 970 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTTCTA ACTAATCTAT AAGTTCTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATTGCCA	240
CGATACTTTT TCAAAAACAT CATACGGTCG TAACATCCTC TCCAACTCGG CTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TTCGCTCCAT GAGTTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GTACTAACTC TTAAATTTCT TTGGATTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTCGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTATACC	780
TTGGATAGCT AGAATCAACT TATCCGCAGA CAGCATAGAC TGCCCTAGTT CAAACTTGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTCGCCAA	900
ACGTAAATCC TTGTAAAAT CCCTCAGTTC CATTCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

## (2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2996 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTTGACCACG GGTAAACTA CCCTAACTGC AGCTATCACA ACTGTTTTGG CACGTCGCTT	60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TCGCTCTATC GATGCTGCTC CAGAAGAACG	120
CGAACGCGGT ATCACTATCA AACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCCTA	180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC	240
TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAACTCG	300
TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCC GTAAACAAC TACGGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC	840
AGGTTCAATC AACCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACTTCCAT TCTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTTACA GGTTCATCG AACTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GACGTTGAGT TGATTCACCC AATCGCCGTA GAACAAGGTA CTACATTCTC	1080
TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATCGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGGCA	1200
AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAAACATT GTTAGAAATC GATTTGACTG	1320
TCCTGATCGA TTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAAAACATT GTTTTAGGT TGTAGATAGA ACTGACGAAG TCAGTAACAT CTATACGACA	1440

1287

AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA	1500
AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAAGAAG AAATCCAAAC CATCAAAACA	1560
CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTTCGT	1620
CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT	1680
GAACAACTCT ATCAGGAAAG TCAAACATAA TTATAGAAAT ATTTTAGCAG CCAAGGTGTA	1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAACAA CGATTTGGCG AAATGTAAAA	1800
AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT CGTAACCATG	1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTTGAAG GCTACAGAGG	1920
CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAGGAG TTAGGTCGTT	1980
CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTACGC	2040
CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAACCAT TGTCGCGTCT AAAAATAAAG	2100
TCTCAATTCA AGAAGACAAG TGAAGTCAC CCCAAAAGTT AGACAGAAAA AATCTAACTT	2160
TTGGGGTGTT TTTATTATGA AATTAACCTA TGATGATAAA GTTCAGATCT ATGAACTTAG	2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATT GGGATAAACA ATTCTAATCT	2280
TAGGTACATG ATTAAATTGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA	2340
TCGTTACTAT TCTCCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG	2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAAGTG	2460
GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC	2520
TGAGAGCGGA GAATGCCATC CTAAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAAG	2580
AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTTCGT TAGATATTCT	2640
TCTAAAAGCC ATTAACTAG CTCGTTTGAC CTAATACTAT CACTTGAAAC AGCTAGATAA	2700
ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC ATTTTATCG AACACAAGGG	2760
AAATTATGCT TATCGTCGGA TTTATTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA	2820
TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTTACAA GCTAAAATGC GACAGAAACG	2880
AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA	2940
ATTTGAAGGC TCTAAAACAA TGGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 837 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTC	120
TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCCTT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCTTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GGCGAGGATA ATGGTTTTCA	540
CGGTCCGAAA GCCCAACCTT AGCCAACCTT TCCTTGCGAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAATTAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 868 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAAC TACGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GGTTTGGTG GTAAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT ACAAACCAAC TGAAGAAAAC AAAAAATTGA TTGCGAAAAT TGAACATGTT	480
GAAAGTCACA ATGCTCAACA AACAGACGCA AACTTCTTTA CAGAATTCCT TGAGAAATGG	540
GATCGTGGAG AATACCACGA CTAAGAGGTG ACCTATGATT TTAACAGTCA CAATGAACCC	600
ATCCATCGAT ATTCCTATC CCTTGGATGA GTTGAAGATT GATACTGTCA ATCGTGTGGT	660
GGATGTAACC AAAACGGCTG GTGGTAAGGG ACTCAATGTT ACCCGAGTAC TTTCAGAATT	720
TGGCGATTCT GTTCTTGCTA CTGGTTTAGT GGGTGGCAAA CTTGGTGAGT TTTTGGTTGA	780
ACATATCGAT AATCAAGTAA AGAAAGATTT CTTCTCAATT AAGGGAGAAA CTCGTAAC TG	840
TATCGCTATT CTCCACGGAG ACAACCAA	868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3744 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG TCTTCATAAG ACTCGAAAGT CACAGTTCTT TCGTTCTTGC TGGCATCTAT	60
ATAGGTAATT TCAATCATGT TAAAACTCC TTGTTTAAT GCTAACTTTA TTTTACTCCT	120
TATAAAGAG AATGTCAAGA AAAATGATTG CGCAGCAAC TTTTTTTAAA ATCATCTTAA	180
ATCAAGAAAT CCAAACCTGC TTCCAAGCTT TCTTCGACAG TCTTTTGTAG CGAGGCCAGT	240
GTCTTTTGCC CATCATTTGT CAGGCAGATA AACTAGAGC GTCTATCTTG ATGGCAACAC	300
ATGCGACTGA GTAGACCGCA ATTTTATAGCT TCCAAGCGAG CCACCATCCT AGAAACTGCG	360
CTCGGGCTCA GATGAAGCTT ATCTGGCAGG TCAATCTGGC GTAGAGATTT TTCTTCAGCC	420
AAGTCCAGAT AGTAGAGCAG GTAGAACTCT TTCAAGGTCA GACTTTGCTC GCTCTGTTGG	480
GCAATGGTCT CTTCCAAGAG ACTTTCAATT TCTTTCTGAC GCCGATTGAA GTCAAACCAT	540
TTTTCCAAAT AGGTCATAGT GTCTCCTTTC TTTTATAGAGT CATAAATAGA AGAAAGTCCA	600
TTAACGGGCA GTCTCTGCGT CACAAGATGA TTGCGCATGC AATAATTATA CTACTTTTCA	660
AGAATGCTGG CAAGCTCTGT TTTTATAGTG TTTTATTTTT GTGTGAATAA TGGGGGAATC	720
CTATTGTTTC AATTTCTAAC TCCTTATCAC ATTCGAATTC AGATTTTATT TCATTCTCT	780
ATCTATAGTT GCTTAGTTTA AAATAAGCAT GGTCTAATAA AGCTATGCAT ATAGTACTGA	840
TTTTAAACAA GGAGCATTAG ATTCCATTAA AGGAGGGCAC AGACATGTCG AGGCGGCCAA	900

1290  
AGTTTTTGAT GTCGGCGTCA GAACTCTCTT CACGTGGGAA AAGAAAGACG TAAACAAGGG 960  
AACTTAGAGC GGAAAAAGCG AGTCGTCAAA AAGCGTAAGA TCCCTTTAGA AGAATTGAAA 1020  
GCCTTTGTAG AGGCTCATCC AGACGCTTTT TTACGGGAAA TTGCGGCCCG TTTTGATTGT 1080  
GCTTTGCCCT CCGTATGGGC AGTTTTAAAG CAGATTAAGG TCATTTTAAA AAAGACGACC 1140  
AGTTTTAGGG AACAAAAGCC TGAGAAAGTT TCTGAGTTTC TTGATATTTT GGATAACCTA 1200  
AAAGATTTAC CAGTCCTATA TATTGACGAA ACGGGAATCG ACCGCTACCT CTATCGTCCT 1260  
TATGCAGGGG CTCCTAGAGG GGAGAAAGTC TATGGCAAGA TTAGCGGACG GCGTTTTGAG 1320  
CGGACTAATG AGGTGGAGCA AAAACTCAAT GGTAGTTTTC TAATCAGATA TATTGATTCA 1380  
CAAATTAGAG AATGAAAGAA TAATTATGCA TAAAAATAGG AATATAAACC AAAAATTAGC 1440  
TGATTTATAC TCATTTGCGT GTCTTTATAA AAAACTTATC TTATAATATA TATATATATA 1500  
TATACAAAAT AGTAAAATGC TTTTTTTTTT TAGCAAAAAT ACCTCAAGTT TCTTGCTATT 1560  
TTGGGTTCCT TATTCTATAA TTATAGTATG GTAATTTATT TATATCCATA CATGAAAATA 1620  
ATACTCGAAA GGAAATTTCA AAATATTTTT TAGACGTCAG AAGGGTGAAT ATAGAGAAAC 1680  
AGACCGAGTA ACTCGGTTCA AATTAATCAA ATCAGGGAAG CATTGGCTAC GGGCCTCGAC 1740  
TTCTCTTTTT GGCTTGTTTA AGGTCTTGCG AGGTGGTGTT GATACTACTC AGGTCATGAC 1800  
CGAAACGGTA GAAGATAAAG TAAGTCATTC AATTACTGGG CTTGATATCC TCAAGGGGAT 1860  
AGTTGCTGCG GGAGCTGTCA TAAGTGAAC CGTTGCAACT CAAACGAAGG TATTTACAAA 1920  
TGAGTCAGCA GTACTTGAAA AAAGTGTAGA GAAACGGAT GCTTTGGCAA CAAATGATAC 1980  
AGTAGTTCTA GGTACGATAT CTACAAGTAA TTCAGCGAGT TCAACTAGTT TGTCAGCTTC 2040  
AGAGTCGGCA AGTACATCTG CATCTGAGTC AGCCTCAACC AGCGCTTCGA CCTCAGCAAG 2100  
TACAAGTGCA TCAGAATCAG CAAGTACATC GGCTTCGACA AGTATTTCTG CATCATCTAC 2160  
TGTGGTAGGT TCACAAACAG CTGCCGCTAC AGAAGCAACT GCTAAGAAGG TCGAAGAAGA 2220  
TCGTAAGAAA CCAGCTAGTG ATTATGTAGC ATCAGTTACA AATGTCAATC TCCAATCTTA 2280  
TGCTAAGCGA CGCAAGCGTT CAGTGGATTC CATCGAGCAA TTGCTGGCTT CTATAAAAAA 2340  
TGCTGCTGTT TTTTCTGGCA ATACGATTGT AAATGGCGCC CCTGCAATTA ATGCAAGTCT 2400  
AAACATTGCT AAAAGTGAGA CAAAAGTTTA TACAGGTGAA GGTGTAGATT CCGTATATCG 2460  
TGTTCCAATT TACTATAAAT TGAAAGTGAC AAATGATGGT TCAAAATTGA CCTTTACCTA 2520  
TACGGTTACG TATGTGAATC CTAAAACAAA TGATCTTGGT AATATATCAA GTATGCGTCC 2580  
TGGATATTCT ATCTATAATT CAGGTACTTC AACACAAACA ATGTTAACCC TTGGCAGTGA 2640  
TCTTGGTAAA CCTTCAGGTG TAAAGAACTA CATTACTGAC AAAAATGGTA GACAGGTTCT 2700

1291

ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGTTCCTTTG CTAAGAAAGG ATATGGATTA ACATCATCTT GGACTGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCTCGGCT TCAGCGTCAA CCAGTGCGTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCTTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCTTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCCT CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TCGGTCAGCC TCAGCAAGTA CTAGTGCATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 795 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTGCTATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCTAGCTAGG CTATTGAACG TTTTGTGATT TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG TTTGGATCCC CAGGCTGCCT TTGATTGAA	480
ACAGATGATG AAGGAACATG CACAAAAAGG GAAGACAGTC TTGTTTTCAA CTCATGTCCT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT TGCCATTTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT TGCGGATGCG TCTCAAGGTC ATTAAAAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC	795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCW TCCTTGACAC TGCTACTACC ATTTCCCATTA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAA GCCATATTCT TTCCCAACTC GGCGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC TACGTGTCAA TTTCAAGTCT TCAAAATCAG	240
CTGCCGCCCT CTCAGATTCT TCTGGTGTC TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT GGGGAACAAC CTTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAACAG AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCAG ACCAAAGGAC ATGATTTTAG AACCCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC TAATTAGATG GCGCAAATGT AACTTGGA	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT CCTTAACAAA AAAAGGTCCT CGCCCTGTCG	660
CTACGCCAAC TAGTACCCCT TGTTCTTTGA CAATCTTAAT CGCATCCTTA GTGGATTTC	720
AAACACTCTT GCGATTGTTG ACCAAGGTTT CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTGTGAT ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT TTACATACGG GTGGAACATAT TTCCATGCAG	900



1293

GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC 960  
CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTA ACCTTCCAAG TCCCCATATC 1020  
AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT 1080  
GGAGTGGTGA TCACACACCG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC 1140  
ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGCGTACtCC AATGAGCTCG 1200  
GTAGTGATGG TGTMTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG 1260  
CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA 1320  
AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTTGGTCTCA 1380  
TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG 1440  
ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA 1500  
TTGATATGCT GGATTTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA 1560  
ATATTCCCAA AGAAACGGCT CAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG 1620  
CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG 1680  
GCGTACAGTT GCAAAAAGCA GCGTTTTCT TTGTAAAGA ACTCAACGCC CAAAAGCTC 1740  
GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA 1800  
TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCCGCT TACCGTATGT 1860  
ATGGTACTGA CTTTCGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG 1920  
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTTCGTCAGT TCTATCTACA 1980  
ACCTCAAAAA CATGTTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAAACATGT 2040  
TTTGAGCTGA CTTTCGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG 2100  
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTTCGTCAGT TCTATCTACA 2160  
ACCTCAAAAA CATGTTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT 2220  
TTTGAGCTGA C 2231

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

GAGTCAAAGG CTCCGAGGTT GACTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG	60
TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA	120
GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT	180
CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGA CAAGTCCTTT	240
TCAGGAACGG GCACCATTTC CTTTTATCAG ACGCACAAGG AGGTTTCATGT CTCACGGCAT	300
TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG	360
CATTTGGTAT TGTTTTATTG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGAA	420
TTCTTCTTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT	480
CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTCCGCAGT TTTTACAGGT TTAAGGCGC	540
TCATCATTGC AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTTATTTGGG	600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG	660
AAAAAAATG GTGGTACAAT GGGAAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG	720
GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT	780
TTGGGGATGC TAAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA	840
ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTGTAGATT	900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA	960
AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTTAAAT	1020
AAAAAAATCT TCACTTCAAC CATCAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT	1080
GCTCTGATTT CAGTTCTATG GTTGTAGAC TTAAAAAAT GAAATGCTGC CTTTAAAAGT	1140
TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT	1200
GATGTAGTGT CAAATGCTTT TAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT	1260
TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG	1310

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5922 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT	60
ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGGTTTGACA GCCTTGCTTG	120

1295

TAGCTATCTG TTTTGGGATT TCAAGCTTCT TTAGCCCACT TCTAGCGATC GTACCAACAG	180
CGGCTACAGC TCCAATCTTG ATTATCGTTG GGATTATGAT GCTTGGTAGC TTGAAAAATA	240
TCCATTGGGA TGATATGTCT GAAGCAGTTC CTGCCCTTCTT CACATCTATC TTTATGGGAT	300
TCAGCTACTC TATCACTCAA GGGATTGCAG TTGGTTTCTT GACTTACACT TTGACTAAGC	360
TTGTTAAAGG TCAAGTTAAA GATGTTTCATG TCATGATTTG GATTTTGGAT GCCTTGTTTA	420
TCCTTAACTA CATCAGCATG GCCTTATAAT AGAATGACCC AGGGGGATT TCCCCCTTTT	480
TTAATACAaG GAGATAGGTG ATGAAAGAGA AAAATATGTG GAAAGAATTG TTGAATCGTG	540
CAGGCTGGAT TTTGGTCTTT TTAAGTGGCG TCCTTTTATA TCAGGTTCCC CTAGTGGTTA	600
CCTCTATTTT GACTTTAAAA GAAGTAGCCC TGCTACAGTC AGGGCTGATA GTTGCTGGCC	660
TTTCAATTGT GGTTCCTGGCT CTATTTATTA TGGGAGCTCG TAAAACCAAG TTAGCTAGTT	720
TTAATTTTTC TTTTMTTAGA GCTAAAGATT TGGCACGTTT GGGCTTGAGT TATCTAGTTA	780
TTGTCCGGTC AAATATACTT GGTTCCTTTT TATTGCAACT GTCAAATGAG ACGACAACAG	840
CTAACCAGTC TCAGATTAAT GATATGGTTC AAAATAGTTC GTTGATTTCC AGTTTCTTCT	900
TGCTAGCCTT GCTTGCTCCG ATTTGTGAGG AAATCTTGTG TCGTGGGATT GTTCCTAAAA	960
AGATTTTCCG AGGCAAGGAG AACTTGGGAT TTGTAGTCGG TACGATTGTG TTTGCTTTAT	1020
TGCATCAACC AAGTAATTTA CCTTCTTTAT TGATTTATGG AGGTATGTCG ACAGTTCTAT	1080
CTTGGACAGC CTACAAGACC CAACGTTTGG AAATGTGAT CTGTGCTTCA ATGATTGTTA	1140
ATGGGATTGC TTTCTGTTTG TTGGCTCTTG TGGTGATTAT GAGTCGGACA TTAGGAATTT	1200
CTGTTTAAAA GTTTTATGT AGGAACCGAC CTCTTTCTAC CAGGGAAAGA TGAATGCAAT	1260
CGTGTCATC TTTTCTTTT TATGGTAAAA TAGAAAAATA ATATGATGAA AATCCTTGAG	1320
GGAGTGACCG ATATGTCAAG TAAAGCCAAT CATGCAAAGA CAGTTATTTG CGGAATTATC	1380
AATGTAACCC CAGACTCCTT TTCGGACGGT GGTCAATTTT TTGCTCTTGA GCAGGCGCTC	1440
CAGCAGGCTC GTAAATTGAT AGCAGAAGGA GCCAGTATGC TAGATATCGG CGGAGAATCG	1500
ACTCGGCCCG GAAGTAGCTA TGTTGAGATA GAAGAGGAAA TCCAGCGTGT TGTTCCAGTG	1560
ATCAAAGCGA TTCGCAAGGA AAGTGATGTC CTCATCTCTA TTGATACTTG GAAGAGTCAA	1620
GTAGCAGAGG CTGCTTTGGC TGCTGGTGCC GATCTAGTCA ATGATATCAC TGGTCTTATG	1680
GGTGATGAGA AAATGGCTTA TGTGGTAGCT GAAGCGAGAg CGAAAGTGGT CATCATGTTT	1740
AACCCAGTTA TGGCTCGACC TCAGCATCCT AGTTCGCTTA TCTTCCCTCA TTTTGGTTTT	1800
GGTCAAACCT TTACAGAAAA AGAGTTAGCT GACTTTGAAA CATTGCCAAT CGAAGACTTG	1860

1296

ATGGTGGCTT TCTTTGAACG AGCACTAGCG AGAGCGGCAG AAGCTGGTAT TGCACCAGAA	1920
AATATCCTGT TGGATCCAGG AATTGGCTTT GGTCTGACCA AGAAAGAAAA TCTGCTTCTT	1980
TTACGGGACC TGGATAAACT ACATCAGAAG GGCTATCCAA TCTTTCTCGG AGTGTGCGCG	2040
AAGCgATTTG TCATCAATAT CCTAGAGGAG AATGGTTTTG AAGTCAATCC TGAGACAGAG	2100
CTTGGTTTCC GAAATCGGGA CACGGCTTCG GCTCATGTAA CTAGTATCGC TGGGAGACAG	2160
GGTGTAGAAG TGGTGCGCGT GCATGACGTA GCTAGTCACA GGATGGCAGT TGAAATTGCC	2220
TCTGCCATTG GTCTGGCTGA TGAAGCGGAA AATTTAGATT TAAAACAATA TAAATAAGAT	2280
GAAAGAAATT GAAAACAATC AGTGGATTGC TAACTACCGG ACGGATCAAC CGCATTTTGG	2340
CTTGGAACGA ATGGTGGAAC TGTTAGCTTT GCGTGGAAT CCCCATCTCA AACTCAAGGT	2400
CCTCCATATC GGAGGGACTA ACGGCAAGGG CTCGACTATT GCTTTTTTTGA AAAAGATGCT	2460
AGAAAAGCTA GGGTTGAGAG TTGGCGTGT TAGCTCGCCC TATCTCATTG ATTACACAGA	2520
CCAGATTAGC ATCAATGGGG AATCGATCTC AGAAGCGAGG CTAGAAGCTC TCATGGCAGA	2580
CTATCAGTCT TTGCTGGAGG GAGAAGCGGT CGCCAATTTA CAGGGCACAA CCGAGTTTGA	2640
GATTATCACA GCCCTGGCCT ATGACTACTT TGCCTCAGAG CAAGTAGATG TGGCCATCAT	2700
GGAAGTTGGC ATGGGTGGAC TTTTGGATAG TACCAATGTC TGTCAGCCCA TTTTGACAGG	2760
AATTACAACCT ATTGGCTTGG ATCATGTGGC TCTACTTGGT GACACCTTGG AGGTCATAGC	2820
AGAGCAGAAG GCAGGTATTA TCAAACAAGG GATGCCCTTG GTAACAGGGC GTATTGCTCC	2880
AGAAGCCTTG GCTGTGATTG ACCGCATTGC GGAAGGGAAA GATGCGCCGA GACTTGCCTA	2940
CGGGACAGAT TATCAGGTTT GTCATCAAGA AAGTGTGGTG ACAGGGGAAG TCTTTGACTA	3000
TACAAGTGCT GTCAGACAAG GTCGCTTCCA GACTAGCCTG CTTGGTTTGT ACCAAATAGA	3060
GAATGCTGGG ATGGCCATAG CTTTACTTGA TACTTTTTGT CAAGAAGATG GTCGAGAGCT	3120
AGCAAGCAAT GATTTTCTTG GTCAAGCCTT GGAAGAAACA AGTTGGCCAG GGCCTTTGGA	3180
AATCGTGTC AAGATCCCT TGATGATTTT GGATGGAGCC CACAATCCCC ATGCTATCAA	3240
GGCCTTGTG GTAACCTTGC AAGAACGTTT TCGGATTAT CATAAGGAAA TCCTCTTCAC	3300
TTGTATCAAA ACCAAGGCCT TGGAGGATAT GTTGGACTTG CTGGGAGCCA TGCCAGTTAC	3360
CGAGCTTACT CTAACACATT TTGCGGATAG TCGGGCGACG GATGAAAACG TGCTGAAAGA	3420
GGCAGCTAAG TCTAGAAATC TCAGCTACCA AGATTGGCAT GATTTTCTAG AGCAGAATTT	3480
GACAGATAAA AAAGAAGAGA AACAAACAGT TAGGATTGTC ACAGGTTCTT TGTATTTCTT	3540
GAGCCAAGTG AGGGCCTATC TGATGGAGAG GAAGAACGAG AATGGATACA CAAAAGATTG	3600
AAGCGGCTGT AAAAATGATT ATCGAGGCTG TAGGAGAGGA CGCTAATCGC GAGGGCTTGC	3660

1297

AGGAAACACC TGCTCGTGTA GCCCGTATGT ATCAAGAGAT TTTTTCAGGT CTTGGTCAAA	3720
CAGCAGAGGA ACATTTGTCA AAATCCTTTG AAATTATTGA CGATAATATG GTGGTAGAAA	3780
AGGATATCTT TTCCATACC ATGTGTGAAC ACCACTTCTT GCCATTTTAT GGTAGAGCGC	3840
ACATGCCTA CATTCCAGAT GGTCGTGTGG CAGGCTTGTC TAAGCTAGCC CGTACGGTTG	3900
AAGTTTATTC GAAAAACCA CAAATCAAG AACGTTTGA TATCGAAGTG GCCGATGCCT	3960
TGATGGACTA TCTAGGTGCT AAAGGAGCCT TTGTTGTCTAT TGAGGCGGAA CATATGTGTA	4020
TGAGTATGCG TGGTGTAGA AAACCAGGCA CTGCAACCTT GACGACAGTA GCTCGTGGTC	4080
TATTTGAAAC AGATAAGGAT CTCCGTGACC AAGCTTATCG TTTAATGGGG CTATAAAAAG	4140
AATCCGCTTC AAGCGGATTT TTCTAGAAAG GAATCATTAT GGATCAACTG CAGATTAAGG	4200
ATTTGAAAT GTTGCCTAT CATGGTCTTT TTCCTAGTGA GAAAGAATTG GGGCAGAAAT	4260
TTGTCGTTTC AGCCATCCTA TCCTATGATA TGACCAAGGC AGCTACAGAC TTGGATTAA	4320
CAGCCTCTGT CCATTACGGA GAATTGTGTC AGCAGTGGAC GACTTGGTTT CAGGAAACGA	4380
GTGAAGATTT GATTGAAACG GTAGCCTATA AACTGGTGGG ACGTACCTTT GAGTTTATC	4440
CTCTTGTTCA AGAAATGAAG TTGGAAGTGA AAAAACCTTG GGCACCGGTG CATTGTGAC	4500
TAGATACTTG CTCGGTAACC ATTCATCGCC GCAAGCAACG AGCCTTTATC GCCCTAGGAA	4560
GCAATATGGG AGATAAACAA GCAAAGTGA AGCAAGCCAT TGACAACTG CGAGCTCGTG	4620
GCATCCATAT TCTCAAAGAG TCCAGTGTCT TAGCGACGGA GCCTTGGGGT GGAGTGGAGC	4680
AGGATAGCTT TGCCAATCAA GTGGTTGAGG TGGAAACCTG GCTACCAGCA CAAGACTTGT	4740
TAGAAACCTT GTTAGCCATT GAGTCAGAGC TGGGACGGGT GAGAGAAGTG CATTGGGGAC	4800
CTCGTTTGAT TGATTTGGAC TTGCTCTTTG TGGAGGACCA GATCCTTTAT ACAGACGACC	4860
TCATATTGCC TCATCCTTAC ATAGCGGAAC GCCTTTTGT CTTGAGTCT TACAGGAAAT	4920
TGCGCCTCAT TTTATCCATC CGATATTAAA ACAACCGATC CGCAACTTGT ATGATGCTTT	4980
GAAAAAATAG AAAAAGTCTA GTTTTCAGTT ACTTGCAACT GAAGGCTAGA GTTTTATAC	5040
TCTTCGAAAA TCTCTTCAAA CCACGTCAGC GTCGCCTTAC CGTACTCAAG TACAGCTTGC	5100
GGCTAGCTTC CTAGTTGCT CTTTGATTTT CATTGAGTAT TAAATAGGT CATTTCCTTC	5160
TGGGAGGAGG ATAGTTTCTC TACCGTCCAT GTCTAAAACC AGTACTCTTG GGGGATAACG	5220
AGGGTCGAAA GGATGGTTAA AGTCAAAATC AATGGCTGTA GGGAGGTGTT GACTTGAAAA	5280
GTGGAAGGTA ATCTTCTCTT GGTATTAAAG CAATTGAAAC TCGAGTTCTT CTTCCAATTC	5340
AAAGACATTT TTTAAGAAAT GGTGATGAT ATACCAAAAA GAGTCAATGA TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAATAATT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCAGAAC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1988 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAAGTATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATTCCGTTT	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCAT TCTCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTTCGATG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTAAAC CCCTTTAGCC ATAACCATCA TTCAGGCCA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCGAG CGCTTGGAT	600
TGTTTTATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTCAGTGTG ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTTCTC TATTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAAT GTTTGGCTTT TGTAGTATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGA TTTCACTCTA TTCTGAAAAA CTTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA	1200
TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA	1320
GTCTTGCAA GAAAAAATT CCTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAAACAACA ATTCGATTG TTAGCTTCAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC	1500
GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTGT AACGGTTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCCCAA ATCGATTAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGTACTATT TAACTTCAAT GCACTATACA TCTAATACTC	1800
AATAAAATC AAAGAGCAA CTAGGAACT AGCCGCAGGT TGCTCAAAAC ACTGTTTTGA	1860
GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTTGA GGTGTAGAT GAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTTATGTA ATTTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAAACAA AAAGGGAAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAATT TCAATCATTG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTTG ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTAAGTACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTCTTTGGT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCCAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACCG	660
CGACGCCAAT GCCGTCCTC TTAGAAATA GTGATGATTT GAAAGAAGT	709

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTATTTTAA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAACTGAT	120
TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTT TATTCTGAAA GATTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTTAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTCTT ATGAACAAGG CTCTCTGGAA AGACTTGGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGACA GCCTCATTGA GCGTGATTAT AACTTGATG CTGCGACAAA	780
TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960



1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA	1020
TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT	1080
GCTGGATTGT TTAGATAAAA ATATTCTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA	1140
TGACTACAAA AAAGCTAATA TTACTATTGA AGAGTACATT GAAATGTCTG AAGTTGATTT	1200
TAATGAAGCT GTTAATTATG AATTTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA	1260
TCAATCTCTT TTTAAGTTTT TTGATAAGAA AAATTTCTCT GGCGATTTAA TTTTACTTG	1320
GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA	1380
TAATCTTAGA GTAATAGGAA ATATATTTC GAATTATCTT ACTAATCGAA AATATAGCCT	1440
CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT	1500
AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC	1560
TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTCGATTTT TTTCTAATTT	1620
TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 598 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG	60
CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTTCT	120
CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA	180
TTTCTACCAG ACCGTTTGGC GTGAgCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT	240
CTGATTGGGA AATTTGGATA AAATTGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA	300
AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA	360
AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CCTTTGATTT	420
TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT	480
GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT	540
TCATAGTTTT CTCTCCTTTT CAGTTATACA AGGTTGTGAT CACTTCCTGT ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1099 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTTT TTCATGACAA	60
GACCTCCCTC TTTTATCTAA CTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAT	120
GATAAAAATA GCAGAAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC	180
TTCTATTATC TAACTTCTTC ATCATTCCAG ACAAATAAAG CTCCGATTGC ATTGAGGATA	240
TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCTTGAA TACCAGCTTT TGTGAGCTGA	300
ACGAAATTGT AAATCAACCA AAAGCCCCAC TGAGTTGTTA GTTTTAATGC ATTCAAAGCA	360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAG ATTCATCTTG	420
CCCCCATATC CGATATAGTT GGTACAAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG	480
ATGGCCGCCA ATTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT	540
TCCCACTTCT TTATAGCAAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC	600
GCCTTATTTT CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAAC AATACCAAAG	660
TAATTTCCCC ATTTGCTTAA TTTCCCCGTG AAACGAGTGG ACAACATGGA AATCCCAACG	720
TTGGTTACGG AAATCAATCC AAAGGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT	780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCAACGAC CAAAGCAACC	840
CCGAAGAGGT CAAACTATTT AGATGTAGCA AAAATTTTGA GTGATTTTTT CATAGGTAA	900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAATAA AATGATAGAA	960
ATAAAACCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAAATCCA CTATAGATAT	1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA	1080
AACAACTCAT TAGAAAGAT	1099

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2723 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA CGTGAAGAGG AAGCCCAGAG AGTAGCCAGG TGTACTGCTA GAACAGTGAG	60
TGAAATTGAA TATTACCATA GAGAGTCAAC CCAGATAGCT CAGGCTTTAG TTGAAAATCA	120
AGCTCGTATC GAGGGAATCT ATAAATACTT TAGCCTTAGC ATGCCAGACT ATTTTACTG	180
GCAATTAGAG CGGAAAGCTT CGCCTTATAT ATCAGTCTCT CTGTATGAAA ATGTTGATGA	240
CCTCTATGTT CGAAATGATT TTGTAAGTGG GGTGGCCATT GCTTTTCAAG ATTACAAGGA	300
AGTCTATGTT TCTACTAAAG ACAAACGTAG GKKAGAAAAA ATCAGGGCTG AGGATTTCAA	360
ACCAGCAGGA AATAGTTTTG CCATTCCAGT GTCAGATCCA GTGTCAGATC AAGACTTAGG	420
AGTGATTTAC ATCTCCTTGG ATCCTGCTGT TTTATACCAT GCCATTGATA ATACTAGAGG	480
TCATACTCCG ATGGCAGTAA CAGTGACCTC ACCTTTTGAT ACGGAGATTT TTCATATGGG	540
TGAGACAGTT GATAAGGAGA GTGAAAATTG GCTAGTTGGC TTAAGTTCTC ATGGATATCA	600
GGTTCAGGTG GCAGTTCCTA AAAACTTTGT TTTACAAGGA ACAGTGACTA GCTCTGCTTT	660
GATTGTGGGT TTGAGCCTTC TCTTTATTGT CATTCTTTAT CTGACTTTGA GGCAGACTTT	720
TGCTAATTAC CAAAAGCAGG TAGTGGATTT AGTAGAATCC ATTCAAGTCA TTGCTCAAGG	780
CGAAGAGGGG CGTCGGATTG ACATTTCCGA GAAAGATCAG GAATTACTCC TAATCGCGGA	840
GACGACCAAT GATATGTTGG ATCGATTGGA AAAGAATATC CATGATATTT ACCAGTTAGA	900
GCTTAGTCAA AAAGATGCCA ATATGCGAGC CTTGCAGGCG CAAATCAATC CTCATTTTAT	960
GTATAATACG CTGGAGTTCT TGCGCATGTA TGCAGTTATG CAGAGTCAAG ATGAGTTGGC	1020
AGATATCATT TATGAATTCA GTAGTCTCTT GCGTAACAAT ATTTCCGACG AAAGAGAGAC	1080
CCTCCTCAA CAGGAATTAG AATTTGCGG TAAATACAGC TATCTCTGCA TGGTTCGCTA	1140
TCCCAAGTCC ATTGCCTATG GTTTCAAGAT AGATCCAGAG TTAGAGAATA TGAAGATTCC	1200
CAAGTTTACC TTGCAACCGC TGGTAGAAAA CTATTTGCGG CATGGTGTG ACCACAGGCG	1260
GACAGATAAT GTGATTAGCA TCAAGGCTCT TAAACAGGAT GGTTTTGTGG AAATTTTGGT	1320
GGTCGATAAT GGTAGAGGAA TGTCGGCTGA AAAGTTGGCA AATATCCGAG AAAAATTAAG	1380
TCAGAGATAT TTTGAACACC AAGCCAGCTA CAGTGATCAA AGGCAGTCTA TCGGGATTGT	1440
CAATGTACAC GAGCGTTTTG TGCTCTATTT TGGAGACCGC TATGCCATTA CTATAGAGTC	1500
TGCAGAGCAA GCCGGTGTTC AGTATCGTAT TACAATTCAA GATGAGTAGA AAGGGAGAAA	1560
ATGTATAAAG TATTATTAGT AGATGATGAG TACATGGTGA CAGAAGGTCT GAAGCGTTTG	1620
ATTCCCTTTG ATAAGTGGGA TATGGAGGTC GTCGCAACAG CCAGTCATGC CGATGAAGCT	1680
CTAGAATATG TTCAGGAAAA TCCTGTCGAT GTCATCATTT CCGATGTCAA TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG	1860
GACTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT	1980
GGATTTGTTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCCCT TCACCATTCCT CACTATGTCT TTGGGTCAAG ACTGGCAGAT TTTCATTTCT	2100
GGCCACCCCT TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTTCCTTA TTACGAACCG ATTTATAGGG TTATCATTC A GGGAAATCTC	2280
AATCAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT	2340
GTTCGATTA CTAAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTTCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC	2460
GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG	2640
CGTGAAACCG ATTCGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCAG	2700
CAGCTCTTGC TTTCAACTAG TGA	2723

## (2) INFORMATION FOR SEQ ID NO: 274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACTTT TTTAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTT TCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTTGTGGT	240
TGAATGACCA GAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCCTC GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAAACTGG	360
CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAAACATA	420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTACTGAT AGGATTGTGG	540
GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTC AACTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTTG GATTTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTC ACTTTTTAGG TGGTCTGGGG CTATTCCTAT ATAGChTCAA GACCATGGGA	60
GACGGTTTAC AACAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTTGT TTGGAGTTCT GGTGGTATT GGGATGACTG CTCTAATTCA GTCTAGTTCT	180
GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTGGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTGGGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATTGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGGGTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCATT GGTTTGAAGC TACGCTAAAT CTAGCACCAG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTTT CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC ATTTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGCACT TAGGAACTA CGCTGCTAAA GCCTTTGACC TTTCCTATAA GTACATCATT	1080
GACTTGGATG AAAAAAGTTGC TGAAAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCGTGATT TGGAACGGAT TGGAGACCAC	1260
ACGGAGGCTC TACTCAATCT GACTGACTAT CTTCAACGGA AAAATGTTGA ATTTTCTGAT	1320
GCCGCCTTGA AAGAATTAGA GGAAGTTTAC CGCCAACTA GTGACTTTAT CAAAGATGCT	1380
CTGGATAGTG TGAAAAACAA TGATATTGAA AAAGCAGCA GTCTTGTAGA ACGTCATGAA	1440
GCAATCAATA AGATAGAACG TGTCTCAGA AAAACCCACA TCAAACGCCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA	1560
TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTGCAG AACAAATCTA AGAACCAAGA	1620
AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCTA AGCAAGACTA GGATGAATGA	1680
AACTGAAAGA GTATTCTGCA GATATATAGT CCCCATTAT TCACCCCAA TCTAAAAACC	1740
ATCCAGAATC CTTGCCTTAG CTTAGATCCT GGATGGTTTC TTTTTCACC CAATGGGTGT	1800
TTTTTACTAG AAAAAAAGA GTTTCCCTT TATGGTATAA GTGTAGAAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTTCCC AGTTGAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCCGCTACT GTCGTTATTC GGATTCAGAT ATCCTTGTC AGTTCCTCTT TCAACTGTTA	2100
ACAGGTTATG GAACGGACTA TGCTTGTAAG GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCCGTTTTCT TTCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTTGCGATGC CTCACCTTG AATgGkCGAA TTCTTTTAC	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTC ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACCT GTTGTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG	60
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1307

TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA	120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT	180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA	240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA	300
GAAGCTGTAG CACTTGCAAA AGAACTAAC TTTGCAAAAT TTGATGCAAC TGTAGAAGTT	360
GCTTACAACT TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA	420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGTTT TCGCACGTGG TGCAAAGCT	480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC	540
AACGACGGTT GGTGGACTT CGACGTAGtT ATCGCTACAC CTGATATGAT GGCTCTTGTT	600
GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCCTAA AACTGGTACT	660
GTAACAATGG ATGTTGGCAA AGCGGTTGAA GAGTCTAAAG GTGGTAAAAT CACTTACCGT	720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT	752

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2643 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCAACATTG ATTTCAAGGC TGTTTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA	60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAAA TCGATTTCTA ACAATGTTTT	120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC	180
CATTTGAACG ATTTCAAATC CTTCTTTTTG GTAAAGATTC TGAGCTCTTT GATTTGCCTC	240
GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT	300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCTGG GGGTTGATAA AAAATCTCCC	360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCCACAA ACTCTTGTTT	420
ATCAAAGATT GAAAAGACTC CTTCCAAGGC TTGAAGTGTC AGTAGAAAAG GAATCCTTGG	480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG	540
AGCGTTTTCT GTGCTCACCT TTTCTTCAAA ACGAATTGTC ATCTTTTCCT CACCACCTTA	600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTTTACG AATAGATAAG TATGATTGAT	660

1308

TTTTATTTT TTCTCGTCGG GAGCATTCTA GCTTCCTTTC TTGGTTTGGT CATTGACCGT	720
TTTCCAGAGC AATCCATTAT CAGTTCAGCC AGTCACTGCG ATTCTGTCA GACTCCCTTG	780
CGTCCCTTAG ATTTGATTCC GATTCTCTCA CAGGTCTTCA ATCGCTTTCC CTGTCGCTAC	840
TGCAAAGTTC GCTATCCTGT CTGGTATGCC CTCTTTGAAT TAAGCTTAGG ACTCCTCTTT	900
CTGCTTTACT CTTGGGGATG GCTCTCCTTG GGGCAAGTCG TCCTAATCAC CGCTGGTTTG	960
ACCTTGGGTA TCTACGACTT TCACCATCAG GAATATCCCT TACTGGTCTG GATGACTTTC	1020
CAGCTAATCC TAATAGCTTC CTCTGGCTGG AATCTGGTCA TGGTCTCCTT CCTCATACTT	1080
GGAATTTTGG CTCATTTTAT CGATATCCGC ATGGGTGCAG GGGATTTCCCT CTTTTAGCT	1140
TCTTGTGCTC TCGTCTTTAG CGTAACGGAG TTAGTGATCT TGATTCAGTT CGCTTCTGCG	1200
ACGGGTATCC TGGCCTTTCT CCTGCAAAAG AAAAAGGAAA GACTTCCTTT CGTGCCTTTC	1260
CTCTTACTTG CTAATTGTTT GATTATTTTT GGTAAGCTAC TGCTTGTCTG ATAAAATCCA	1320
ATTTCTGCCA TATATCCTTC ATGAAATTAT TTCACAGTTA AATTATAAAT TATTTCTTTT	1380
GTACAAAGGG ATGATGTTAT CAAATCGATC TGTCTTCTA TCTTCTTGAT ACTGATCAAA	1440
AAATTTCAAT TCGACTGAAA ATATTTGCTT TATAAACTGT AAACGAATAC TTTGTTTAGA	1500
CATTATAGTC GCTAGACTGA CTAGATGATT ACTCAAAACG ACGTCCAGAA TACTCTTTAC	1560
TTTGCTTGGT TTTTAAACAA AAATTTGATC ATCCAAGGGT TCAATCATTT TGTAACCTTT	1620
TTGCGCAATT TGACGATAAA AGTAAGAATG TTGCTTTGGA GTCAATAATC CTAACCTAAA	1680
AGCTCGATAC TCTAAAGCCT GTATCGAAAC ATTCAAATCC GACTTCAATA AAATATAACT	1740
ATCAGGATTG CTGACACGCT TGCCAACCCT CTCTTCAAAT TTGACTAAAA ACTCTTCTTT	1800
TGGCAATAAA AAACATGATG CAAAATAATT TGCTTCTTGC TCCAAACGAT CGCCATCTTC	1860
ATTCATATCT TTATATTTAT GTAAAAGAAT ATGTCCTAGC TCATGAGCTA AGTCAAAATT	1920
TCGACGTACA GATGATTTAT TCGTTCCTAA CACAATATAA GGTCTTCCCA ATTTTGACCA	1980
TGCGCTATAA GCATCAGCTT GGCCATTAAT TAATCGTTCC ACGATATAGA TGCCTGAACG	2040
TTCTAATTTA TAAAGCAAAT CATGATTATC TTTTGAAATA CCTAATTTTT CCCTGGCATA	2100
AAGAGCCAAT TCCTCAATGG ATTCTCCCTT ATGATAAGAT TCACTCACTA CATTACTTAG	2160
GTCATGAATT ATAATATTAG GTATAATTAC AAAACTTTCA AAATAATCAA TCAAACATC	2220
TACCTTATGT AAATACATAG TTTGAATATC TATTGTTTTT CGTGTTGCTA GGTCTGCATT	2280
TCTAAAGGCA ATTACAGAAG AATCAAATCG AATGCTCTCT TCTTCTGTT CAAAATAAGT	2340
TAAATCAACA TGAAATTGGT TGGCCAAATG CATTTTGGTT GATAATTTAG GTTTCGTTTC	2400
GTTGGACTCA AACTGCCAAA TGGCTTGTTT CGTTAAATTA ATTCTCTGAG CTAATTCTGC	2460



1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT 2520  
ACTCCTTACT ACTTTTGACC TTCTTGTTTT TCTATTCTTG GAATAATTC AAAATCTTCT 2580  
GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640  
GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 582 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG 60  
GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG 120  
TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGG CAAGCTGGAG AGTCAGAGTA 180  
TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAaAGGAG TTGCTCAAAC 240  
CTTCTTAGAG GGCTTGATTG AAGGTTTTGA TTATCTTGAT TTTCGCTCAG ATACGCATGC 300  
TGAAAACAAG GTTATGCAAC ATATTTTTGA AAAACTTGGT TTAAACAAG TCGGTAAGAT 360  
GCCAGTAGAT GCGAAGCCT TGGCCTATCA AAAATTAAAG AAATAATGCA AAAGAAGTAT 420  
GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480  
TTGTATGGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG 540  
ATAGAAGAAG TTGTWAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AAACCTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTTAA 60  
ATTTATGAT GAATTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120  
CCCCTAGTAT AACAAGTTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCAAAG CCCCCTGATA GTCAAAGCCG GTCACCTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTTAT GAGCACCATC CAAATAAATC TGTGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

## (2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 766 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTTGGTTGTG GCTAAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATTCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAAGTCT CAACACTATC CAGCCTTGAA ACTTTTGTAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAAAATCATG	360
TTTTCATTAC CTCGGCTTTG TACGGTGTG TTCCAGTCTT GTCACCCATG GTCCTCACC	420
GTTTGGATTT TTTGATGAAA TTAAAAGTCG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG	480
CAGCCTATGA TGAAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCCCGC GGGGCCTTTC	660
TAACAGCTTT AATAGAAAAT CAAGTACAAA CTGTGGGGG AGCACGTCGC TTGAACTTTG	720
CTGGATTTGT TTACCGAGAA GATTTGTCAC AACCACAGGG GGATGG	766

## (2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 901 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1311

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CCGGCCACGG TTCCATCCAA CTTACAGGT GTGCACTTGA TTGTGTATGT AATTGTCACT	60
AACGGTAGAA TTTCACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG	120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGCAAA	180
TAGATTTTAA AATTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTTGA CGACCTTGT	240
ATTGCCTAGT TTTTCGCGTG CAATTTGAG AATGGCACCT GAGTCTTTG AAGCAAAGAG	300
GAATTTTCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCCTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATTGACATC	420
TGGGTAAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTTC CCAACTTTCC CAGCGATAGA	480
GAGGTAGGAA GTGCCTGTCTG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT	600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG	660
ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC	720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTC TGCATGATCT	780
ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAWCGTCG ATACCTGTTG GCATATGTTT CCAACCGATG	900
T	901

## (2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1765 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG	60
CTGCATTCTGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTCCA ACTCTTCCCC	300

1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTCCC CATTTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTTCG CTTCTGAGTC TTCTGGGATT GGTTCGAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTC AATTGTCCGT CTTCTCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTACCA AATTCTTCTT TTCCATCAAT	600
TGTCAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTAT ATTAATAATT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTCTTGCG	780
CTTATTGCGA CTGATATCTG CTTGTTCAAT CAACATGCGC TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTTCATG TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CTTGTAAAGT ATCAACCAAT TCCTTAACGC GGTCAAACC AAATTGGCCT	1020
TGTTCTTCAT TTATCTGGAT GATTCAAGC CCTTGAGCTG TAAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTTT TGAACCGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTC ATCAGCTCA	1200
TACTTACGGA TTTGATTTCG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTG GTTAATTGGG TTGTAACCTT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT	1380
GTTTCTTCAG TAAATCCCAT TCTAACCCC TCTTCTCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTTCTGTCC	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTCCGTTG CGCTCAATAG TTTTGTTTCA AGTTTGAAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTG	1765

## (2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1346 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGGT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAGG ACACCATTCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAAACTA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTCACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTCTT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGCA TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTGTTT	1140
GAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AAACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG YTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 900 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTCTAG AATTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTC TCTCTAGTAT TTTATTTAGA AGATTTAATC	240
TATCCTTGGA TTGTTAAACC TTTGGTTT GAGATAAATP CATTGCGTGA AAAAGGTTTA	300
CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTTA TAACAAATAT CCCGTTTTAC TGAGGCAAAT ATCGGAGTCT	420
TGTCTTCGGT TCTATACTTA TTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGGG AAATTAAATG ATATAAAAT TGGAAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCTATCG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 862 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTATCA	60
GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTT TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGCT GGAGAAGTAA GGGAAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTTACAGA TTCCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTTACTTA GAGGACTTGG AGGGAAATGG CATTGAACTC TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAACGGT 540  
 GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA 600  
 CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT 660  
 CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT 720  
 TGCCCAACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA 780  
 AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA 840  
 TGAAGGTAGA GCATCAATTG TA 862

## (2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC 60  
 GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATTCCA 120  
 AAGCGTTTCT CCTCATTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA 180  
 TCATTTACTC TTTATTTTAC GATAATTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG 240  
 TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCTT TTTCTGTTGC TCCATTTTCC 300  
 ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG 360  
 ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT 420  
 TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA 480  
 GATAGTGTA TATCCCCAAT TGGAAACCAT TCTCCCTTCT CTTTGACTTC AATCCAAAAA 540  
 AGCTCACCAT GCCGATyCAr ATAGGAATAC ATGGCTTCCA AGGTCGcTtG ACTGTAAGGA 600  
 AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC 650

## (2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCTCATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAACTTTG	240
TAAAATTTTC TTGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTTCCAACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAATCACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAAC GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAGA GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTCTT CAAAACAAC CTTTGTCAAT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTTGTTCA AGCTTTGCAA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATAA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AACTCTGTA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATTCCTC GTTCATCACG AAGGCCGCCG AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCCG	240



1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCTCCTC	300
AAAAGTGCGC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA	360
GGGTGCGAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCAATTT	420
CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTGGCAT GGTGACTCAA GCGTCCTTTC	480
AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC	540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1949 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTCG ACCAATTCAA GGTGAGGCA TCGCAAATA TGGACTGTTC CCCCCTCAGT	60
TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT	120
TGGAAAGTAG GCATCAGCTG ACAATCTTT ACAAGCATAG TCCGTTCCAT AACCTGTAA	180
CAGTTGAAAG AGGAACTGGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG	240
GTCATTGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC	300
CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA	360
AAAAGACTTG TTTTGAAGT GATGATTTGG TAACTGTTT ATGTGAGTTT CCTTTCTTTT	420
TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAACTCT TTTTGTCTA GTAAAAACA	480
CCCATTGGGT GAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT	540
TTTGTAGATT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG	600
ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC	660
ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCCGAAA GTTTATTAAA AAAAAATCC	720
TGCCAAAGAA TTTTGGCAG GAAACCAAT CAATTTATCA GTTCTATCA ATCGCTTATC	780
GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAAT GCGATACTCT ATTATTTAAG	840
AGTAACTGAA GCTCCAGCTT CTTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC	900
AACGCCTTCT TTAACAAGTG CTGGTGACCC GTCAACAAGT TCTTTAGCTT CTTTAAGACC	960
AAGACCAAGT ATTTACGTA CAACTTTGAT AACGCCAACT TTTTGTGCG CTGCAGATGT	1020
CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC	1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAAA TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTC AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT TATAATAGTT TTTTTCGTAG CTAGkTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTTC TTTGCTTTCT GCAACCGCTT TGA CTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC TTCTTTAGAT GCGACAGCGC CTTGATTCG	1440
ACCACCTTTA ATTTCAAGTG CTTGAGCGTT TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGCTAC TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTTT CAGCTGCACG ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTCCACGAA GCTCAGCAG AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC AGCTTTCATT TTTTCAGCTA CACGTCAACT	1740
AGTTCCGCTT TTTTAGCAAT AATTGCTTCA CTCATTAGTG TGTTACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTCAA AAAGAAAAAC GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTGTCTCT CGGTAGGATA TTTATGAGTC GAGCTCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG	1949

## (2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1023 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT TTTTGAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT ACTTGCTCTC ATTTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAATGGA TTTCCACAGT TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCTACGATA GTTGGGTTGA CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTTCCCA TCCCAAAGCT CACCTTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT CTTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAACG CCACCTGTAC AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATTGTGGTA ACTCACGGAA GTTGCGAATA TCTGGGCGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG	600
TATCTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGGAGA CAAGTAAGCA CCTGTTGTTT	660
CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTCTT	720
TCTTGTAGCG AACAAACATC TTCTTGAAGG CTTGTTTATT TTCTTCGTCA ATCTTGAACC	780
AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAGTCCAT GTATTTTGA GTTGTTCAT	840
AGTCACCTGA AACTGTTCCG TTAATTCCTT CGTCAGCGAC TAGGATACCG CCTTTAAGGn	900
CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATTG CTCTGCATTT TCAATTGGAG	960
TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTGTA TCTCTTATC	1020
TAT	1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3831 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTTAAT AGTTTAAAGC	60
ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAATATG	120
GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA	180
TTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA	240
CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAAACA	300
CACCATCGGT TATTATTATG GATAATGTAA GATTCATAG AATGGGGAAG CTAGAACTTT	360
TATGCGAAGA GTTTGGGCAT AAACCTTTAC CTCTTCTCC TACTCGCCT GAGTACAATC	420
CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA	480
ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG	540
ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC	600
AAATTTGTC CTTTCTTTT TGAAGTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT	660
GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTTGGCG TTGGAATAAG GTAATTGAAG	720
GGCGTTGACG ATTTCTCTT TATCTTTGAG GAAGGTTTAA AACAAAGTCT GAAACAGAGG	780
TGGAAGCA AGAGCTGATA GAGATTATAG TGGTGTAA AGTCTTCGGA ATAGCTCAAA	840

1320  
AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAAATCGT 900  
TTATCACTCA GTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG 960  
TATTCATGGG ATTTCCGATG ATGGCTTGTG TTCTGCTCTC AAGAACAGTT ATGATATTGA 1020  
GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC 1080  
CCGGACTGTT TCAACsTCCT AGGACATAAT CTCAGGAAGA ESEGAAAAAT CATGCTCAAA 1140  
GTGAAAATCA TTGTTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT 1200  
GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGTTGA TGATACAAGG 1260  
AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA 1320  
GCACTTAAAA CGGCCTTTTC TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAAT 1380  
CAGAACCATA ATACCTATAT AAAAATATTA TAGTTCTAAT AGGATTTACC CAAAAGTTT 1440  
AAGGCGGTCT TTTAGAACT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTCTATTT 1500  
TGTCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT 1560  
AGTGAATGTG TAAAATTTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT 1620  
TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA 1680  
TGGTCCTACA TTTGGTGATA ATTTTGACTG GGAACATGTT CATTTTAAAT TTTAATTTA 1740  
TTATTTAGTG AGATATGGCA TTGGTTGTG TAAGGATTTT ATTGTTTACC ATTATCGTGT 1800  
TGCTTATCGT TTGTATCTTG AAAAATTGGT AATGAATCGG GGTMTTATTT CTTGTTGAGG 1860  
TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT 1920  
AGTAATTTTT CTAAATCATT TTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT 1980  
CTTGATAAAA AGGCGATTTT TTATTATAAT AAATGTAAG ATATAATTGC AGGTGAGAGT 2040  
CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT 2100  
GTTGTTGTAG GTACCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCTTTCA 2160  
GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG 2220  
ATTGACGGTA AGAAATTTAA GTTGCACTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA 2280  
ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCCTAAAT CTCTTGTAAG AGAGTTGAGC 2340  
TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCGTA TTTCTGATCG TGCGCATGTT 2400  
ATTTTGCCTT ATCATATCGA GTTGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG 2460  
ATTGGTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGA 2520  
ATTGATATTG CAGATCTTTT AGATAAAGAT ATTTCCGTG AGCGTTTGA ACCTAACCTT 2580  
GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTCGATGAT 2640

1321

ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT	2700
GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT	2760
GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTTGTTA CGTCATCAAA CCCTGTAGCT	2820
GGTGGTGTGA CAATTGGTTC TGGTGTCCGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA	2880
TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCTTTCC CAACTGAGTT GTTTGATGAA	2940
GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACTGG TCGTCCACGT	3000
CGTGTAGGTT GGTGTGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT	3060
AACCTTTCTT TGAACCTCTAT TGATGTTTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG	3120
GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA	3180
CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGGTTCAG AAGATATTAC CGGAGTTCCG	3240
AATTTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTT GTCGTGTGAG TGAATTGGTT	3300
GGCGTTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCCGT AACAAACAAA TATTTTAGAA	3360
AGTGTGTTGGT CCTAAGAGAT TTTTAAGATT TGTTTAAGAT AGGTCGGGTA TACTATAGAC	3420
GGTTACAAGA AGACCTCCTA ACTTGTGTGA ACAAATATCC TAACTTTTC TTTTCATAA	3480
TAATCTCCCT ATAGAGTCAC CGCATTCCGT GGCTTTTTTT GTGTTGGGAT TCATGATATA	3540
ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG	3600
AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC	3660
CAATTGGTTG TGTGATTGTC AAAGATGGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG	3720
AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT CGGAACCTGA	3780
GTGAGGAGAG TCGCCTTGCT GGATTGCACA CTTTTTGTTA CCATTGAACC G	3831

## (2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1441 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTCC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG	60
TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTATT TTCAACTCTT	120
ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGT TTTATTTTTT	180

1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATPGGTAC ATATTGAAGA GGGCCGCCCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGCTGAATT GATTTTTTAC	720
GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTTGCGCT GAAACTGCGA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAATT CATCATCTGT CATCGCTTCA AGTTTTGCTT	900
TGAATGCTTC AAGAACTGTT GGAACGTGTT CACCCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAA CGGCCTGCTT	1080
CCTCTAAGAA TGGTTTTGCC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGAATTG CTGAGGCGGT	1200
TTTCATCAA AAGTTTAATG AATTCTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCCGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGACCGGGTA	1440
T	1441

## (2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCTG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCAATT TCGTTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGGA TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAATTTG TAACCTTGAA TTCATCGGGT GACCCTGTGG	540
AAGCCGCAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG	600
ATCGTGTTC AGCCTTGCTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTGAA ACGGATATTG	720
AAGCGCGTTT CCACTTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAAT ATTCGTCAGT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAAATCTA CTTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA	1020
CAGAATTAGA GAGTTTTGAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACCTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATTCTTT ACGGCAAGCA	1320
ATAATACCGA GGATTAAATG GTTGAGTTAG AACAAAAAAT GATTAACATT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT	1500
TTGATGAACG CATTCAGAA GCATTTAACG AAGCTTTAGA TATTTTGTAA AAAGAATTTG	1560
ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGGA AGTGGCAGAG CCTGGTGTA	1620
CCAATCGCTT TGTTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAGA	1680
AAAAGATTTT ATTGTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAAACA	1800
GTGTTTTATA CTCTTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA	1860

1324

GTACAGCCTG AGGCTAGCTT CTTAGTTTGC TTTTGTATT TCATTTAGTA TTAAAGTGAT	1920
TTCGCCAGTC TTATCTGCAG CTTCAAATCT GTACTTTGAG TAACTTGGTA ACCGTCCAAT	1980
AACGAAGTCT ATTGAAAAAT CTCCAGACTA GAGAACTCAC GGATAGTTCC TAATCTGGAG	2040
ATTCTTATT TGCACTTTTT TGTACAAC TTAGTCCACG GTAAATAGAC CTCTAAAACC	2100
TCTTTGTTTA CGAGAGTTTC CTCGTTTGA AGACATTCTA GAAGATAGGA TAGATATTTT	2160
TCGCTATTTA TACTAGACTA AAATCAAAAA GCATTATATA ATAGTGATAT GAAATCAACT	2220
AAAGAAGAAA TCCAAACCAT CAAAACACTT TAAAAGACT CTCGTACAGC TAAATATCAT	2280
AAACGCCTTC AAATCGTTCT ATAGTAAAT GAAATAAGAA CAGTACAAAT CGATCAGGAC	2340
AGTCAAATTG ATTTCTAACA ATGTTTGA AGTAGAGGTG TACTATTCTA GTTTCATCT	2400
ATTATATTTT GTCTGATGGG CAAATCTTAT AAAGAGATTA TAGAACTTTT ATAGTAGATT	2460
GAAATAAGAT GTGAACAACT CTATCAGGAA AGTCAAATTA ATTTATAGAA ATATTTTAGC	2520
AGCCAAGGTG TACTGTTATA GATTCAATAC ACTATAGACT GTAATCAAAC AACGATTTGG	2580
CGAAATGTAA AAAATATGA GGAGTTCGA CTCGACTCTC TCCTTCAAGA AACACGTGGT	2640
GGTCGTAACC ATGCATATAT GACAGTTGAG GAAAAGAAAG TCTTCTTGC CCGCCATTTG	2700
AAGGCTGCAG AGGCAGGAGA ATTTGTTACA ATTGATGCCT TATTTCAAGC TTATAAAAAG	2760
GAGTTAGGTC GTTCCTACAC ACGTGATGCC TTCTATCAAC TGTGAAGTG CCATGGTTGG	2820
CGAAATATTA TGCCACGTCC AGAACATCCT AAGAAAGCAG ACGCTCAAAC CATTTGTCGG	2880
TCTAAAAATA AAATCTCAAT TCAAGAAGAA AAGAAAGCGC TTTAAAACCA GTAGACGTTT	2940
TCGTAAGGTT CGCTTGATGT ACCAAGATGA GGCTGGTTTC GGTAAGATCA GTAAACTGGG	3000
ATCTTGTGG GCTCCAATAG GAGTAGGTCC ACATATCCAT AGTCACTATA TACGAGAATT	3060
TCGCTATTGT TATGGAGCTG TTGATGCCCA TACAGGCGAA TCATTTTCT TAATAGCTGG	3120
TAGATGTAAT ACTGAGTGA TGAACGCCTT TTTAGAAGAG CTTTCACAAG CTTATCCAGA	3180
TGATTATCTT TTAATCGTTA TGGACAATGC TATATGGCAT AAATCAAGTA CCTTAAAGAT	3240
TCCGACTAAT ATTGGTTTTA CTTTATTCC TCCATACACA CCAGAGATGA ACCCCATTGA	3300
ACAAGTGTGG AAAGAGATTC GTAAACGTGG ATTTAAGAAT AAAGCCTTTC AAACTTTGA	3360
AGATGTCATG AATCAACTCC AAGATGTTAT ACAAGGATTG GAGAAGGAGG TGATAAAGTC	3420
CATCGTTAAT CGGAGATGGA CTAGAATGCT TTTGAAAAC AGATGAGTAT AAAAAGAAAG	3480
TCCTCATTTT AATAGAAATC ACGACTTTCT GATGGATTTA TAGTAAAATG AAATAAGAAC	3540
AGGACAAATC GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTTAGAA GCAGAGGTGT	3600
ACTATTCTAG TTTCAATCTA CTATATTTTT GGAGTGATAG AAAAGCCCTT CATAAGCTAG	3660



1325

TCTACTTGTT CAGGTGCGAG AGCTTTGACA TCTTTTCTG TACTTAGCCA AGTCAGTTTT	3720
CCGTTCTCAA AGCGTTTATA TAGTAGCCAA AATCCTTGAC CATCCCAGTA AAGGGCTTTA	3780
AAGCGGTCTT TACGTCCACC ACAAAGAGA AAGACTTGAC CGGAGAAAGA ATCCAATTCA	3840
AAGTGGGTTT TAACTACATA GGCTAATGAG TCTATTCCCT GCCTCATATC TGTCTTGCCA	3900
CAAACAAGGT GAACTTGACC TAAATCACTT AGTTGAATTA TCATAGTACA ATACCTTTCC	3960
TCCGATAATT ATTTTATC TAGTATACTG GAAGTTGGG AATTAGGATA GATACCTTGT	4020
TATGACGCGC TTACGTAAC TGTAAC TAGC TGCCTAGTTT GATCTTTGCT TCTTCATTGA	4080
TTAGCAGTAG ATTTCAAAT GATAAAACG CATAGTATCA GGTATTGAAA TGTACTGCCC	4140
CAAAAGTTAG ACAGAAAAA TCTAATTTT GGGGTGTTT TGTATGAAA TTAAGTTATG	4200
ATGATAAAGT TCAGATCTAT GAACTTAGAA AACAAGGATA TAGCTTAGAG AAGCTTTCAA	4260
ATAAATTTGG GATAAATAAT TCTAATCTTA GGTATATGAT TAAATTGATT GATCGTTACG	4320
GAATAGAGTT CGTCAAAAA GGAAAAATC GTTACTATTT TCCTGATTTA AAACAAGAAA	4380
TGATTAATAA AGTCTTAC	4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 718 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTT TAG ACTTTGCTT TAATCGTTT TTTTAGGGA TGATTGCGAC ACCTTCTTTT	60
GGCTATTAAC TTTAGCAGGA GGGATTATCC TTGGTCTAGC GCCGGCTAGT GCCACCTTGA	120
TGAGCTTATA TGCAGAACAT GGTATAGCT TTCGGAATA CAGTTTGAAG GAGGCTTGGT	180
CTCTTTACAA GCAAAATTTT GTCTCAAGCA ACCTGATTTT CTATAGCTTT TTAGGTGTGG	240
GTCTAGTTT GACCTATGGT TTGTATCTCT TGGTGCAATT GCCTCATCAG ACCATTGTTC	300
ATTTGATTGC GACCCTTTTG AATGTCCTAG TAGTTGCCCT GATCTTTTGG GCTTATACAG	360
TATCTTTAAA ATTACAAGTT TATTTTGCCT TGTCTATCG AAATAGTCTC AAATTATCCT	420
TGATTGGCAT CTTTATGAGT CTAGCAGCTG TGGCTAAGGT TCTCCTTGGG ACTGTGCTAC	480
TTGTAGCAAT TGGTTATTAT ATGCCTGCCC TGCTATTTT TGTAGGAATT GGGATGTGGC	540
ATTCCTTTAT CAGTGATATG TTGGAACCTG TCTATGAAAT CATCCATGAA AAATTGGCGT	600

1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG 660  
 ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG 718

## (2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTAAACAGAT 60  
 TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG 120  
 GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT 180  
 GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAAT AAATGCAATT 240  
 AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA 300  
 ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC 360  
 AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT 420  
 TCTTATTACA ATATTTTGT CATTAAAGCT TGGAACAAAA GAAATTAATA TCAGAGATTT 480  
 TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA 540  
 TGAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT 600  
 ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC 660  
 AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCTTTTAG GGAATTCATC AAGCATAA 718

## (2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1436 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACTAATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG 60  
 TTTTCTTGG CATAATGACT TTTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA 120  
 CCAAGTCCAC SCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT 180  
 CCAGGTGGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT 240

1327

GAAGGCAAGG CCACGTCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGGTTGTTGT CATGAGGTGC CCTATCAGTG TGAATAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GCTTGGTCAA TAGTCAAGGA	840
TGAGTTTGT CTTCCCTTAC TATAGTGA CTAAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTGTC TTAAACAGGC CTTGAAAGAC AATGCCTGAG CTACTGGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTGAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAAATCATG TAGAGGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTTGGCC AAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTGCGGA AAGAACGTAA GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT	300
ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT	420
GTCATTAAAG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTCCGTCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAATATTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCATTAG AACATCACCC TTTGAGCCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCCTTTT GTTTTCTCG CTTTAATCCA GGTGCCCCAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAAA TCATCTAGTT TTGAAGTAGG AGAAAACTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCTTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTAAT AGTTATTATG CAAAGTCTAA	1200
AAGGTTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTTGGGA AAGAACGTAA	1320
GAGTTTGCAG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT ACACCATCTG AAAATGAGCA	1620
GTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1022 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1329

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA	60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTCGATG TTCGCAGGTG	120
CATTTTAAAC CTTCAGTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTG	180
CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG	240
TTTTTTTGAA TGCCGAGTTG GTCACCTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT	300
TAAAAAAAT CTCTTGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC	360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA	420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG	480
TCTTGCTTGA GCGGATTTTG GCAAATATTT TTGTAAATAT TCGGATTCTG TCATTATTTT	540
TGGTCAAAGA TGGTGGTGCC AAACCTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT	600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CGCGATTGTG AAATTCAGTG	660
TTGCTGCCGA TTCAATTGCC AACTTCGGTG TTGAAATAT GCTTCGCCAC TGGGGTGTGA	720
CTTTCATCGG AAACCTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA	780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT	840
CATTTTCAAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT	900
AIACTATAAC TCAAGGTGCT ACAATATCCT TAATAAATA ATATGGAGGT CACCTTATGA	960
CTTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA	1020
CT	1022

## (2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGGAAATATCG ATATAATGGC	60
TTCAATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAACT	120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA	180

1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCCTGGA GGAGTTTTTC CTATTCTGAA	300
GTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTTCAT ATATAGGATA	360
AGAGGTTGTT TCGTCTTTGT TCCCATATAA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTTGTT TTTCTGCTCG	480
TATTTTTTCA AGTAAACTT CGACTGATTC ATCATTGCGG TCTTGTTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATTCTT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

## (2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAAACAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTGGTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTGCAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTTCAGCT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAC AGCCTAAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAAATCT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTGTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTTGA G	881

1331

## (2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 949 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```
CCTTTTAA TACAAGTTAT TTTGATTAA CCGGCTGTC TTGAGCTGTC TGCAAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA      120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT      240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCCTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCCTT AGGAAGATTT TTCACGATAC TGTCCAGTC ATCCTTGTA TTCTCAGGAT      360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA      420
GCATGATTTC ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG      540
TGCCATCAGC AATTCCCAA CTGTTTGCAT CTGCCCCTTC TGCCATCACC TTGGTCTGGC      600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGTGGTGC CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTTG GACAATAGGT GTGTTCTTGC      780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC      900
AATGGAAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT      949
```

## (2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 622 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```
AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT CGAATTAAAG      60
```

1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA	120
AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA	240
AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT	300
TACAACTTCT TAAACAGACT CTTGAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTACG AATAAAATAG GAGTTATGAA	540
ATGAAAATTG TTAAGTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT	600
ATTGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAAACTCAA	60
TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA	120
ACGTAATTTC TAAATCAGGT ACAACAACTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAACTG	240
ACCGCCAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG	300
TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAAGTGC GAATGCAGCT CGCAAAGACT	420
ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGAATG GTGGAAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT	600
ACCCAAC TTC AGCCAAC TTC TCAACTGACT TGCACTCACT TGGTCAATTT ATCCAAGAAG	660
GAACTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTTT GGAAGAAGAC CTTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAAGCAACT GACGGTGTTT TTCTTGCCCA CACAGATGGT GATGTACCAA	840



1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTTACT TGAATGCTAT CAACCCATTT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAAT	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTTT TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CCGTGGTGAC TGGGTTATCC	1740
AAAAGAAAGA CGGTTACCCA ACTTACAAC TGGCCGTTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATTGAGC CCTTCCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT	CCAGTCTACA	ACTTCTCTAT	CCCTGGTACA	GTGAAAAACT	TGCTTGACTG	300
GCTATCTCGT	GCCCTTGACT	TGTCTGATAC	ACGTGGCGTT	TCTGCCCTTC	AAGACAAGTT	360
TGTCACAGTA	TCATCTGTAG	CCAATGCAGG	GCACGATCAA	CTTTTCGCTA	TCTACAAAGA	420
CCTCTTGCCA	TTTATCCGTA	CACAAGGCGT	TGGTGATTTC	ACTGCTGCAC	GTGTTAATGA	480
CTCTGCCTGG	GCAsACGGAA	AATTGGTTCT	TGAAGAAACA	GTCTAAACT	CACTTGAAAA	540
ACAAGCTCAA	GACTTGGTCG	AAGCTATCAA	GTAAC TAACA	CTCAATAAAA	ATCAAAAAGC	600
AAACTAkGAA	GCTArCCGCA	AGCTACTCaA	gCACTGCTTT	GAGGTTGTAG	ATAGA ACTGA	660
CGAGTGTnna	ACATATATAC	GGTAAGGCGA	CACTGACGTG	GCTTGAAn		708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTTCTTTTCT	TGGAAATAGG	TGTATAATAC	GTTTATTAAA	TTTTTGAGGA	GTTGTCTATG	60
AAGAAAAGTT	TTATCCATCA	ACAAGAAGAA	ATTTCTTTTG	TCAAAAACAC	TTTACCCAG	120
TATTTGAAAG	ATAAGCTAGA	AGTTGTCGAA	GTTCAAGGTC	CTATCTTGAG	TAAGGTCGGT	180
GACGGAATGC	AGGACAACCT	GTCTGGTGTG	GAAAATCCAG	TATCGGTCAA	GGTCTCCAA	240
ATCCCTGATG	CTACTTATGA	AGTGGTGCAC	TCACTTGCTA	AATGGAAACG	CCACACCTTG	300
GCTCGTTTGT	GCTTTGGTGA	AGGAGAGGGT	CTCTTTGTCC	ACATGAAAGC	CCTTCGTCCA	360
GATGAGGATT	CCTTGGATGC	AACCCACTCT	GTTTATGTTG	ACCAGTGGGA	CTGGGAGAAG	420
GTTATCCCAA	ATGGTAAGCG	TAACATCGTT	TATCTAAAAG	AAACAGTTGA	GAAGATTTAT	480
AAGGCTATTC	GCCTGACTGA	GCTAGCTGTT	GAAGCCCGCT	ATGACATCGA	GTCTATCTTG	540
CCAAAACAAA	TTACCTTTAT	CCATACAGAA	GAATTGGTAG	AACGCTACCC	AGACTTGACA	600
CCGAAAGAAC	GTGAAAATGC	GATTTGTAAA	GAATTTGGAG	CCGTCTTTT	GATTGGTATC	660
GGTGGCGAGT	TGCCAGATGG	TAAACCGCAC	GATGGACGTG	CACCAGACTA	TGATGACTGG	720
ACAAGCGAGT	CTGAGAATGG	CTACAAGGGT	CTAAATGGTG	ATATTCTTGT	CTGGAATGAG	780
T						781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

CCCGCATCTT GTAGGGTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC	60
GCTTCTAGGG CTGTTTGGTA GTTGTTTTTC GCGTCCCGAT GCGCCTTTTG TTCTTCTTCG	120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC	180
TTCTTATCAA TACCTCCAAT GTCTCCACACA TTACCATCGC GGTCAATGGT ACCTGTACCG	240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA	300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG	360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTGGCC ATTTTCCAAG	420
GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTTCATAGGT GACCTTGACG	480
GAATCCCCTA ATTTTGGAGA ACTGACGTAA TCAATCAAGT CTTTGGAACT ATCAAAGGTC	540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGAATTA	600
TCCGTCACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT	660
TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAGAATTG ATTGATTGCG	720
ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA	780
GGTGTCAACC AACCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG	840
AATTGT	846

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 829 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC	60
CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG	120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT	180
GACTAGGGTC AGCAAACCTGA TTAAATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC	240

1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GCGGATGGTA GGTAGTTGCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

## (2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCGCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTCGCTT CGCTGTGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCAGGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC	360
GGTGACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGCGGATGA GGCGCACGCA GGCC	464

## (2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCTATAA TGGTAATAGA TTTTATTGAG AGGTTTTTAT GTCATTTCTA TCAAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTTGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCCTA TAAACAACTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTTGT CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTC TGCCATGCA GCGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCCT	540
CGGCACCTGG CTTTCTATCT CCAATGAAGG CTTGCGCCTC TTTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTTCTATCC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTTATCC TTTACTTTAT CCTTGCCTCT CTCCTCACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTTCTTTAC TCCTCTCAA GAACCTCTTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAAAATCC ATTCATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1939 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTTC CCGCCCCTTA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG	540
CTTCGATTGG AGGAATTCCT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TTCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTTT	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCCTA ACCGATAAGG TGTCGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAATGGTT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTCAGAC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAACTC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAGC	1080
AATTTGGACT TGCTGTTCCCT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCAT TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATGCGA ACAGGAGAAA TACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTTACGGA GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATTGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 907 base pairs
  - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTGGA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAATTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCAGTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTAAAG ATTTCTTTGA TAGTATAGCC TTTTTCAGTT	420
CCTAAGTTAA AGATTGAGA AGAACTGTCT TCTTGAAATA GGTAGTTCAT TCCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCGTAGTCAT CTCCAAATAT TTTAAGCTA TCATTTTGTC CCAATGCGGT CTTGTTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTCAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTTGTC TCTGCATAAG GGTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTTGGTT CATACCAGCA	900
ACGTTGG	907

## (2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTGGGCGATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCA ATAACACAG	180
GAATCATTCA TTTCTCCTTT TGAGTTTAA TTTGTTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA	TCTTGGTCAA	AAAAGGTCAA	ATTTTTGCTC	TGCTTTCATT	AGACAGAAAC	300
AAAAACCCAA	CCTCCTTTTCG	TGACTGGAAA	TACTTTTCCA	AGTCATTCTT	CTTTTCGATC	360
TTATTTTGTA	CCGAACAAGC	GGTCTCCAGC	ATCTCCAAGA	CCTGGAACGA	TATAACCGTG	420
TTCGTTCAAA	CGTTCATCCA	AGGCTGCTGT	AAAGATTTCT	ACATCTGGAT	GAGCTTCTTG	480
AAGGGCTTTT	ACACCTCTCTG	GAGCAGATAC	AAGGCAGACA	AATTTGATAT	TTGATGCGCC	540
ACGTTTTTTA	AGAGAATCAA	CAGCCAAGAT	TGCTGAGCCA	CCTGTTGCCA	ACATTGGGTC	600
TACTACAAAA	ATTTGACGTT	GGTCAATGTC	CTCAGGCAAT	TTCACCAAGT	ATTCAACTGG	660
TTGAAGTGTT	TCTTCATCAC	GGTACATACC	GATGTGGCCA	ACTTTAGCAG	CTGGAACCAA	720
GTTCAAGAGA	CCATCAACCA	TCCCGATACC	TGCACGCAAG	ATTGGGACGA	TGGCCAATTT	780
CTTACCTGCC	AATTGTTTTT	GAAGTGTMTT	TGTAATTGGT	GTTTCGATTT	CCACATCTTC	840
TAGTGAAGA	TCACGAAGTA	CTTCATACCC	CATCAACATT	GCAATCTCAT	CTACTAGCTC	900
ACGAAAAGCT	TTTGTAGAAG	TATCTGTACG	ACGCAAGATT	GACAATTTGT	GTTGAATCAG	960
TGGGTGATTA	ATAACTTCAA	TTTTTCCCAT	TTTGGGAATT	CCTTCTTTCA	ATTTATTCTT	1020
CTTATTATAC	CAAAAAACGG	TTTAAAAATC	TTTCTAAACC	ATTTATTTTT	GATAATTTTT	1080
ACATTAGATC	AGCCTCTTTA	AGAGCTGTCT	GTAAGTGTCT	AAGTGGTAAA	TGGGTCAATT	1140
CTGTCCCTTT	TTCTTGATAA	AGGTATTGGG	CGTAGTCGTC	CATTCCGTAC	TGGTTGATAT	1200
AAACCACGCG	CTTGCAGCCG	ACCTGAAGCA	ATTGTTTTGT	ACAGTTGAGA	CAAGGAAAAT	1260
GGGTACATA	GGCTGTAAAG	CCTTTGGGAA	CACCACGCTC	AGCACCTTGA	AGGATAGCAT	1320
TGACCTCAGC	GTGAAGGGTG	CGAACGCAGT	GGCCTTCAAT	GACCAAACAT	TCGTGATCAA	1380
TACAATGCTC	AGTCCCTGAC	ACCGAACCAT	TGTAACCAGT	GGAAATAACC	TTATTATCTT	1440
TTACCAGAAT	CGCGCCCACT	TTAGCACGTT	TACAAGTGGG	ACGATTCGCA	ATTAGTAGAG	1500
CTTGGGCTGC	AAAATACTCA	TCCCAGGCCA	GTCTTTTTTC	AGTCATCTCT	TTTCTCCTTT	1560
TTCTCTATTT	TTTAAAAAAT	GGTAAACCTA	AATCTGCAAT	CTTTTCAGCT	GGTACCTTCA	1620
TGCCATCCTT	GATCCATTTT	AGAAGGACAG	AGACGATGGC	TGAGCTCCAG	AAGGAATGAA	1680
GATAAGAGCT	GACACCTTTT	GATTTCCCAT	GGTATTTTTT	TAGAAATTCC	TGCATGGCTT	1740
GGACAAAGAT	TTTTTCCAGA	TGGTAATCCA	AGGCCAATTG	AATTACTCTA	GCTTCCTTTC	1800
TGGCCTCCCG	GAAAAGGTGA	ACCCAAACCA	AATAAAGGTC	TGTCTTTAAA	TCGTAATGAT	1860
GCAGCTGTTC	CATAATATTG	TGGACAGTTC	GTTTAAAGAC	GCTCTCTAAA	ATTTCTCTTT	1920
TGGAGTCATA	ATTGCGATAA	AAGGCCGCAC	GCGAAACACC	TGCACGTTTG	ACCAATTCAG	1980
AAATACTAAT	CTTGGTCAGT	TCCTTTTTTT	CCAAGAGTTG	CAAGAGGGCT	GTTTCAATGG	2040



1341

CTTCTCTGGT TAATAAATTG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100  
CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160  
CTTTTGTTTC 2170

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60  
AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGA ACAAGCTCGT CGTCTTGCCC 120  
TTTCACTTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG 180  
GACCAAACAA CCGTTCTAAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAAC 240  
TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCGTAA CTTGTTGTA CAAGCTACAA 300  
AAATCAAAGG CGGAATCCTA GGTTCAACT TTATGCTTCT TTTGGAACGT CGTTTGGATA 360  
ACGTTGTTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420  
ACGGTCACAT CCTTGTGAC GGGAAACGCG TTGATATCCC ATCATCCGC GTAACCTCCAG 480  
GTCAAGTGAT CTCAGTTCGT GAAATATCAT TGAAAGTTCC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTC TCCTTCTCTA CCGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60  
CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTT GCCGTCGTAT 120  
AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATCTCTT TTCAAGTTTC TTAGGTCTAA 180  
CAGGACCTGG ACCTGGTCTT GATCCACTTT CTTCCGCTGG AGAAGAAGGT ACATCTTGAC 240  
TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTACTTTT TTCTAAATCT CTCAGAACTCT	480
GCTCTTTAAA GCGTAATTTT TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTCCCTG CAAAGGTTGA	660
CTGGGAA	667

## (2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GTACTATTCG TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT	540
AAATATTAAG AATCACCCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTUC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCCAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CAAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTCAGATT GAACCATTA CTAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT	1080
TAAAAATCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGTAACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAAACA CTAAAGACCT	1260
ATTAGATTTA AATAAACAGG TGGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTWT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATAAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG	60
ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAATCATT TTGAAAAGAC	120
GTAAAAATCA TCTAAATCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC	180
TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTTT TCTTCAATTT GAGTTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC	420
ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATTCCTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATATT TCTCTTTCAT TTATTAAACG ATTCACAGAA TCTCTATTG TAAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC	660
TTTATAAACT CCACCTTTGG CATTTT TAGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTTA TATCTTGGA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT	780
TTTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT	900

1344

ATACAATATT TCTAATTTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT TGAAATTTAT CTTCTTCTCT CTAGAAAATA TAAAATCAAA	1080
GAATTTTTTA GCAACCAAAT TAGCATTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAAT ATATAACCA TGTTCATCAC TAAAATTATC	1200
ACTAATTTTA TATTCTAATA ATAAATTATG GTATGCGTCT TCTATTTTCTAG TTTTCATAGTC	1260
CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTTCTCCATA AATTTTTTAGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAAC	1380
TTCAGTCCTC TATTTGTAA TTCCTTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA	1560
ATTCTTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCCTTAAAA AGCTCACAAT	1620
AAAATTTTAA ATTTCTATAC AACAATCCGA GAGTAGTCTC ACAATTTGAA CATTTCACAT	1680
CACTCTTAAT ATATAAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TCGCGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCCC CAGAAGGCGA TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTC CGACAATTC AAATTTTCTA	1980
ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTCC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTTG ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAAACT TACTTGACATA TTGGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTCAA AATCAAATTG CTAAAAATAA TTTTAAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAATTGTT TTGAAATTAG TAAATTAAAA TAGGTTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAATTCTG CCCATCATAA AATATCTATT TAAGTAAAC AAAAATTTTA	2340
TAATTTTTTG ATTTTAAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1049 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1345

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCAGTA CTCAAAACT TACTTATCA CCAGTTTTAG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTCTT TTGGCATTIT GAAATCGGAG	360
ATGTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTGGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAAT TACTATATTC ACAATGTTAT CCAGTGTTTT TTCTCTAATA TTTAAGGAGT	660
GTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTAAATPAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGGCCCG TCCGATTTTC	900
TAATTGCCCC ATAAACATTT CCTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATTGC AGAGTCCTTA CTTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTTCCGG	1049

## (2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 776 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAAA TTATGCTGAT AAATACAAAA	120
TGAATCCTAA AGTAATTTAC CCTCATTCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACACAAAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACG ACTACCTGCT ATTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACCTAT GAATTGGGT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTATAAATAAAGG TGTTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTCTCTGT TGGATAATGA TTACTACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGT TATTAAAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGGAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTG AAAGTCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACTT GTCCTCTCCG TTATTTTATA AACAAATTGAA AGCAAT	776

## (2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTTCG CCAGGCTCAA GCGCGCATG	180
CCCGACGGCG AGGATCTCGT CGTGACCCAT GCGGATGCCT GCTTGCCGAA TATCATGGTG	240
GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTCGC AGCGCATCGC CTTCTATCGC	420
CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTGCAACAG CCGCCTAATG	480
AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC	658

## (2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
  - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTTATAT GAGTACCGAT GTTATTCCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAATGTG AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGTATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATTG TTCACCTGAT CTACTTCTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTGTAGT	840
CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA	900
ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTTT ATATCTTCTT TTAATATATT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTTT CATTACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACTT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC	1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA	1260
TATTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTTAC	1320
TATATCTCAA ATTGAGTATG ACGAAGTGCG CTCCCATGTC CTGGGAACGC ACTTTCTTCA	1380
TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACAGGATG AGATTTACAG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTT ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTTT GGTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGGAAAC AGCTCTTCTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAA-ACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCCGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TCGGTGTCGG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAGGTCCA GCCTTTTTC A GGTCTGGCCT TGCTGGGTA GGCAGCCGAG AAGAACTCTT	540



1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG 600  
GCATTTAGAC GGTCAAACGG AACGAGCAG TAGGGTACTG TGC 643

## (2) INFORMATION FOR SEQ ID NO: 323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TCGAGTTGA 60  
AGTCAAGAAG AGGAAAAAAA CAAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120  
AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAAACTCG TCGCTGGAAT CCTAAGATGG 180  
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAACTGTAA 240  
AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300  
TGTTCTGTTG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTTCA 360  
GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAAGTCT TACAAACTGG GGAACAATCC 420  
AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTTGAAG 480  
TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TGCGCGTCTT GAAAAATTCT 540  
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTATG ACCCACATAA 600  
AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGTTTGA 660  
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720  
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

## (2) INFORMATION FOR SEQ ID NO: 324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAC 60  
AGGTGTCGAA TTGGAACTAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTC	300
GATTCAAGAG ACGATGGCGA AAGATTTGCT ACAAAATTCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAAATC AGGACAAGTG GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGGATTG TGGAAAAATA TCCTGATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1237 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAGTACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCCTGCCA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCCTCG	300
ATTCCGGTAG GTCAATTTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTAATCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTTCGG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTG ATATTGATAA TACACCATTT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTTATAATC CTAATACTGA	780
GTAACATTG AATTTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTCGGC CTTTCCTTTT TGATGTTTCAG AGCGATAAAA ATCCGGTTTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGTAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA	60
AGTGCATTTT CTTTGTAGTCA AAAATTGAAA AAGCTAACCT TTTCTCAAG TTCAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAACT AACATTACCA	180
AAATCGGTTA AACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTTGTT TTCAAAGAT	300
AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAATT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTACT TTTGCATTTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTTCAAAA GTTTTATTTT GATTATTTTG	180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTA AACAATTTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTGTGAA AATAATTTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTCCC TTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTTCTGTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTCTGAA AGTTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA AATCGATTTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT TAATTTATAT GAGTTTAAAC CGATTTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTGAAG GTTTTGTGATT CTTTACAATT	720
AACCGACAAA CTTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTA TATAAATCTG TAGCTCCACC AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTTCTA CGGAACCTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCTTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCCATAAT CTTATTCGAA CCAGTCTTTG GTAATTTTGT TTTKACATCT ACTATYTCTT	1020
TAGATTTATT AATATGATTT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTGCG TCTGTGTCATT CATTTGTCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCTCTTT GTTTTTTCT TTTTCGTTT TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCAT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTGTC ATTAGATTTG ATGAATGATA TATACTTACC GGATAAATTA TAAAATTGGT	1380
TATTTAAAAC GGTTATTTTA CCCTTTGAAT CCTCAATAAC AATTCCTTCT TTACCC	1436

## (2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTCCTGAT	60
ACGTATTTTC CGTCTTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTCGATTTGC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC CATGATGCGA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTGA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG	240
TGTTGACAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCGTTCTTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTTCTAGTG	360
CCATTTCAAC CATTCCTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG	420
ATGCTTGTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACAGG ACTTTGGATT TCTTCACGAA	540
TACGGGTAGC AACAATTTCC CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTGCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTGTAG	60
GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTTGCCT	120
AAAATTGCCG AGATTCTGTC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTTGTAA GGTGGTATT	240
GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTGCCGCG GAATATGGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTTATG	420
CTTGGATCTA TGTTTGCTGG AACTGATGAA GCTCCAGGCG AAAGTGAAT CTTCCAAGGA	480
CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC	540
GACCGTTATT TCCAAGGTTT TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT	780
AATGAGGCAC CAAATTATTC TATGTAAAA ACAATGAAAA GAACTCCAGT GAAAACAGGA	840
GTTCTTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTTAACTGTC TAGTGTGTC AAGTTCACCTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAGATTC GGATAAGTTT	1260
TGTTTGTGAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGCTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAATCTT CAGGAGCAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTTGTG AGTTTAAAT TACTCCCAT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAA ATACTAGATT CTATTTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTTCTA TTTTATGTC CAGTCCAGT ACCGGAGAAA	180
TATTGTTTTA ATATAATATC TCTTTTTGTC TTCTAAGCTC TTAAAAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTTTATCC ATTTTCAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCATATAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAATTT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGGAAGT	540
TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTTATAGG TAGTTCAGTG TTTAAAAGAA GAGTTTCAGC TACATTCATT	660

1355

CTTTTCTTT GAGTGACTC TGTAATGCTT TGACAATATT TTTCCTTAAA TAAATTTTTT	720
AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTTAC ATTCGTTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTCTA AGGCCTTTGT AAGTATTATT TGATTGCGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCTGGAT TAATGTAAAT AGATGCTAAA TGTTTTCTA TTAGCTCTTT TTTAAAACCM	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACCTGAA TAAATTGAAA CATAGTCTGA CATACTATAA	1260
GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACCTT	60
GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTGTGATCC GGCCTTATTT	120
GAAATTGAGA AAAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTTAT	180
TTGACACATA AAGAATTGGA TAAATTGTTT TTTTCATGATG AACGTCTTCA ATTGGAATAT	240
AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTATG CCAATGATCG AATAGATTTT TTTTCCTAG GTGATTTTAA TGAGGTTGAA	360
ATCAAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTTCA	420
TATTGTCAAC CTTATTCTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC GAATTTTGTT TTGTCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAAATAGT TGTCAATTGC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACCTAGGA ATGTAGTCTC	240
TTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTGTCTTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTCTG CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAACCTACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAwGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCTG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC AACTGGTCT TGGAAACGG CAAAACCTCT GAAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGGACAGA TTGGCAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180



1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATG AGGAATTCCC TGGTGAGTTC	240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGCAGaA GcATTAAACAG AAAGGAAGCC TATGACCTTT AAACCTTCTCA GCCAAGAAGA	360
ATTCATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG	480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC	533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC	120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCanna ACCACACCTA CGGCAAAGTG AATCTGAAGT	240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAAATCGTC TATGTCCGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGA TTATGCCTGG TTTGGTCAAT TGTACACCCC	480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAAGT AGGGGTTTCCT TTTTGTATA TTTTCAAAT AACGCCTCTA	60
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1358

CACTATTTGT AGCAAATCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAT TGGTTTAAAT	240
AGCGTAGTCT TTTAACTAG TTTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGATTAGCT AATGGATACC TATCCTACC	349

## (2) INFORMATION FOR SEQ ID NO: 336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAATTTG AATCAATTTT GTGATTTGTT TCTGACGCTA	120
AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCCA CTTCTTTGGG AGTCATTTTC	240
TTGGTTCCCT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTCCCCGGG	300
ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTT	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACCGGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTTT CACCGTCAAC	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTCTTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTTA TTTGTCTAAA TACATTCAAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC	960
CCTTATACCC TTTTTCGGG CATGTTGCCT TCCTGTTTTT GCTCACCCAG AAAACGCTGG	1020
TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAACCTGA	1080
ATCTCCACA GCAGTTAAGA TCCTCTGACA GTTGACACG CCGCAAGAAC TATPCCCGAT	1140

1359

GAATGAGCAA CTTTTAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG 1200  
GCCCCG 1206

## (2) INFORMATION FOR SEQ ID NO: 337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60  
GAAAAAGGCC ATCAGGTAT TATTACGACA GGTGCGCCTT ACCGTATGTC AAAAGATTTT 120  
TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAACCTCA ACGGATCCCT TACTCATTTA 180  
CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAATA TCTGCTAGAT 240  
ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300  
TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360  
TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420  
TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAG 480  
CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540  
GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600  
GATTTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660  
GGTTATGCCA TGAAAAATGC CAATCCAGAG CTAATCCCTT ATGCAGATGA GCAAATTTCC 720  
CTTACCAACG ACCAAGATGG GGTTGCCAAA ACCCTACAAG ACTTATTCTT ATAACCTATA 780  
CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

## (2) INFORMATION FOR SEQ ID NO: 338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGCAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACTTACCTT ATGCCCAAGC GCCAGGTATG GGACTCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTTCAATGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CAGCTATTTTC AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

## (2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCTGTGC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTTC CACCAGTATC GATTATTTAA	240
TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTGCGAG ATTAGTCGGG	660
TGTTATCCTC TATTCCGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTGC	720
CCTTAGTATT CATTCTACTT GGAATAACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCGATCGT GTAGATTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840  
CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60  
GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120  
CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180  
AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240  
AGAGAACAGA GTTAGTAAAC CTAAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300  
ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360  
AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTTGT AAAGCCTGAT AGATAATGCC 420  
ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAAATCATC TGACCAAATA AGATCAAAAA 480  
CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAAGTACTA GGAGACTTAG CATCTGATGG 540  
GAAATAAGTC CACGACTCTT TTCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600  
TTCATAGATT TTGAAAACT CCATAACGCC GATAAACAG AAAAAGCTCA TAAACCTGTT 660  
GAAGGTGCG TCAAGACTTC TCTGGCTATT TTTTCCACAC CTTCATAGAG GCTTGGGGGG 720  
CAGACGTCTT TCATAAAGCC CAAAATTCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT 60  
TTTTATGCAG GTTGGGCGCT TCATCAGACA GGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGGGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTAT	540
CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAAGTGC CTACTATAGT	600
GCTGCAACAG GAAGTTTGG GGATGCGWTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTAATTCTAA AATTTTAGAG AATATGTTTT TTTAAGG	707

## (2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 762 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCATTT CGAACCAAAT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAGTAG	360
AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA	480
AAGCCTTAAA CCTGTACAG CTAAGTCACG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCTT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA	762

## (2) INFORMATION FOR SEQ ID NO: 343:

1363

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTGTCTTC	60
TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTGTACTT GGCGAAATTT GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAACCTACA	360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCAGGACT	480
TC	482

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTAA TAAAGTCAAT ACCTGTCTTT ACTTTTTCTT AAAAAAGTT TATTATGTTT	60
TTTAAGGAGG TGTAAACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAAT	120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAA CCTACTAAAA	240
ATTGCATCTA TTGGAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACACG ATGATATAAC AAATAAGCG TTACAGATCG CTCAAATAC CATTTCTAAG	420
ATTGATTATC AAATTTTACA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA	480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT	520

1364

## (2) INFORMATION FOR SEQ ID NO: 345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

GCATCAAATC CGCCATCAAA GAAGTTCTCT GGATTTACCA AGACCAGTCA AATAGCTTAG	60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG	120
GAACCATTGG TGAGCGCTAT GGTGCCGTTG TTAAGAAACA CGACATTATC AATAAGCTTC	180
TCAAACAGTT GGAAACCAAT CCTTGGAACC GCCGCAATAT TATTCGCTC TGGGATTACC	240
AAGCTTTTCA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTT	300
GGCGTGTGTA TGGGGAAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC	360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC	420
ATTTTGGCTG GAAGGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA	480
ATCAATTTGA ACAAGCTCAG GAATTGCTCC GTCGGGAGCC GTCAAACTGC CAACCACGCT	540
TGGTTTTAAA TGTTCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT	600
TGGTGGATTA TGACCTGTT AAGCCACAGT TGAAGTTTGA CCTAGCTATT TAAAAGAATA	660
GAAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTGTTT TTAACGTGAT ACGCGGCGAC	720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTGATTA	780
CTTTCTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG	840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG	900
CCAGCCTCCT CAAGAGGTCA CATTTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA	960
CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA	1003

## (2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC	60
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1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGAACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTGTTT ACGATTTATT TCTCTCTTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCTGGAGCA TATTTTCTT CCCAATTATC	300
TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC	420
AAACTGCCG TAGGTGAAGT AAAGCGTGT C AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGTCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATTCTTCT ATTTTAAAAC CAGCCCTATG GGTGACCCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTTAT CCATCATGTG GTGGAAAGTC TTGACCTTAT TGAAATGATA	720
GTCACGGCTG ACAAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAGTGGG TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCAKTTTGT CTTGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAgT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 673 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA	300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTTCAG CCATACCACC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTC	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAAC TAAGTAGGT	60
TGGACAGGAA CTTTGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 891 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG	180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG	360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGGCGTC	420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC	480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAGA CAGGGCTAAT AAAGTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT	600
ACACAGAGAT AGAAAAAATA CTGAACTGAA AAAATCCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA	720
GACCAAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG	840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A	891

## (2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTTTTA TTTTAGAGT AAGCTAAGCG CTTCAGCATC	60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT	180
AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG	300

ATGCGTTTGA CTGTCAAATG GAGTG

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(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 344 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TCGGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG	180
AGTCAGTAGA TCCGTTTACT GCGGAAATAA ATAAGAGGAA GTAACGTTAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 692 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT	300
GTAAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTGG CGGGATTCTC	360
AGCTTGCAAT TCCTAGCTGG AATGGCAATTT GAAAAAGCTC TTGCTGTGGG GGTCTTCCC	420
TTTATCATTC CAGACCTTGG CAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTTAT TTTGAAAACT TATACTCAAT GAAATCAAA GAGCAAATA	600
GGAAGCTAGC CGCAGGCTTG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

## (2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1005 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTCC ACTTGATGAA GGAAATTGGA	120
GTTAATTCTT TCCGCAC TTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTAC CAGTGGAAC TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTTGC CAAGACTGCT	360
TTACATGCT TTGGAGATAA GGTTCATTAC TGGACAAC TTCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC	540
TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTTAA AGGAACTTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTTCTTG GAGTAACTA CTACCATCCA AAACGTGTTT AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

## (2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 973 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAAAA GAGTAAACTA TTAAGTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTGTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTCG	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAACCT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCG TCAAATCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCCTTGAT GGTMTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTTCCAC ATTGTGGCTA CCTGGAACAC CGATTTTCATT CGCTGCCATG	420
ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA	480
AGTGTTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCCTGGAT ATTCCACTTG	600
GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAAGA AGAAAGTTCC	720
ATAACAAGCG TGTCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTCCCCGGn TCCTCTAGAG	840
TCG	843

## (2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 807 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTTCT GCATTAAATT GTCTATTTTT GCTCGTGCTG TTACGCTCTT TGTATCATGT	120
ATTAAGTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA	240
GTAAGTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAAATCCT TAAACGCGAA	300
GGTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGAATT	480
GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATTAG GAAGTTGGAG AAGTTTGTTC ACAAACAGGC CAACTTATCT ATTTTGCACA	660
GTTCTTAGAG CGTGTTCAGT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	720
CTGGCCGTGC TGGCATGTTT GGGTAACAGG AGAATAATAA CATGTCACGT ATTGGTAATA	780
AGTTCAGCTA AGGCCTTCGT AAAAGTT	807

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## (2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC	60
TTAACCATCT tTGAACAAA TCCTCAGGCT CAGGTCAC TA TTTTCGGTGC CTTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCCTT CTGCCTAGCA ATCCTAAGTT GGCACCCTAT	180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAA GTGTACGCTT CTAACGAATA	360
TATAGATAGG GAAGTGTCGG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGGTC	480
TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG	540
ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA	600
GCCAGTTAGA CAAAAAGAT TTGGAAGTGG TTGTCAGCGA CCGTTTGCAA GAA	653

## (2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 641 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT	60
GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCAGTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCCTAGAG CAAGTGCTAG AACCTTGAC TATTATCACT GGTGGACACA	300
ACCACAAGGA CCAGTTGACC TATGCTTGGA AAACACTTTT GCAGAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG	420



1373

TCAACCAAGT AGGAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAAG GGTAAAATTG 480  
CTACGGATAA GGCTCAAAGT GACTATCTCT TTA CTGTCAT TAACACAGGC TTGCATGATA 540  
AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTC AAG GAATTGCACC 600  
CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G 641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1958 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA 60  
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTT TAGA TGGCTTTAAT 120  
AGCGAAATTA TTGCTTTTAA TCTTTGACT TCACCCAACT TAGAACAAGT ACAAACAATG 180  
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC 240  
TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT 300  
ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA 360  
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA 420  
GCCATTATAG ACTATATTGA TTA CTACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA 480  
CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG 540  
GGTCAGTACA AAACCTCTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT 600  
CTCAAATCGA GTTTTTACTC AATTTTCTTA CTGATTGGG ATTGAAATTC CAATTAATTT 660  
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT 720  
CAAGAAAAAT TCTTGAATGG TTTGATTTT AGGCTCACGA ATAGCACGGT GTTTGTTTGA 780  
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA 840  
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG 900  
TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTTCTCCG ATTTTCTAAT TCTATTATAG 960  
CACTTTTTGA ATAAAGTCGC TTGATTTATA CTCAATGAAA ATCAAAGAGC AACTAGGAA 1020  
GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT 1080  
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG 1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCC GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTC TCCACATGGT AGGAACCAAG CACCATTGGG TTCTTGAACA	1440
AGAACAATTT GTTTTGTTC AGGATTAGGG ATAACGTCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCACGT AATACCATTT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
TACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGAAGTGTG TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

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TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATc TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAACGTAAA AAGATTTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAATAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTTT GGAAAGTAGG	180
CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTTCCATA ACCTGTTAAC AGTTGAAAGA	240
GGAACGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAGA	360
TAAGACCACC ATACTGGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAGTG ATGATTTGGT AAACGTTC A TGAGTTTC CTTTCTTTT GTGTTTTTTT	480
CTACACTTAT ACCATAAAGG GGAAACTCTT TTTTGTCTAG TAAAAACAC CCATTGGGTG	540
AAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG	600
GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAATTAC	660
TCATCAACCT TTAGTGGA A TCCAATACA TTTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGTATAT GAGCCCATGT TTTCTCAATA GGATTGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTTAATG	960
TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GCTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

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ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140  
GATAAAAATA AGTATCGAAT CCTGTTTC 1168

## (2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CCGCTTCAGC 60  
GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC 120  
GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC 180  
TTCAGCAAGC ACAAGTGCCT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC 240  
GAGTGCCTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA 300  
ATCTGCATCA ACCAGTGCCT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC 360  
CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC 420  
ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC 480  
ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGCCT CAGCTTCAGC 540  
AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC 600  
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC 660  
AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCTTCA GCCTCAGCAA GTACTAGTGC 720  
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC 780  
AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCTTCG GCTTCAGCAA GCACCAGTGC 840  
GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGCCT CAGCCTCAGC 900  
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCC GCTTCAGCAA GTACTAGCGC 960  
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGCCT CTGAATCGGC 1020  
ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC 1080  
ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC 1140  
GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGCCTCT GAGTCAGCAT CAACGAGTGC 1200  
GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CAGCCTCAGC 1260  
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCCTCA GCTCAGCGTC GACAAGTGCs 1320

1377

TCrGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCGGCTTC AGCAAGTACT	1500
AGTGCAATCAG CTTAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAGTGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCGTCAG CTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCACTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCAAT CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAGCTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCAAT CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT	2580
GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCTCT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGCAAT CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCAACCAGT	2940
GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT	3540
ACCAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGCGT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCGTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA	3960
GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA	4020
ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGAT CCGGTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCGTCA	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TCGGTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA	4380
CCAGTGCGTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCG	4440
TTCGGCATCA ACAAGTGCTT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2550 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCTTCCGC	CTCAACCAGT	GCGTCCGCTT	CAGCAAGCAC	AAGTGCGTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACTT	CCGCCTCAAC	CAGTGCGTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCAsCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCGTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCACA	TCAGCTTCTG	AATCGGCATC	AACCAGTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGATC	AGCTTCAGCA	TCAACGAGTG	CATCGGCTTC	AGCATCAACC	480
AGTGCTTCGG	CTTCAGCGTC	AACCAGTGCG	TCAGCTTCAG	CAAGTACCAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGCG	TCGGCCTCAA	CCAGTGATC	TGAATCGGCA	660
TCAACCAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGATCAG	CTTCAGCATC	AACGAGTGCA	720
TCGGCTTCGG	CGTCAACCAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCGTC	AGCTTCCGCA	780
TCAACAAGTG	CCTCGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAGTGCT	840
TCGGCTTCAG	CAAGTACCAG	TGCTTCAGCT	TCAGCATCAA	CCAGCGCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGCGCCTCGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCTTC	GGCTTCAGCA	1020
AGCACAAGCG	CCTCGGGTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCGTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCGTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	TACCAGTGCG	1440
TCAGCCTCAG	CAAGTACCAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCGTC	GGCCTCAACC	1500
AGTGATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGATCG	GCTTCGGCGT	CAACCAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACt	TCCGCATCAA	CAAGTGCCCTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCTTCGG	CTTCAGCAAG	TACCAGTGCT	TCAGCTTCAG	CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAGTGCG TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGCG TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAGTGCA TCTGAATCGG CATCAACCAG TCGTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTTCAGCAAG	2280
TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTTCAGCAAG	2400
TACCAGTGCG TCAGCCTCAG CGTCGACAAG TCGTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GCGTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAGTGCG TCAGTTCACG CATCAACAAG	2550

## (2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TCGTTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAGTGC GTCAsCTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTTCAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCGTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAGTGCG TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600



1381

TCAGCAAGTA CCAGTGCCTC AgCCTCAGCA AGTACCAGTG CTTCAGCCTC AGCGTCGACA	660
AGTGCGTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGCGTCCG CTTCAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCGTCGG CTTCAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TCGCTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTCAGCTTC AGCAAGTACC AGTGCGTCGG CTTCAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAGTG CTTGGGCTTC AGCGTCAACG AGTGCGTCTG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCTTCGCA	1200
TCAACAAGCG CCTCGGCCTC AGCAAGTACA AGTGCTTCAG CCTCAGCATC AACCAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAGTG CGTCAGCTTC AGCAAGCACA AGTGCGTCAG CTTCAGCATC AACCAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 735 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTGCTG ACCAGCACCC GTTCCTGCCA TAATTTCTT TTTACCCATG	60
CGTWTGGCAA GCCAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTGCGT	180
AATAAAGAGG AGTTTCACGT CCTACGTACT GGCGCAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGGTC TGCCTGACTT TCACGGTAGG CTTCTCCAA CTCCAAACT GCTGTCATCA	300
ATGTTCTGG GACAAAACGT CCGCCGAATT TTCCGTAAAA TCCATCTTA TTTGGTTCCT	360
GATATGCCAT GCTTTACCCT CTCTATAAAT CTTCTAATCT TTTCATGATC TTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCAATTAAG GCCACCTGCG ATAAAGAAGG GCTGTGCTAG TCCAGTCGTA	540

1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCA	TTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AATTCTCAAA	TAAATCATCT	GCCACCTGAC	CGTGAACCTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGGGTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCATCGG	CTTCAGCGTC	120
AACGAGTGCG	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCAAGTGG	TCAGCCTCAG	CGTCGACAAG	TGCGTCCGCT	TCAGCAAGTA	CCAGTGGGTC	300
AGCCTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGGGTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGGGTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCATCGG	CTTCAGCATC	AACCAAGTGA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAGCT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGGGTCGG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCCG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGGGTCGT	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGGGTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGGGTCAG	CCTCAGCAAG	TACCAAGTGT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCCGCC	TCAACCAGTG	CATCTGAATC	GGCATCAACC	AGTGGGTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGGCTCGG CTTAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGGCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACGAGTG CG	1702

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACCTCAG CAAGCACAAG TGGCTCACTT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAAGG	360
AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGGCTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGGCTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGGCTCGG CTTAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT 900  
TCAGCAAGCA CCAGTGCGTC GGCTTCAGCA AGTACTAGTG C 941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 869 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA 60  
GTGCATCAGA GTCAGCAAGT ACCAGTGCGT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT 120  
CAGCAAGCAC CAGTGCGTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA 180  
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT 240  
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA 300  
GTGCGTCTGA ATCGGCATCA ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT 360  
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA 420  
GGCCTTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT 480  
CAGCATCAAC GAGTGCGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA 540  
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT 600  
CAGCGTCGAC AAGTGCGTCG GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA 660  
GTGCGTCAGC CTCAGCGTCG ACAAGTGCGT CGGCCTCAAC CAGTGCATCT GAATCGGCAT 720  
CAACCAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT 780  
CGGCTTCAGC ATCAACCAAGT GCATCAGAGT CAGCAAGTAC CAGTGCGTCA GATTCCGCAT 840  
GCAACAAGTG CCTCGGCTTC AGCAAGTAC 869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 750 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA 60

1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TCGTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TCGTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TCGTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCCTGGTA GCGGGATTGA	240
TTGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGAATATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACCAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGA CTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGCAGTCA	900
TAAGCGTCCG ATTGGTTCCT TTATGTTCTT AGGGCCTACA GGTGTCGGGG TATCCGA	957

## (2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

## (2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

1387

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGGCTCCG CTTAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGGTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGGCTCAC CTCAGCGTCG ACAAGTGGCT	240
CGGCTTCAGC AAGTACCAGT GCGTCASCTC AGCAAGTACC AGTGGCTCAC CTCAGCGTCG	300
ACAAGTGGCT CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACC AGTGGCTCAG CTTCGGCATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCGGCG TCAACCAGCG	540
CCTCGGCTTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGGCTC GGCCTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGGCTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGGTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCTTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAGTGGC TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGGCTC AGCCTCAGCA AGTACCAGTG	1020
CTTCAGCTTC AGCGTCGACA AGTGGCTCGG GCTCAACCAG TGCATCTG	1068

## (2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGGCT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGGCTCT GAATCGGCAT CAACAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCCT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

## (2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAACTAGCAA CCACTATCAA GTCAGCGGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGGC GTGTGATTTC	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTGCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATCGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

## (2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



1389

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTCC CATCGTACCG CCGAAAATCC CAGCGCCTCA GCCATCAAAT ATCCTATCAA	60
CGTTCTCAAA AAAAGTGACC GCTCTCTCAT CATGTTTCCA AGTGGTAGCC GCCACTCAAA	120
CGATGTCAAG GGGGGCGCAC ACTskATTGC CAAAATGGCC AAGGTCCGTA TCATGCCCGT	180
TACCTACACC GGTCCCATGA CTTTGAAGGG CTTGATTAGC CGTGAACGTG TCGATATGAA	240
CTTTGGAAAT CCAATCGATA TCTCAGATAT CAAGAAAATG AATGATGAAG GCATTGAAAC	300
AGTCGCCAAT CGTATTCAAA CAGAATTCCA ACGTCTGGAC GAAGAAACGA AACAAATGGCA	360
CAATGATAAA AAACCAAATC CACTCTGGTG GTTTATCCGC ATCCCTGCCC TCATCCTTGC	420
TATTATCCTC GCTATCCTAA CCATCATCTT TAGCTTTATC GCAAGCTTCA TCTGGAACCC	480
AGATAAGAAA AGAGAAGAAC TTGCATAGAA GAAATGAACC TTGGCCAAAC AGCTAAGGTT	540
TTCATTTATA TAGTAGATTG GwACTAGAAT AGTACACCTC TACTTCTAAA ACATTTTtag	600
AAATCGATTT GACTGTCCTG ATCGATTGTG CCTAATCTTA TTTCAATT	648

## (2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 690 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT TTCAGCATCG ACAAGTCCGT CTGAATCGGC ATCAACGAGT GCTTCGGCTT	60
CAGCATCAAC GAGTGCGTCA GCTTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	120
GTGCGTCCGC TTCAGCGTCA ACCAGTCCGT CGGCTTCAGC GTCGACAAGT GCTTCGGCTT	180
CAGCATCAAC GAGTGCGTCG GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCGCCT	240
CAACCAGTGC GTCCGCTTCA GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT	300
CTGAATCGGC ATCAACGAGT GCGTCGGCCT CAGCAAGCGC AAGTACCTCA GCGTCAGCTT	360
CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC GTCAGCCTCA GCAAGTATCT	420
CAGCGTCTGA ATCGGCATCA ACGAGTCCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT	480
CAGCAAGCAC ATCAGCTTCT GAATCGGCAT CAACCAGTGC GTCAGCCTCA GCATCGACAA	540
GCGCCTCAGC TTCAGCAAGT ACCAGTGCTT CAGCCTCAGC GTCGACAAGT GCGTCGGCCT	600
CAACCAGTGC ATCTGAATCG GCATCAACCA GTGCGTCAGC CTCAGCAAGT ACTAGTGCAT	660

CAGCTTCAGC ATCAACGAGT GCATCGGCTT 1390 690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1003 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTT CAATATGTGC ACGTTGGAAT GTTAGTGCTT 60  
ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120  
CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180  
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTTATA TACTAGTGGT GTTTTGGGG 240  
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAAA 300  
GAGCTTGTAG AGAAGAATTA GTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360  
CACAGGATAA CCTGATGCAT TTTTGTAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT 420  
TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC 480  
TTAGCTTAGA TCCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTTA CTAGACAAAA 540  
AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAAGAAAG GAAACTCACA 600  
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG 660  
GAGGTCATTT AACCAGTAT GGTGGTCTTA TCTTTTTTCA GGAACTTTTT TCCCAGTTGA 720  
AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT 780  
ATTCCGATTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG 840  
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG GAAGGAGGGC 900  
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC 960  
ATAGTTTGCG ATGCCTCAAC CTTGAATTGG TCGAATTCTT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 738 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT	120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT	240
TATTCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCT CAGATATTCA	300
CCTTTTGTGG ATTGGTCTGA AGTTTTCTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCAcKGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc	420
GACTCAAAAC ACCGTTTTGA GGTTGTAGAT ATAACGACG AGcGACTCAA AACACCGTTT	480
TGAGGTTGTG GATAGAACTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA	540
CTGACGAAGT CGcTCAAAAC ACCGTTTTGA GGTTGTGGAT AGAACTGACG AAtgctCAAA	600
ACACCGTTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGCGACG	660
CTGACGTGGT TTGAAGAGTA TTAAGTCTTA TATTTTGGT AAAAATCAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 695 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT	120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG	300
GACGAACTTC TGGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAACGC GCTTTCTTGG	360
CTTGAGCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT	420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT	480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC	600

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTTC CAAAACTTCT GCTACTAGAC 660  
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG 695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 691 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT 60  
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT 120  
CAGAAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC 180  
CAGAAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCAA TGGGTGTTTT 240  
TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAAGA 300  
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA 360  
CTATCTTTCG ATGGAGGTCA TTTAACCAG TATGGTGGTC TTATCTTTT TCAGGAACCTT 420  
TTTCCCACT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC 480  
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTCA ACTGTTAACA 540  
GGTTATGGAA CGGACTATGC TTGTAAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG 600  
TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GWTTCCTTC CAGAACTGAC 660  
GAGGAAACAG TCCATAGTTT GCGATGCCTC A 691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 750 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC 60  
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT 120  
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT 180  
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG 240

1393

TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGTAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTGTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCA GGTGCGAGAG CTTTGACATC CTTTCTGTGTA	600
CTGGACCAAG TCAGTTTTC GTTCTCAAAG CGTTTATATA ATATCCAAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 738 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCCT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTTG	240
ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTTGGC CATCTACATA TCCCCTTGT	420
ACCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCAA AGATGAACCA	480
AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGCAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CTTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACTTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 657 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT	60
TAGGAAGTAT ATATGAGTTC TCTAGTCTGG AGATTTTTC AATAGACTTCG TTATTGGGCG	120
GTTACTTTTCG AAACCTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTCCTTT	180
GGGGTCAAAC TCAGTAACTT ATTGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC	240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTCT	300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT	360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT	420
TCGCAGAAAC CATCATAATT GGAGTTTGA CGCCTTTGGC TCTCAGCCGC TTACAACTT	480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTCTGTCTT	540
CTGCCAAAGC TAAGGCCTTC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC	600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 586 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG	60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC	120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC	180
ACCAGTGCGT CGGCTTCAGC ATCAACGAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT	240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA	300
CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGGGTCAC	360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC	420
CAGTGGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA	480

1395

TCAGCATCAA CGAGTGGCTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC 540  
AGTGGCTCAG CTTCAGCATC AACGAGTGCG TCAGCTGCAG CAAGTA 586

## (2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 451 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT TCAGCTTCAG 60  
CAAGTACCAG TGGCTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG 120  
CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180  
CGTCAACGAG TGGCTCTGAG TCAGCATCAA CGAGTGGCTC ACCTCAGCAA GCACATCAGC 240  
TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC 300  
AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360  
TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGCGT CAGTTCAGCA 420  
AGCACAAGTG CGTCAATTTA GCATCAACCA G 451

## (2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60  
CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120  
GGCTTCAGCA AGCACAAGTG CTTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180  
ACGAGTGCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240  
GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC 300  
ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360  
GCTTCAGCAA GTACCAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG 420

ACAAG

1396

425

## (2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 572 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAGT	60
AGACAACTC TTCATACTCC AACACTTGCC CATTATATGC GAATCTCATC TATTTTTTCT	120
TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTTG	180
AGCAAGTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT	240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTTCG	300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT	360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT	420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC KAGTKTGCTC	480
TTTGATTTWC ATTGAGTATC AGATTTAGGA AATTAAGTTC CTCGKCTCCA AAAAAKAGCT	540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

## (2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT	60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT	120
CAACAAGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT	180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGGCTCA GCCTCAGCAT	240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT	300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA	360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT	420



1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480  
GCGCCTCAGC TTCAGCAAGC ACCGG 505

## (2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC 60  
AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120  
AACTTTAAC TTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180  
GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA 240  
ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG 300  
ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360  
AGTGTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420  
GGATAGAACT GACGAAGTCG GTACCGA 447

## (2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 572 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGTAATAT TTTATTGAAT AAGATAGGCC 60  
TTGATATTAA GCACTTTGGG ACGTCTCCC TTAGTGCTTT TTTGATTCT CTTAGTATCC 120  
AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA 180  
CCAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA 240  
AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCA 300  
AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360  
CCACCAAGTA TAGTGATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420

1398  
AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT 480  
TCTATAATCT CTTTATAAGA TTTGCCCCATC AGACAAAATA GAACGATTG AAGGCGTTTA 540  
TGATATTTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

**DENMARK**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

**SWEDEN**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

**UNITED KINGDOM**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

**NETHERLANDS**

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

**SINGAPORE**

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

**NORWAY**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

**AUSTRALIA**

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

**FINLAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

**ICELAND**

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

**What Is Claimed Is:**

25           1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.

30           2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

35           3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

40           4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:  
45           a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;

          b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

50           c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.  
55

60 7. A method for identifying an expression modulating fragment of  
*Streptococcus pneumoniae* genome comprising the step of comparing a database  
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a  
representative fragment thereof, or a nucleotide sequence at least 95% identical to  
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a  
nucleic acid molecule comprised of a complementary nucleotide sequence to said  
65 target sequence, wherein said target sequence comprises sequences known to  
regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*  
*pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of  
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a  
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*  
*pneumoniae* genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a  
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,  
wherein said fragment modulates the expression of an operably linked open reading  
frame, wherein said fragment consists of the nucleotide sequence from about 10 to  
200 bases in length which is 5' to any one of the open reading frames depicted in  
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*  
*pneumoniae* genome of claim 8.

12. An organism which has been altered to contain any one of the  
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the  
fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

- a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;
- b) identifying members of said library which contain sequences that hybridize to said target sequence; and
- c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

- a) isolating mRNA, DNA, or cDNA produced from an organism;
- b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;
- c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.



19. An antibody which selectively binds to any one of the polypeptides of claim 17.

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20. A method for producing a polypeptide in a host cell comprising the steps of:

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a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1

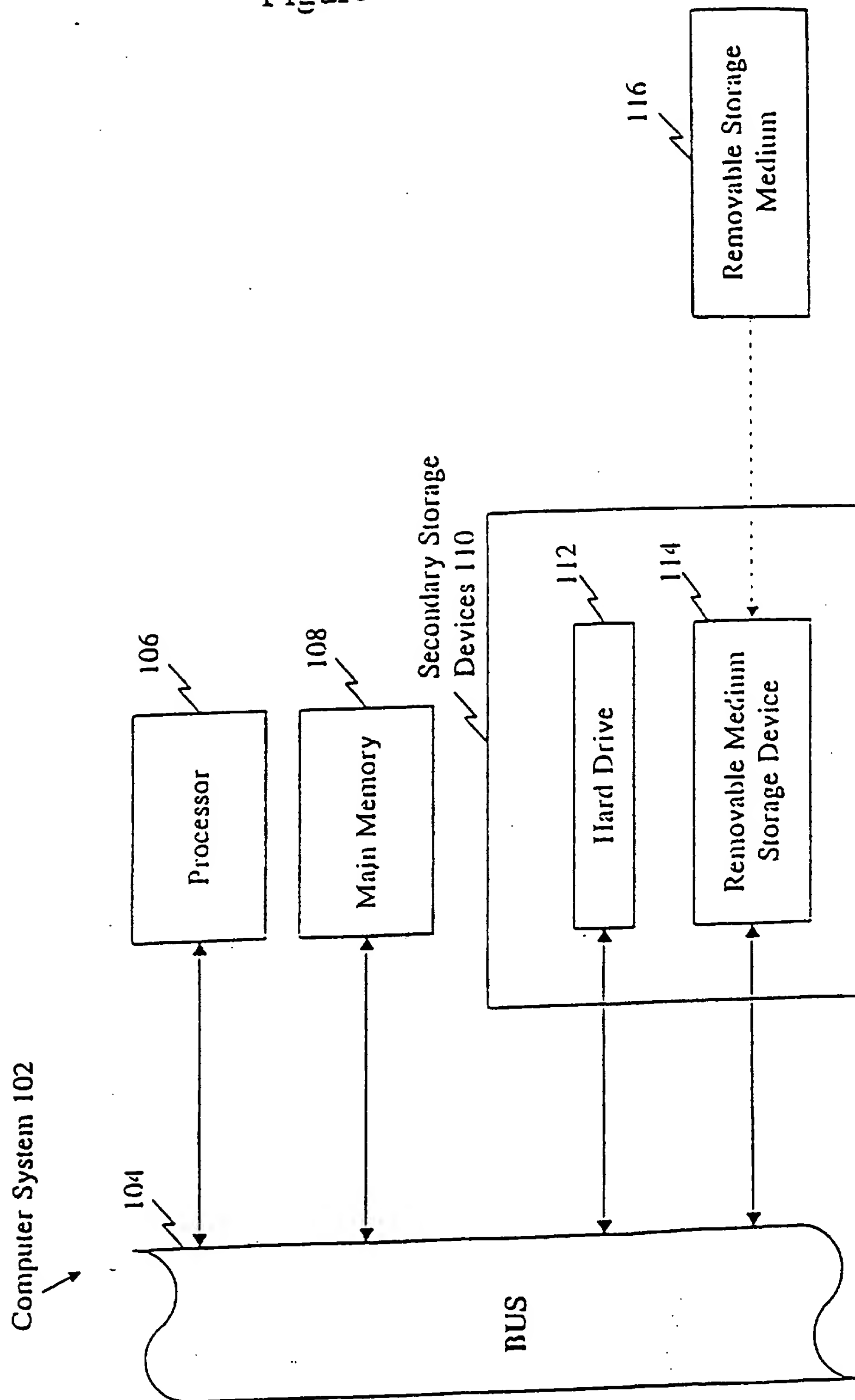


Figure 2

